	CAAAGTCGGT	TTAGTAACAT	GTATGTATGT	AAATAATGTA	ACTGGACAAA	TACAGCCTAT	420
	TCCACAAATG	GCTAAAGTTA	TAAAAAATTA	TCCTAAGGCA	CATTTTCATG	TAGATGCGGT	480
5	TCAAGCATTC	GGCAAAATTT	CAATGGATCT	CAATAACATA	GATAGTATTA	GTTTAAGTGG	540
	ACACAAGTTT	AATGGTTTAA	AAGGACAAGG	CGTCTTACTT	GTAAATCACA	TTCAAAATGT	600
	TGAACCAACT	GTCCATGGTG	GTGGTCAAGA	ATATGGTGTT	AGAAGTGGAA	CAGTTAATTT	660
10	GCCAAATGAT	ATTGCAATGG	TTAAAGCGAT	GAAGATAGCT	AATGAAAACT	TTGAAGCATT	720
	GAATGCATTT	GTTACTGAGT	TAAATAATGA	CGTCCGTCAA	TTTTTAAATA	AATATCATGG	780
15	AGTTTATATT	AATTCTTCAA	CTTCAGGTTC	ACCATTCGTT	TTAAATATTA	GTTTTCCTGG	840
	CGTAAAAGGT	GAAGTATTAG	TTAATGCTTT	TTCAAAATAT	GACATTATGA	TATCTACGAC	900
	AAGTGCTTGT	TCATCTAAAC	GTAATAAATT	AAATGAAGTA	TTGGCTGCAA	TGGGATTATC	960
20	AGACAAATCT	ATTGAAGGTA	GTATAAGATT	ATCATTTGGG	GCTACTACAA	CTAAAGAAGA	1020
	TATAGCGAGG	TTTAAAGAAA	TATTTATCAT	CATTTATGAG	GĄAATTAAGG	AGTTGCTAAA	1080
	ATAATGAAGT	ATGATCACTT	GCTTGTTAGA	TACGGGGAGT	TAACATTAAA	GGGTTCAAAT	1140
25	AGAAAGAAAT	TTGTAAATCA	ATTAAGAAAT	AATGTAAATA	AGTCATTAAA	AGGACTTGAT	1200
	GGGTTTGTCG	TTAAAGGCaA	ACGAGATCGT	ATGTATATTG	AACTTGAAGA	CCATGCaGAT	1260
30	ATAAATGAAA	TAACATATCG	ATTATCAAAA	ATTTTCGGTA	TTAAATCTAT	TAGTCCAGTA	1320
30	TTAAAAGTAG	AAAAAACAAT	AGAGGCAATA	AGTGCAGCGG	CAATTAAATT	gCGCAGaATT	1380
	TGAAGaAAAC	AGCACATTTA	AAATTGATGT	GAAGCGTGCC	CGATTAAAAT	TTCCCCAATG	1440
35	GATACGGTAT	GGAATTACAG	CGTGGAATTG	GGGTGGTGCC	AGTATTGGAG	CACTTCGCCA	1500
	TATTTCCAGT	GGATGTCCAA	CGTCCCAGnC	CCAGGAATT			1539

(2) INFORMATION FOR SEQ ID NO: 563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 968 base pairs
- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

ATAnCGTATA	CATGTGTTCT	TTAAAATTGT	GATAAGGAGT	TTAGGATGGT	TTATTTAAAA	60
TCAATAGATG	CCATTGGATT	TAAGTCTTTT	GCAGATCAAA	CCAATGTTCA	ATTCGATAAA	120
ССТСТА В СТС	CAATTGTTTGG	TCCAAATGCA	ACCCCTAAAA	GTAATATTAC	AGATGCTATT	180

	ATCTTCTCAG GTGCAGACA TCGCAGAGCT CAGAGTTATG CTGAGGTACA GTTAGGATTA	300
	GATAATCATT CTAAAAAGCT CAGTGTTGAT GAAAACGAAG TTATTGTAAC AAGAAGATTG	360
5	TATCGAAGTG GTGAAAGTGA GTACTACATA AATAATGACC GTGCAAGATT AAAAGATATT	420
	GCCGATTTAT TTTTAGATTC TGGATTGGGA AAAGAAGCGT ATAGCATTAT CTCGCAAGGT	480
	AGAGTTGATG AAATACTAAA TGCTAAACCA ATTGATAGAC GTCAAATTAT TGAAGAATCG	540
10	GCTGGTGTAC TTAAATATAA AAAACGTAAG GCTGAATCAT TAAATAAACT TGACCAAACA	600
	GAAGATAATT TAACGAGAGT AGAAGACATT TTATATGATT TGGAAGGTCG CGTAGAACCT	660
15	CTAAAAGAGG AGGCAGCTAT AGCTAAAGAA TATAAGACAC TTTCACATCA AATGAAACAT	720
	AGTGACATTG TAGTTACAGT SCACGATATT GATCAATATA CAAATGACAA TAGACAATTA	780
	GATCAACGTT TAAATGATTT ACAAGGCCAA CAAGCAAATA AAGAAGCTGA CAAGCAACGT	840
20 -	TTAAGCCAAC AAATTCAACA ATATAAAGGT AAACGTCATC AACTTGATAA TGATGTTGAA	900
	TCGCTTAATT ATCAATTAGT AAAAGCTACG GAAGCCTTTG AAAAATATAC GGGACAATTA	960
	AATGTTTT	968
25	(2) INFORMATION FOR SEQ ID NO: 564:	
3 0	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 436 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:	
	TTGTGTGTAT GCATTCAATG TGCTCTGTTT GTAAATGGCT AGCTATATAA TTTAGGATTC	60
	GAGGATCGTC ATCGACAACA AGACATTGCA CCATAGCTAT AAACTCCCTT ATCTTTTTCA	120
40	TTTATTATAC ATGTAAAATA TTTTTGCGTA AAAAAACAAT TGTTCATATT GAGTTCATAT	180
	TTCAACCTTA TACTGACGCT AAAGAAGAAA TAGGGAGAAG TGAATCGATA TGAAATTAGC	240
	GATAAAAGAG ATTATGTTTT ACAAATTTCG TTATATTTTA ATCACATTAA TCATTCTTTT	300
45	ATTAAGTATT ATGGTGTTAT TTATTAGTGG TTTAGCTCAn GGGCTTGGTA GGGAGAATAT	360
	TTCGTWATTT GAACACTTTG GATAATGATG aaTATGtTGT TCaAAAAATG AAAGAGCCGC	420
	aAATTGAGAA ATCGCA	436
50	(2) INFORMATION FOR SEC. ID NO. 545	

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2554 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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	(xi) SE	QUENCE DES	CRIPTION: S	EQ ID NO:	565:		
	ATGTTTTGTC A	ATATCAATT	GTTTGAGATA	AATCCGCTTG	TATAAAACGA	ACTTTATCAT	60
10	CATTAAATTT G	CTAGTTAAT	TCATTTATAT	CAGTACGATA	ATATTGCACA	TAAACTTCAA	120
	ATCCATCAGT T	AATAATTGT	TTGACTATCT	CAGAACCAAT	TGAACCAGAA	CCACCTAATA	180
	CTAATGCTTT C	ATTACTTTT	TAATCTCCAA	ACGACTATCG	ACTTGCTGAT	CTAAATTTAA	240
15	ATATAACGAT G	ACGTTTCGT	TAATACTATC	TAACGTGATA	TTTTCAACAA	TGTCTAACAT	300
	GTCAAACACG C	TAACACCTT	CAAAATACAA	TTTAGTATAT	TGATTAGCAA	TATATTCAGG	360
	TGAGTTTAAA C	TTGATATGA	ATTCACCTAT	AAATTGCTTT	TTCAAAAGTT	CAAATGCTTC	420
20	TGCATCTTGG A	AALTGCCTT	TTTTATCACG	CAACTCATCT	AATAATAATT	TTTTAATTTT	480
	ATCTGGTTCT T	CAGTAGCAC	TTGTCACGAT	TGAAAAACTA	TACGTCGGCT	CTAGTACAAA	540.
25	TTGATAACCA A	ATGTATCAT	CGATAAGTCC	TTCGTTTAAT	AAATTCTGAT	AAAAATCTGT	600
	TTCTTCCCCA A	AAATTAACT	CAAAGAATAA	TGACATTTCT	AAATCACGTT	GTACATATTT	660
	TTGAGGCGCT T	CTTGTAATG	GTTTATTTTT	AAAACCAAGC	ATTAGTCTTG	GTGATTGAAT	720
30	TTTCATAGAT T	CAGTAACAA	ATGCTTCTTT	AACATCCTCC	GGTTCATCAA	CAAGTCCTCG	780
	TTCGATTTTG G	GTTGGTTAA	CTTTATTACG	AGCATCCTCG	TGTTGTTTTA	CTATTCGACA	840
	TATTGCTTCA G	GATCCACAT	CGCCAACAAC	AAATAAAACC	ATATTTGATG	GATGATAAAA	900
35	CGTTTCATAA C	ATAGATACA	AATCATCTTT	TGTAATATCG	TATATACTTT	CTACACTACC	960
	GGCAATATCA A	CACGTATTG	GATGTTGTTG	ATACATTGCA	CGCAALGTAT	Taaacattaa	1020
10	TTTATATCCA G	GTTGCTCTT	Gatacatttt	TATTTCTTCT	GCAATAATAC	CTTTTTCTTT	1080
40	ATCAACAGTT T	CTTTTGTAA	AATAAGGCGT	TTCaACCATT	GTAAGTAAAC	GTTTAATGTT	1140
	GTTTTCAATA T	LATCAGTTG	CACTGAACAA	GTAGCTTGTA	CGATCAAAGC	TTGtAAACGC	1200
45	ATTTGCTTGT G	CGTTATCTT	CAGCAAACGC	AGTAAATAAG	CTTCTTCTTC	TTTTTCAAAT	1260
	AATTTATGTT C	CTAAAAAGT	GAGCAACTCC	ATCAGGTACA	GTAACAAATT	GGTCTTGTCC	1320
	AAGGGGTTTG A	ATTGATTAT	CTAATGAACC	AAATTGTGTA	GTGTAAGTGA	CAAATGTCTT	1380
50	TTGAAAACCT G	GTTKGGGGA	TAATAAATAA	TCGTAAACC	TTTTCTAATL	CTTGTTCGAA	1440
	tACTCTTTCG T	CTATTAATT	CATAATAACG	CTCTTTCATT	ATTTATCCCC	TCCTTTTGTC	1500
	AACACATAGA I	TEGTATCTAA	AAATGCTTTT	TCAGCAACAG	AAACAATATC	TTCGCGACTT	1560

	TIAIGCATAA	TCTCTATAAT	ACTTTTCGGA	CGATCTTCAG	ATTCATATCG	ATGAGAAATG	1680
	ATTACTTTTT	TAGCTAACTC	TAATTTTTCT	TCAGTGAAAT	CTCCTGCTTT	TATTTTTCA	1740
5	AATTCACTTA	TAATAGTGTC	TTTTGCAGTT	TCGTACTTAT	CACTTGAAAC	CCCACTCAAA	1800
	ACAAATAAAT	AGCCATTTTT	GCCATCAATT	TGTGAATGTA	TAGAGTACGC	TAAACTTTGC	1860
10	TTTTCTCGCA	CTTCATTAAA	TAAAACAGAT	GAAGGATCTC	CTCCAAACAT	CATGTTAAAT	1920
	ACAACAAAGG	CAGCATATCC	ACTTTGTCCA	TATTGTGTTG	GAAAACGGTA	TCCCATATTT	1980
	AATTTAGCTT	GATCCACGTC	ATCATATTCA	ACAATATAAT	CAACTTCTTC	ATCGTGTAAA	2040
15	TGATGAGTAG	AATGTTGGAA	TTGATGTTTA	TCGAATGGTT	TAAGTGCAAA	TTTTTCACGT	2100
	ATTTGTTTCT	CAACACTTTC	AGGTTCTACA	TTGCCGACAA	CATAAACAGA	ACATTGATCA	2160
	TTATTAATCA	TTGATTGATA	TGTATGATAT	AGTGTTTCAG	CAGTAATATG	TGGGATTTGT	2220
20	TCTAGTTGTC	CTGTAGATAA	GTATTTATAT	GCTTCATTTT	CAAACATATG	GTCGAGTAAT	2280
	TTTAAAAACG	AATATTGTGC	TTTATTATCT	ACCATTGCTT	CTATTTTTT	GGCTAATAAT	2340
25	GTTTTCTCTT	GGTTAACAAA	ATTATCATTG	AATGCTTTAT	TTTCAATTAA	TGGATTCCAA	2400
	ATGATTTCTT	GtAATAAATC	TAATCCTTGa	TTAAATAATG	AwTCACCGkT	TCYTAAATAA	2460
	CGkkCaTTAA	CAATTYCTAA	tGaAAATGtA	ATGACaTGCT	Gatctttgaa	TTTTGAAATT	2520
30	GTACTATTCA	CATACGCACC	ATATAAATCG	GCTA			2554

(2) INFORMATION FOR SEQ ID NO: 566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

THTCGCTATT TTHAATTGGT TTTGTATGGT TTAAGTTATA TCAATATACA ACAHACCCTA 60

AAGCTGATAT CCCAGGTATC ATTTTTAGTA CGATTGGTTT TGGTGCTTTG TTATATGGTT 120

TCTCAGAAGC TGGCAACAAA GGTTGGGGTT CAGTAGAGAT AGAAACAATG TTTGCGATTG 180

GTATTATCTT TATTATTCTA TTCGTTATTA GAGAATTAAG AATGAAATCA CCAATGTTGA 240

ATTTAGAAGT ATTGAAATTC CCCAACATTTA CATTAACAAC AATTATTAAT ATGGTTGTAA 300

TGTTAAGTTT ATATGGTGGT ATGATTTAT TACCGGATTTA TTTACAAAAT TTACGCGGAT 360

TCTCAGCATT AGATTCCGGA TTGTTATTAT TACCTGGTTC TCTAATTATG GGTCTACTAG 420

	TTGCTGTAAT	GACTTATGCA	ACATGGGAAT	TAACTAAATT	AAATATGGAT	ACACCATATA	540
	TGACAATCAT	GGGTATCTAT	GTACTTCGTT	CATTTGGTAT	GGCATTTATA	ATGATGCCAA	600
5	TGGTAACTGC	AGCTATTAAT	GCGTTACCGG	GACGACTTGC	CTCTCATGGT	AATGCTTTCT	660
	TAAATACGAT	GCGTCAATTA	GCAGGCTCTA	TAGGTACAGC	AATCTTAGTT	ACTGTAATGA	720
10	CAACACAAAC	TACACAACAC	TTATCAGCTT	TTGGGGAAGA	GTTAGATAAA	ACGAATCCTG	780
70	TTGTACAAGA	TCATATGCGT	GAATTAGCAT	CACAATATGG	CGGACAAGAA	GGCGCAATGA	840
	AAGTGTTACT	ACAATTTGTA	AATAAACTAG	CAACGGTTGA	AGGTATTAAT	GATGCATTTA	900
15	TAGTTGCAAC	GATATTTAGC	ATCATCGCCT	TAATTTTATG	TTTATTTTTA	CAAAGTAATA	960
	AAAAAGCAAA	AGCTACAGCT	CAAAAGTTAG	ATGCAGATAA	TAGTATCAAT	CATGAATAAA	1020
	TAAAATAAAT	TAATTGAAGT	GTGACTAATC	AAAAATTATG	TTGTGGGGAC	ATGATTTTTA	1080
20	AAGTATCGGT	GCCAAATATG	GTTATCGATA	CTTTTTTTAT	TTGTTGATTT	ATAGAATGTT	1140
	AGAGGAATTA	TATTAAAATT	TGGCATTGAC	GTAGTAGGTC	ATTAATAAAG	AAAAAGCAGG	1200
05	AAGTGGGTCA	ACGAAATGAA	TTTTGTGAAA	ATAACATTTC	TGTCCCAATC	CCTACTATAT	1260
25	AACATTATTT	TAAACGAGGC	ATGCGATTAC	GGAAGAATAA	GCTTATAACA	AGTAAACCGA	1320
	TGCTACAGCC	AAGTAAAATG	ATGCCGTTAT	GAATAGCGTC	ACTTGCTGTA	ATCACTTGAT	1380
30	CTGGTGGTAC	ATTTAAATAA	TATTTTTTGA	AAACATCTGC	AATT		1424
	(2) INFORM	ATION FOR S	EO ID NO: 5	67:			

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

TCTCCCATGT TCTGCTAAAT GACGCATCAC TTTTACTTCA TGAGGCGTCA ATACACGTCC 60 TTCACCAGCA TTCAAACCGA CAACATTTAA AGGCCCATAT TCAATACGAG ACAGTTTCGT 120 CACTTGATGA CCAAAATGTT CGAACATTCT TCTGACTTGG CGATTACGAC CTTCTGTAAT 180 TGTAATTTCA ACCAATGTTG TGTTTTTATC TTTATCTTGT TTCTTAACTT TCACTTCAGC 240 300 CGGTTGCGTC ATACCATCTT CTAATTCAAT ACCTTTTTCT AGCGCTTTCA CTTCTTCTCT CATTAAATAA CCTTTTAATT TCGCAACATA TTTTTTCTTA ATTTGATATC TTGGATGTGT 360 CATTAAATTA GTAAATTCAC CATCATTTGT GAGTAATAAC AATCCAGAAG TATCATAGTC 420

	ACGTCCTCTA TCATCAGATA CACTTGTKAT CACTTGAGTT GGKTTATGGA AKAAAATGKA	540
	AALTTTGTCT TCTAGTTCTA TTTTAATACC TTCAACTTCA ATCGTATCTG ATGGCTTCAC	600
5	TTTTGTTCCT AATTCAGTGA CAGTCGTACC ATTCACTTTC ACTTTTCCTT CAGAAATTAA	660
	AGTTTCTGCC TTACGT	676
10	(2) INFORMATION FOR SEQ ID NO: 568:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 454 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:	
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20	GAAACGGTTC TACCAAAAAA CAGTAAGGGC TAAACCCAAT CATGGTAAGA CAAAAAGTAC	60
	AAATAGCCAT GCCCAAGTTG AACTCGCTGT ACGCCTATTT CTTTCTAAAA AGATAATAAT	120
25	AAAAGCCAAT ACTAAATTAA TGATGAATCC AATGGCTAAA ATAATAGTAA ATAACGTTCC	180
	TAAATCGTTT GAAAATGTAA ATCGCATAGT CTTTTCTCCT ATAAAGAAAG GCACAAAAAA	240
	ACATTTTGCA CCTTTCACGT CATATTATTT ATTCACAGAT AAAGTTAAAA TTGCATTGAA	300
30	TTCTTCTTCA TTATTTGGGA ATGTTCTTTC TTCTATTTCT TTAATAGTAA TATTTACTAA	360
	TTTTAAATTT GTAGCTTCTT CAGAACTTAA AAAAGCATTA ATGTTTTTTT CTAATAACTC	420
	KARAGTCTCA GCTGLAAAAG TTTTAAGTTT AATT	454
35	(2) INFORMATION FOR SEQ ID NO: 569:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 894 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:	
	ACGATATTAC CACCCTCTGA AATAACATCA ATCATGTGAT CTGTAAAGTC CCAAGGATGA	60
	CTTGTTGTGA AACGAACTCT TGGAATCGCT ATTTTAGAAA TTGCTTGTAA AAGATCTCCT	120
50	AAGTCATATT CTATATCCTG TAAATCTTTA CCATAAGAAT TTACATTTTG ACCTAAAAGC	180
	GTTATTTCTT TGTAACCTTC ACGAGCAAGT TCACGTACTT CATCTATAAT GTCTTCAGGT	240
	CTACGGCTTC GTTCTTTACC TCTTGTAAAT GGAACAATAC AATATGTACA AAACTTATCA	300
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	TCAATAACGT CTCCTTCTTT AGACCATACT TCAACAACCA TTGCTTTAGA TAAGTATGCT	420
	TCTTCTAAAA TTTCTGGTAA ATGATGAATA TTATGTGTAC CAAATATCAT ATCTACATTT	480
5	TGATACGATT TTAAAATTTT ATTCACTACT GACTCTTCTT GTGACATACA ACCACAAACA	540
	CCGATTAAAA TATCAGGTCG TTCTTTTTC AAATrCTTCA AATTACCTAT TTCACTAAAC	600
10	ACTITGTTCT CGGCATTTTC TCTAATCGCA CATGTATTAA TTAAAATAAC ATCTGCAGTG	660
	TTAATATCAG TCGTkGCTTG aTAGCCTAAT GCYTCMAGTA TACCAGCAAT GACCTCAGTG	720
	TCATGTGCAT TCATTTGACA TCCATATGTT TTAATTAAAA ATGTACGCTC GTTCCCCATA	780
15	CCGCGATATT TTYCATCAAT TEGGGAAATC NCTATTATAA CGAACTTCTK GTETACCNCC	840
	TTTTTTnCGC TCCTTTAAAA TTAAGGCGGC TGATAAACAG GTCCAAAATA TTAC	894
	(2) INFORMATION FOR SEQ ID NO: 570:	
20 25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 441 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:	
30	TATCAATCCC ACAGCACATG CTGAACAAGA TCAAACATGG GAGAAGATTA AAGAACGCGG	60
	TGAACTTAGA GTGGGTCTTT CTGCAGATTA TGCACCAATG GAATTTGAGC ATACAGTTAA	120
	TGGTAAGACT GAGTATGCAG GTGTAGATAT TGATTTAGCT AAAAAAATTG CGAAAGATAA	180
35	TAATTTAAAA TTAAAAATCG TCAATATGTC ATTTGATAGT TTGTTAGGAG CTCTTAAAAC	240
	TGGAAAAATT GATATTATTA TTTCCGGAAT GACTTCAACG CCTGAACGTA AGAAGCAAGT	300
40	TGATTTTTCA GATTCATATA TGATGACTAA AAATATCATG CTTGTAAAGA AAGATAAAGT	360
40	TAATGAATAT AAAGATATCm AAGACTTTAA TAATAAAANA GTNGGGGCAC AAAGGGACTG	420
	AACCAGAAAA AATCGCTCAA C	441
45	(2) INFORMATION FOR SEQ ID NO: 571:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1205 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:	

	AAGTCGTTCA	TCTTTTTCTA	CAAGGGTGTA	AAAATAATCA	ATCATATCGT	ATAACGCTTC	120
	TTTACCAATG	ATGTCATATG	GTGTTGTTGT	CATTTAATCA	CCCATTTTCA	AAAATTTACT	180
5	GTTACGAACT	TAAGTTAATA	TATAACTAAT	ATAACATGAT	TTTAAACATT	TGAAAGAAAT	240
	ATGCATATTT	GCCAATTTAA	TTTATATTGT	TTGAAAGTGT	TICTTTTTC	TTGAAAAAAC	300
10	GTTGAACTTT	ATTTAAAGGT	tGATGATGTT	CGAGGTTTAG	TTCGTTtAAT	AAAGATtGGA	360
	ACTITITGTAA	ACCTTGATTA	TAGTCTTTAA	CTTCGAACTC	TAACTCATAA	TCCGTAGTAT	420
	CGAAATACTC	ACTITIATET	AAAACCAGTA	AATCACCTTT	ATATTTAGTT	TCTTGGCGAT	480
15	ATGTCGTTAA	TGCACCAAGT	ATTGATAAAG	TTGTATCTTT	TACACCAAAC	TGTTCAACTA	540
	TAATTTGACG	AATGTCATCT	GGAAGATTGT	CGTTTGAAAT	AATCAAGTTC	ATCTCTGGTT	600
	TAATGTCGAC	GATATAGTTG	TATTCTAATA	GACCAACCTT	TGCTGGTGTC	TTTAAAGTCA	660
20	TTTCATATTG	ATTGTCTTTA	ACTCTTATGC	GTAGTGCAGA	GCGATGTTCC	TTTAATTTGA .	720
	AATCGGGTGT	ATCAATATAG	TAATTGACTT	GCTTAMAAAG	CACACTGTCT	TTAAAAATT	780
25	TCTCTTGCAA	TTTATTATAG	ATTGALGCAG	TTATCATTTG	TETAAATTCT	ATTTCATGAT	840
-5	TTGTTGCCAT	GATATGTATA	CACCTCGTAT	CAAATTCAAT	TTATCTTAAC	TATATTATGA	900
	ATGACAAAGT	TGAATTTTAA	AAGTAATTTC	CTTTATCTAT	TATCAATGTT	AATTTGACCA	960
30	TTAAAAATAG	TGTTCGTAAG	TGTTTTGTAT	TATTGAATTG	TGTTAAAATG	TTATGGAATA	1020
-	AGAGGAGGAT	TAAGCATGsG	TTTWTATATT	AATGAAATTA	AAATTAAAGA	TGACATACTT	1080
	TATTGTTATA	CAGAAGATTC	TATTAAAGGA	TTATCTGAAG	TAGGACAAAT	GCTCGTTGAT	1140
35	AGTGATAATT	ATGCCTTTGC	GTATACATTA	GATGATGGTA	AAGCGTATGC	TTATCTCATT	1200
	TTCGT						120

(2) INFORMATION FOR SEQ ID NO: 572:

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(i) SEQUENCE CHARACTERISTICS:

- _ (A) LENGTH: 570 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

TGAAGAATA GCAATGATGA AATGCCGTAT GTTATATGAG ACGGGGTCAT TTCTTGAATT 60

AAGAGAAGAA ACAATTGTCT TATTGAAAAC TGGCATACAA CAATATGATG CATTGATGAT 120

TTATTACGTG AAAAGTTTGA TTGGTTTGGG ACAATATTTT GAAGCGGTAG AAGTAATTCA 180

ATTTGCTAAG TCAAAATTAA TTGAAGATGA AAAACGATTG ACTCAGTCAT TAGCTGATTT	300
TGTTACGTTA TCAATGAGGG AACAGACGCA CTTGATTTTG AAGTTAATAG ACAATGGTCA	360
TTTTCAATTT CAAGAAACGG TATTATATAT ATKAAAAYCT AATACGTACA GTtATAACCT	420
CATTAGTTTA ATGATTGAGT ATTTAAGGTT CGCAAATTGT ACACAAGAAC TGACAATTGA	480
AAAGTATGGT ATGGATGTAA CTTTTGTACC AGCTAATTTA AAAGGGCTAG AACATACAAC	540
ACTTAAAGAA AAAGTTATAC CTAACGTTAT	570
(2) INFORMATION FOR SEQ ID NO: 573:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 939 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:	
GTTGAATGGT TAGCAGCTGC AGTTGTATTA TATTTCTGTG GTGTAATTGT TGACGCTCAT	60
GTATCATTCA TGTCCTTTAT TGCAATATTT ATCATTGCTG CATTATCAGG TTTAGTCAGC	120
TTTATTCCTG GTGGTTTCGG CGCTTTCGAT TTAGTTGTAT TACTAGGATT TAAAACTTTA	180
GGTGTCCCTG AGGAAAAGT ATTATTAATG CTACTTCTAT ATCGTTTTGC GTACTATTTT	240
GTACCGGTAA TTATTGCATT AATTTTATCA TCATTTGAAT TTGGTACATC AGCTAAGAAG	300
TACATTGAGG GATCTAAATA CTTTATTCCT GCTAAAGATG TTACGTCATT TTTAATGTCT	360
TATCAAAAGG ATATTATTGC TAAAATTCCA TCATTATCAT TAGCAATTTT AGTATTCTTT	420
ACAAGTATGA TCTTTTTTGT AAATAACTTA ACGATTGTKT ACGATGCTTT LATATGATGG	480
AAATCACTTA ACGTATTATA TTCTATEGGC AATTCATACT AGTGCTTGTT TATTACTTTT	540
ACTGAATGTA GTTGGTATTT ATAAGCAAAG TAGACGTGCC ATTATCTTTG CTATGATTTC	600
AATTTTATTA ATCACAGTGG CGACATTCTT CACTTACGCT TCATATATTT TAATAACATG	660
GTTAGCTATT ATTTTTGTTC TGCTTATTGT AGCTTTCCGT AGAGCGAATA GGTTGAAACG	720
CCCAGTAAGA ATGAGAAATA TAGTTGCAAT GCTTTTATTC AGTTTATTTA TTTTATATGT	780
TAACCATATA TITATTGCTG GAACGTTATA TGCATTAGAT ATTTATACGA TTGAAATGCA	840
TACATCTGTA TTGCGCTATT ACTTCTGGCT TACGATTTTA ATCATCGCTA TCATCATAGG	900
TATGATTGCA TGGTTGTTTG ATTATCAATT TAGCAAAGT	93:

(2) INFORMATION FOR SEQ ID NO: 574:

5	(A) LENGTH: 1059 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:	
10	GAATTAATTA AATATTACAC ACAGCCTCAT TTTTCATTTT CAAATAAATG GCTATATCAA	60
	TATGATAATG GAAACATTTA TGTTGAACTT ANGAGATATT CATGGTCAGC ACATATATCT	120
	TTATGGGGCG CTGAAAGTYG GGGAAATATT AATCAGTTAA AAGATCGTTA CGTAGATGTG	180
15	TTTGGACTAA AAGACAAAGA TACTGATCAG TTATGGTGGT CTTATAGAGA GACATTTACA	240
	GGTGGCGTTA CACCAGCCGC AAAACCTTCT GATAAAACTT ATAATCTTTT TGTGCAATAC	300
20	AAAGATAAAC TACAAACGAT TATTGGTGCG CATAAAATAT ACCAAGGCAA TAAACCAGTA	360
20	TTAACATTGA AAGAAATCGA TTTCCGTGCA CGAGAAGCGT TAATAAAAAA TAAAATATTA	420
	TATAACGAAA ATCGTAATAA AGGTAAGCTT AAGATCACCG GTGGCGGTAA TAACTACACT	480
25	ATTGATTTAA GCAAAAGATT ACATTCAGAT CTAGCAAATG TTTATGTTAA AAATCCTAAT	540
	AAAATAACTG TTGACGTCCT CTTTGATTAG TATATGAAGG TGACTTATAC TTCATGCACT	600
	TTAATTCCAA ATCAGATTAT TTAAATGATA ATTTTTAAAG TGTATGATGT ATATAATAGG	660
30	TAAAATTTC TATATATTA AATGGAATTG GGAGTAGGAA TGTGACAGAA ATAGTATTTT	720
	ATAAAATTTA TTCtTGTCAC TCCCCAACTT GCACATTATT GTAAGCTGAC TTTCCGCCAG	780
	CTTCTATGTT GGGGCCCCGC CAACTTGCAT TGTCTGTAGA aTTTCTTTTT GAAATTCTCT	840
35	ATGTTGGGGC CCCGCCTATA ATTGAAAAAT GCTTGTTACA TGGGCATTTT CATTCGGTCA	900
	ACTACTACCA ATATAATATT GEAGAGCCTA AGACATTGAT TTATTATGTC TTAGGCTCTA	960
	TTCCTTCATT TAATGATTAA nTTATTATAG CAATACTTTA TTGTCCCATG ATTAGTGTTC	1020
40	TTTTAATGAG ACATAGTAAC TATAAAGTTT AATAATCGT	1059
	(2) INFORMATION FOR SEQ ID NO: 575:	
	(i) SEQUENCE CHARACTERISTICS:	
45	(A) LENGTH: 574 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:	
	GTTTGCTTTA GGTCCTGTTT CATATTTATA CTTCGAAGGA TTTACCTTTT TGAAGTCTGG	60
CC		

	TTCAACTKGC TTTTTATTCT TTTCGAAATC AGCTGGTTGA GTAGTTATGA GTTCATTATT	180
	TTTATTAGMA TAAATCTTAC CATTAACATA TTTATAATCT TTTGTTATAA AGTCACCATT	240
5	TCTGAATGGA ACTACTTGAT TATGACCTTT AGAGAATAAA TCAGTACCGA ACATTAAATA	300
	GTTCTTCGTA TCTATACCAG CCAAATGTAA AATTGTTGGC ATTACATCGA CTTGACCAGC	360
10	ATATTCATTA TTGATACCAC CAGATTTACC AGGGATTTTA ATCCAGAAAC CAGTTCTGTT	420
10	TAAATCTGTA AATTTAGCCG GTGTGATTTT TTCACCTAAT AGTTTTTCCA TGGCATTGTT	480
	ATGGTTTTCA GAGATACCAT AGTGGTCACC ATAAATCATA ATCACTGAAT TGTCATATAA	540
15	TCCTTTTTC TTCAAGTCAT TAATATATTC TTCT	574
	(2) INFORMATION FOR SEQ ID NO: 576:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 796 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	-
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:	
	CAATGTTTTA TAGTACAATA TATTTTTAAT AATACTCGTT AAGGAGAATG ATATGATATC	60
30	AATTCACGCA ATTTCGACAG GAAAAATCCA AGATTTGCCT TATAGCTCGA AAAGACCGAT	120
	GCGCTCTGCT TTAGATAAAA CTAAGATTTC ACAAACAACA TGGTTATCTT CAACTGGTTT	180
	CACTGGTGAT GAACAGGCTT ATAAAGATCA TGGTGGACCA CATAAAGCAG TTTGTGGGTT	240
35	TAGTAAGCAT AATTATGCAC TGTATCAAGA TGATTTACCT ACACTACCTA CTCATGCGAT	300
	GTTTGGAGAG AATTTAACAT TTGATTATTT AGACGAATCT GATGTTTACT TTGGTAATCA	360
40	ATATCGTTTA GGTGAAGCGT TAATTGAGGT TTCTGAAATT AGAGAACCAT ACTGGAAAAT	420
40	TCAAGCAAAA TATAATATTC CTGATTTAGT GAAGCGCATG TCTACATCTG GTAAAACAGG	480
	TTTCTATTTC CGGGTATTAA AACAAGGCTA TGTATCTCCA AATGATCAGC TTTACTTAAT	540
45 ·	ACAAGAAGCA CCAATCGAAC ATCGTTTATC TGTACAACAG CTTAATGACC TTTATTATAA	600
	TGATAGACAA AATCAAGATA TGTTACGATA TGCACTAAAC AATCCATTTC TGTCACCAAC	660
	AAGACGCGAT AAACTTCAAA AAATGTATAA CAGAACATTG GAAATAATTA CCTTTCATTn	720
50	ATAAGTGTTA AATGAACTTT TCAAAACAnA AAGGAATCAA CTTCACACAT CGTTTGTATG	780
	AATAGTCTTA TCTATA	796
	(2) INFORMATION FOR SEQ ID NO: 577:	

(A)	LENGTH: 1095 base pairs
	TYPE: nucleic acid
	STRANDEDNESS: double
	TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

10	AGAAATTATG	ACAAAATATA	AAGATGGAAA	GTTAGTTTAT	GCATCAGTCG	AACCAGGATC	60
	TTACGTAATA	CATAAAGATG	ATGCAATTAA	ATATGACGAT	TATTCTAAGT	TAAAAAAATT	120
	AAGTCAGCTA	ACTAAACTTG	ATCATCCAAA	ACCAGTTCCA	TATAGCGTaC	TCAAATCAAA	180
15	TCTTTCGGAG	TACCTTTAAC	AAGCGTTTCA	TTTATGACAC	ATGGATCAAA	GGATACTAAA	240
	GATGAAGTGT	TGCCGGCATT	GGCCTATTTC	ACTTTTTCAC	CAAAAAATTA	TGAAGACAAG	300
	TCTAATCCAG	ATCCAAAAGT	TTTAAATTTA	GTACATATGG	ATTTCTTAAA	TGCATCTAGT	360
20	GATTTTGGTA	ACGCACATTT	TGTTGTTTTA	AGTAAATATA	TTAAAGAGTA	TGAATCAAAC	420
	TATGAAACAG	CGTCAGATGA	TTCTTTAAAA	TAGTATTTAC	TGTGTGAAAA	ATAAATAGTG	480
25	TACTACATTA	AATAATCGCA	ATAATAATCC	CGATAAACAA	TCAGCATTAC	TGCTTATCAC	540
	ATAGAGTTCG	TAATAACTAT	AACTCTATGA	TTCGCAAATA	ATAAATGATT	GTCATCGGGA	600
	TTTATTTTTA	TCAATTTATA	AAGTGACATT	ACCTTGTTCA	TCAGCAGGTT	TGAAAACAGT	660
30	AATCACTGCA	CTAATAATTG	CTAAAATGTG	TGGGATACCT	GTCCAACAGA	ATATTAAGTG	720
	TAGAATACCT	TGCATATTCT	TGCCGGCATA	AAATTTATGA	ATACCAAAAC	TACCTAAGAA	780
	CAATGCTAAT	AAAATATAAA	TAACTTTGTT	TACTTGCATT	TCTTTCCCTC	CAGTTGAATT	840
35	GCTTATAATG	ACATTAGCTT	CTCTTTTTAT	TATACCCACT	TTTAGTTCAA	ACATTCTAGT	900
	TTAAGCATTC	CCAATCATCT	AAATTTCAGT	TATTCAATCC	TTACAATAAA	TTTAGGATTA	960
	CATTTCAGTT	GCATTGTATT	ATTTTACGTG	TGAAATATAC	GTAATGAATC	ACATGACAAy	1020
40	CTYCAAATTG	AAAAATATAC	ATTCTATGAT	GTAAGGTCGC	ATTTTTAATA	TATTTACGTn	1080
	AAAATAGTTT	GGATG					1095

(2) INFORMATION FOR SEQ ID NO: 578:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

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ACTGCCAAAA	TAATCATAGC	CATGTTCTAC	AGCTGCTTTC	GCTACAATAT	CCAAACGCAT	120
TTCAAAACAA	GCGGTACAAC	GTAAGCCGCC	TTCTTTTTCA	TCAGCTAATT	CTTTATCCTT	180
CACCATTTTC	ACAAACTTAT	GTGGTTCATA	AGGTGCTTCA	ATATACTTCA	CATTCGCACC	240
AGTCTTGCGA	TTAAAATCTT	CCACAAATTG	TTCTTGCACT	TTAGCACGTC	GTAAGTACTC	300
ATTTTTCGGA	TGAATATTTG	AATTCGCGAA	ATAAATTGCA	ATGTCTGCAT	ATTGTGTTAA	360
AAACTCTAAT	GTATATGTAC	TACAAGGTGC	ACAACAACTA	TGCAATAAGa	TTTTAGGTCT	420
GATTGCTTCT	CTTTCCCACT	GSCCGATTAA	TnTCTTCAAC	ACCTTGTCCA	TAATTAATTT	480
GTnGATTTn						489

(2) INFORMATION FOR SEQ ID NO: 579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

CGTACTGCAT	CATTTGTTGA	AAAATTTGCA	AACTTCTTCA	AGATGTTATG	GCTTAGACTT	60
AAAGCGATGA	AGCACTACAA	AGCCTTAAAT	AAAGAATCTA	AGAAGCAAGA	ATTTGAAAAT	120
TCATTCAAAG	ATGTTCAAAA	AATTATGCGT	ATTGTGAATC	ACAATATTAT	TTTACGCTTA	180
AAAGAAGAAC	AAAATAGTAC	AAATGTACTT	GAGGTTAGCT	TAGTCATTAA	TCATTACTAT	240
GATATGAGTC	GCTCATTAAA	GTGGCGTGCA	CAACGTCGAA	AAGAACGTCA	AGAAAACAGC	300
AATCAAATCA	TACCGCAAGC	TATGTTCCAT	AACCACAAAT	TGGAAGCATT	GTACTTACAA	360
CGTCATCTTT	TAGATGAATT	AATTCGCAAA	AATAAAATCA	ACAATATCGT	TGCAGCTCAA	. 420
ATTCGAGAAA	ATATCAATTa	CAACGAAATT	GTCTTGTCTT	TACAGTCCAA	ACATTAAGCA	480
AGaCwTaCaw	TmCCCCCGTA	CATATGAGAC	AAAGTCATTA	TCATCTCATA	TGTACGGGGT	540
TTTTATATTC	AACATCAAAA	AATCAGATTG	ATGAAAAGTA	AATAACCTTT	CATCAATCCG	600
ATTTGATTAT	AGAATCTATT	TTTTAAGTTT	AAATGGAATT	GTACATACGT	TAACATTCTT	660
TTGATAAATT	AAATACAATT	TCATACGCAA	ACTAGTTTGA	TTGTGTAATA	AATTATGCCA	720
ACGTTTCTTA	GTAATAAATT	CTGGTATCAC	TACTGTAATC	ATATAGTTTT	GATCGTTGGC	780
TTTACGATTA	ATCTTATCGA	TAAAACGTGA	AATTGGTCGT	ATAATACTGC	GATATTCCGA	840
ATGTAAAATA	ACTAATCTTA	CATCTGGGAA	ATGACGTTTC	CATTTCTCTT	GGAATGCTTT	900

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TGCGTAATAA	ATAGACTTAT	CAACTGCTGT	TGTAATACTT	GTTATCGGCA	CAATTGCTAA	102		
ATTACGATCT	ACCACGTCCA	CATTAAGAAC	ATCAATGTCA	GAACGTAATT	GTTCTGCGAT	108		
ATCTCGATAA	TGKTTGKTAA	TTTTCAAGAA	GAAAATCACC	ACGAACGGCA	AGAAAATAAG	114		
TATCGGCCAT	ACTTGGCTAA	ATTTAGTTAT	GAGTAAAATC	CATAANAACA	ATAAATGTCA	120		
CGATACCACC	AAGTAAGTTC	ACAGACAACT	TACTTAACCA	ATTCTTAGGA	CGTTCATGAA	126		
TCCATTTAAT	AACCATACCG	AATTGTG				128		
(2) INFORMATION FOR SEQ ID NO: 580:								

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

A GTTGGGAATG GCTTATTCCC TATCCCAAAC	TTGGGAATG	GGGTGTCCTA	CTATATCCAT	GCCTCCTTTC
C TAAATCGCCT nTCTATACnT CCATnCATTT 12	AAATCGCCT	CACTGTATAC	TCAAGACTAT	ATCTGTCAAT
T ATTTTAAATA TCATTATCAA TCCAGAAGTA 1	TTTTAAATA	TTGTTTAATT	TTGGAACAAT	CATTTTCCAG
TA TITAACTACA CATGGGTAGT CGGTGGTTTG 2	TTAACTACA	TAATCAATCA	ACTITTACAA	TTTACTATTC
TA TTGTTATTGC CAAAATTAGG TGCAACATTA 3	TGTTATTGC	TGGCAATTTA	GCTTTTTAAC	CTTGGGGTTA
T ATTATGGGTG TCATTATTGA TACATTTGGA 3	TTATGGGTG	GGGTCAAATT	CAACAGTTGC	ACTGTAATTG
AT TTAATTAAAG CAATTGGAGT ATTGTTACTC 4	TAATTAAAG	TGATTTTAAT	CTACAATTCA	TTATTTGGCG
T AACAAGAATA ATTTATTACT AACTGATCAA 4	ACAAGAATA	GAATCAATTT	TCGTCATAAT	ATTGTCGGCA
SA TTTATTTTTG GTTTCTTTCC ACCTATTCAA 5	TTATTTTTG	TCTATTAGGA	TGTTTTGGCT	AAGTATTTAC
AT ACTCATTCAC CAGCCTTTGC ATCATTAGTA 6	CTCATTCAC	AGCTAGTCAT	ATAGTGCTTT	ACGACAATTA
rg attitaaccg ctattittaa tcgttcttta 6	TTTTAACCG	AGCGCTATTG	TTGGGTCAAT	TCATTTACAA
ST AAATTAAAGC CTATCTATTT TACTGGCGGT 7	AATTAAAGC	AAAATTCGGT	CAAGTCATTT	AAACTAAAAA
AC ATTATCTTAA TGCCTCATAT GGGTGCAGCA 7	TTATCTTAA	AACAGCTAAC	TGGCTTTTGT	ATACTTGGCA
AG ATTCTAATGG GCATATTGAT AGATCACTTT 8	TTCTAATGG	GTTTGGCCAG	TTATTGGGAT	TTAACAACAC
NG ACATCCAGAA AAACTATTGG TCTATTATGT 9	CATCCAGAA	AATAGCAATG	GTTCACCTAA	GGATTATTTG
TA TTTTAAATTA ACTTTTAGCT TATCATTTTA 9	TTTAAATTA	TTTAAGATTA	GCATTATACT	ATTTTGACAG
T ATTTTTTGT GGTCTAAAAA TCTTTAGAAA 10	TTTTTTTGT	GTGATAAGCT	ATTITTAAAA	ACTTGTAATT

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	CAACTCATTC TTAAGACCTA AATTAATGTT ATNTTTTAAT AATTTACACC AAATTAATAG	1140
	CAAAAATTAT GTTATTCGTG CTAATATTTC ATAGTTGGTT ATTCAATTAA TTAAAAATAA	1200
5	GTCAAAATGC ACAACTTTTT ATn	1223
	(2) INFORMATION FOR SEQ ID NO: 581:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 454 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:	
	CACCTTTTTA TCATGCTTAG TTATCAATAA ATCTATATTT TGCTGTTTTA CAATTTTTTT	60
20	AACTTTATCA ATCTCATTAT CTTGGACTAA ATAAATATAT GATCTTGCAT CTGTTGCTAG	120
	AGCTTGTTCG TGTTTTTCTG ATAAAACATA TGTGATGGAA GCGTGAATAA TAATGCCTAA	180
	TGTAACAAAA CTGATAATTA ATATACTGCT TATCAATAAC ATTAAGCGGT GGTGAAACTT	240
<i>25</i>	CATCATTGTT CTTTAGGTCT TTCCAATTTA TAGCCTAAGC CACGCACAGT TTTAATAAGT	3 0 0
	TGTGGCTTCT TAGGATTATC TTCTAATTTA TCTCTTAAAT GACTGATATG TACATCAACA	360
	ATTCTTGAGT CTCCTGCAAA TTCATAATTC CATACCGTAT TTAACATATG CTCTCTCGTA	420
30	ATGACTCTGC CTTGTCTTTC TATCAAATAA AGCA	454
	(2) INFORMATION FOR SEQ ID NO: 582:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 452 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:	
	TITATAAGAT TITATTTACA AATAATTGGT TITCATATGT ATAAACACTT TIGACTTTCA	60
45	AATCTTAACG ATAATTCTAT TACAATACAA TCCCCTATTA GAATGATITA TGTAATAAAA	120
	AAAGCGGAGT TTCCCCCAGC TTTTCTAAAC GACTACATAA AATATAAGAT TGCAATTAAA	180
50	TGCAATAGTG ATGCTATTAC AATAAAAATA TGCCAAATCA TATGAAAATA TGGTCTATTC	240
50	TTTTGTGCAT AAAACCATGC ACCAATTGTA TAAGACACAC CACCTAAGAA AATGAATAAT	300
	ATGAATATCC ATGATGTGCG AATAAAAATA ATTGGTAACA AGATAATACC TACCCAGCCC	360
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	AAAATCCCCC AAAGTGTCGT TCCCCATAAT AA	452
	(2) INFORMATION FOR SEQ ID NO: 583:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1472 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(b) Torobogi: Timedi	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:	
	CGCTTTTTGC AATAAGTCAT TAGCCGCTTT TAAGCCTTCT TCTTTTCGAT CTACAACAAG	60
15	TAAAATAAAT GGCTTTAACG CTTCTTCTTT TTCACTTTCA AGCATATCTG GTTTTTGAAC	120
	CATTICAAAT GGAGATITCA ATCCATTATT ATCGCTCATT TCAATAATTG CATCATACTG	180
20	TGCTTGTGAC ATACTTGCAA TAGCCTGTTT TGCATTTTCT TGAAGGAAAT ATAAGTTTTT	240
	CAATTTAGGA TGCTTATTTA ATGTACTTAA TGTAATCGGT GTAATGTCTT TCTCATAAGA	300
	CACTTCAATC ACTGTACTAT TTGTTCTACC AGGAATTGGT GGTTTTTCAT GAATATGCTT	360
25	TGATACTICT CCAATICCAA CGACAGATIG ATTITTCGTT CGATTATAAA AAATAATATT	420
	GTCGCCTTCT TCTAACTGAG TATAAAAATG ATAACCATTA CGTTTAATAC CGTTGTACGT	480
	GTGCGTATAA ATCGTATATT GGTTTCCAGG TTCAAATTCT TCAGTTTCAG CTAAAAAGAA	540
30	ATAACGCGGT ATCTTAATTT CGCCTTTACC AAGACCACTT ATTAAATCAA ACTCTTCTGC	600
	AGTGATTTGA TTGAACAATG TCTCTTTCAT ATNACTTATA CGAAATTCCA AAGCTTCACT	660
	ACGCTTTAAA TAATCTGCTG TTAATGGTTT CAATTGTTCA TTAAAACGAA ACTGTACACG	720
35	TATTTTATTT TGTGCACCTG TTTCAACACT AATAATTTCA CCACATCCAA GTAGTCCAGT	780
	ATCCGTCTGA ACTTGATAAA AGATGACTTG ATCTCCTACT TTAGCCTTTT TAAACGCTCT	840
40	AAATCCTTGA GATGGGTTAA AATGTGCGCC TGATTCAAAT AAAGCTGTTT GTCCTACTAA	900
40	CGGTTCATTA TGATTCCAAC GGTTATATCC ACAATTCAAC CAAAAATAAT TCGTTTCTGC	960
45	TGTCATCTTA ATACTCCTTA ACCTGAATAA ATTTTAGAAA CACTATGAAT TACATTCTTT	1020
	LAGTGTTTCT TATGCAGTTG GACGCGTATG CGAACAACTG TATACCCTTT GTTCACTGCG	1080
	ATTTTAATCG CATTTCCTAT AACATTGTAG CGCCCAGGAC ATTAATTTAC GTCCCAGACC	1140
50	CTTATCGTTT TCACTTCTAA GTAAGTCGAA CTATTTTGCT TTACAACAAG TGCGACTCTA	1200
	AATACAGTTG GACACACATA CGAGCAACTG TATACCTTTT AATCAGTTTT CTATATTTTA	
	TTTATTATAT CTCTCTTAAT GATAAAATT GTTACAAACA GTTTAACATA TTTAGCTACC	1320

	AIGHIACONC INICCIOCO INICCIONA OCCUMINA INCACATITA INCACATITA	1110
	TACTGCCGTT AGAATTTTAT CATGTCTHAA TT	1472
5	(2) INFORMATION FOR SEQ ID NO: 584:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 787 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:	
	GGTAGTGAAT GGGGTTCAAG ACAACAGTAT TGGAAGTACG AATGAATCAC AGTTTTTAGG	60
	AAATTATATT GTAATTAAGC ACGCAGAAAA TGAGTATAGC TTAATAGCTC ATTTACACCA	120
20	ATATTCAATC ATTGTGAATG AGGGGCAAAA TGTTAAATAT GGTGATATCA TTGGGAAGGT	180
	TGGGAATTCT GGCAATTCTA CTGAACCTCA TATACATTTT CAAGTAATGA ATGATAAGAA	240
	TATTGAAGCA TGTACATCTT TAAAAATTCG ATTTATAAAT AATCGAGAAC TTATCAAAGG	300
25	GGATGTGGTC TGCGGATTAC AAGCTGAATG ATGGCGATAC TTATAAAATC TCGACACTAT	360
	AAAAATGGTA TAGTGTCGAG ATTTTCTTGC TTATTTAGTT AATTCAAAGT GCACGCCGGA	420
20	TTCATTAGAA GTCGACGTAT TTTTGTTTGT AATAGAGTAA CCGGTCATTG AAATTTTAGA	480
30	TTCAATATCT GAAGCGGAAT TTGTAGATTC AGGATTATAG AAGCTACATT CATAAGTGTT	540
	ATCATCTTTC TTTTTAAGTA TAAACATACC TTTGGCTTTA ACTTCGACTT TAGTGTTGTT	600
35	AATGTCAAAA GTTTGAGTGC TATTACTATA ATTAACACCA GCCCAAACCG ATTCATTATC	660
•	TTTCACAACG GGGAAGTCAT CTTCTTGCTT AACGACGTNA CTTCATCTTT CTCTGTCTTA	720
	AAGACATCTT TAGATAAGCC TGGATACAAC ACATATCCAT ATTTATTGTC AGAATTAGAA	780
40	TGCTTTT	787
	(2) INFORMATION FOR SEQ ID NO: 585:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 830 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585:	
	ATGCTAAATT AGGGGGAATA TTTACGATAA AGAGACCAGA AAAATAATAA AACACATGCT	60
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	INAMATGAAG ACTATITITT ATTACAAGAA AATGTATCTA GTAAACTTAA AGTAGCAAGA	180
5	CCTAATAAAT TTAATGCATG TTGTGCACCT TTTTTACCTT GGCCAGCTTC GAAATGTTTG	240
3	TAAGCAGCTA CACTTAAAAT GCCTATCGTT GATAGTGATG CAAGGCGAGA AATGTTTTTA	300
	TTGATAAAGC TAGCTGAGTA TAAAGCAGCA GTAGTTGCTT CTGCAATGCC GACGTATTTT	360
10	ACAAGTTCTT TTTGCAAGCC AAAAGTATGT TCAAACAGTT CAATCATACC CTTATCTTCT	420
	TGCAATTTAG GTTTACTGGC TTGGTATAGC TCTTTCGCAA GTTTTAAATT CGTTGCGTAA	480
	CGCAAAATCA TATTTAATTC CTCCCAATAT TTGATTTTTT GTGAAAGATG ATTACTTTAT	54,0
15	CATTTTTACC CGTTTCTATA AAAATGAATC AATTATGTAA CGTATGTGTA GTTTAGGAAT	600
	GTTTGCTATG GAAATATAAT TCTGTTCACT CAAAATGTAT GAAATTAATG TGTAGTTTTG	660
	TCGAGTTGCT CTTTTAATTT GGTTAGATTG TTTTTTAGAG AAGCGGTACT ATTTTTAAGT	720
20	GCATCAACAG ATTTACCTTC GTTTTGAGAC ATTGAGTTTA TTACAGCACG AAGTTCTGTT	780
	TCTAGTATGT CAGCGTCGCL TTAGCATTAG AACTTAATAL TTALACTCTT	830
25	(2) INFORMATION FOR SEQ ID NO: 586:	~
30	(A) LENGTH: 412 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586:	
35	TTAGGACGTT TTTACAATCA GTACAATGAG CTCATTGTTA TTAGTCCTTT AACGGCGTCT	60
	TITAATGCTG GCGCTACATT TGGGCGATTT CATCATTTAA TTGATACTGA AACTTTAGCA	120
	AAATTAGAAC ATGAAAAAGG ACATTATTAT CAGAAGATGA TATGTGATGA CAATGTAGAA	180
40	ATGATTTCTA TAAATAACAT ACCGAAATAT CCGAGAAATC ATAATGTATT AACTAATCAT	240
	GACTCATACG AATATTCATT GAATTTAGGA AGTAGTAATA GTTATTCAAA GTATGAGCTT	300
45	ACCTTAGATG ATATTTATGT TGGTGCTACC TTTLAACAAA TTATATTTAT ATTCTAGCCM	360
	ACTAAATAAA AGGGKaCtaT TTGAATCAAA CMATATGTAT TAACCTTTTT TA	412
	(2) INFORMATION FOR SEQ ID NO: 587:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 4709 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587:

	TTCAGTTTGA	AATTAATCAT	ATAAATTTCT	TATGGGAGGG	TTGATATCTT	AATGATTAAC	60
5	ATTATTTCAG	CTATAGGATC	TATTGGAACA	TTTATTATGG	CTTTATTTTA	TTTTGTATCA	120
	GTTTCAGTTC	AACTTTATCA	AATGAAAATT	AGCTTTCTGC	CAGCTTTAGG	TTTTAACCAA	180
10	ATTTTATTAG	AAAGGGAGGA	GGATCAACTT	AATATAATGA	ATTCGGCAAC	AGAAGAGCAT	240
10	CATCATAAAG	ATTATATTAA	ACTATATAAT	TTAGGTGGCG	GTGCTGCTAA	raaaattgca	300
	ATAGAGGTTT	TATTGGGGAA	GGATArAGTC	ATTCAGAAAA	AATACGTGCA	TATTKTACCT	360
15	AGTAAAGAAG	GGTACATGTT	ACCAATTAAT	AAAAATGTGT	ACGAAGAATT	AGAAAGAACG	420
	ATTGASAACA	ATGGTCATGA	AGCTGATTTG	AATGTACGTA	TGACTTATTA	TCATAATGTA	480
	AGTCGCAAAC	AACAGGAAGT	TATATTAAAA	GGTCAAATCG	ACCGTTTTAA	TACTTATAAT	540
20	aataaagaaa	TTTATGATTT	GCAGTTTATC	TAAAAATTGA	TTTAAGAGGG	TAGTTGTTTA	600
	TTGCGAAAAA	TATCATTCAA	TTTTAATGAA	ATAATGGCGT	CATTACTATA	AAATATTACT	660
	TTATGTTGTA	ATGCATTTTT	CTATAAGATA	GAACTAAAAG	GAGGGGCAAA	GATGCAAATT	720
25	AGACAAATAC	ATCAACATGA	CTTTGCTCAA	GTGGACCAGT	TAATTAGAAC	GGCATTTGAA	780
	AATAGTGAAC	ATGGTTATGG	TAATGAATCA	GAGCTAGTAG	ACCAAATTCG	TCTAAGTGAT	840
30	ACGTATGACA	ATACCTTAGA	ATTAGTAGCT	GTTCTTCAAA	ATGAAGTTGT	AGGGCACGGT	900
30	TTACTAAGTG	AAGTTTATCT	TGATAACGAG	GCACAACGGG	AAATTGGATT	AGTGTTAGCA	960
	CCTGTATCTG	TTGATATTCA	TCATCAAAAT	AAAGGTATTG	GGAAGCGATT	GATTCAAGCA	1020
35	TTAGAACGAG	AAGCAATATT	AAAAGGATAT	AATTTTATCA	GTGTATTAGG	ATGGCCGACG	1080
	TATTATGCCA	ATCTAGGATA	TCAACGCGCA	AGTATGTACG	ACATTTATCC	ACCATATGAT	1140
	GGTATACCAG	ACGAAGCGTT	TTTAATTAAA	GAATTAAAAG	TGAACAGTTT	AGCGGGAAAA	1200
40	ACAGGTACCA	TAAATTACAC	ATCTGCTTTT	GAAAAAATAT	GATTTCAAGC	TAGGATTACA	1260
	TTAGGTAGAG	TTCATATTAA	TAATAAAAA	TGTTTGCAAT	CAAATCGTAC	GTTGTCGTTT	1320
	GTAATTCTTA	AAATAGCAAT	AAATAAAATG	TTTGTTAGTA	AAGTATTATT	GTGGATAATA	1380
45	AAATATCGAT	ACAAATTAAT	TGCTATAATG	CAATTTTAGT	GTATAATTCC	ATTGACAGAG	1440
	ATTAAATATA	TCTTTAAAGG	GTATATAGTT	AATATAAAAT	GACTTTTTAA	AAAGAGGGAA	1500
50	TAAAATGAAT	ATGAAGAAAA	AAGAAAAACA	CGCAATTCGG	AAAAAATCGA	TTGGCGTGGC	1560
35	TTCAGTGCTT	GTAGGTACGT	TAATCGGTTT	TGGACTACTC	AGCAGTAAAG	AAGCAGATGC	1620
	AAGTGAAAAT	AGTGTTACGC	AATCTGATAG	CGCAAGTAAC	GAAAGCAAAA	GTAATGATTC	1680

	GICAAACACI	AATAATGGCG	AAACGAGIGT	GGCGCAAAAT	CCAGCACAAC	AGGAAACGAC	1800
_	ACAATCATCA	TCAACAAATG	CAACTACGGA	AGAAACGCCG	GTAACTGGTG	AAGCTACTAC	1860
5	TACGACAACG	AATCAAGCTA	ATACACCGGC	AACAACTCAA	TCAAGCAATA	CAAATGCGGA	1920
	GGAATTAGTG	AATCAAACAA	GTAATGAAAC	GACTTCTAAT	GATACTAATA	CAGTATCATC	1980
10	TGTAAATTCA	CCTCAAAATT	CTACAAATGC	GGAAAATGTT	TCAACAACGC	AAGATACTTC	2040
	AACTGAAGCA	ACACCTTCAA	ACAATGAATC	AGCTCCACAG	AGTACAGATG	CAAGTAATAA	2100
	AGATGTAGTT	AATCAAGCGG	TTAATACAAG	TGCGCCTAGA	ATGAGAGCAT	TTAGTTTAGC	2160
15	GGCAGTAGCT	GCAGATGCAC	CGGTAGCTGG	CACAGATATT	ACGAATCAGT	TGACGAATGT	2220
	GACAGTTGGT	ATTGACTCTG	GTACGACTGT	GTATCCGCAC	CAAGCAGGTT	ATGTCAAACT	2280
	GAATTATGGT	TTTTCAGTGC	CTAATTCTGC	TGTTAAAGGT	GACACATTCA	AAATAACTGT	2340
20	ACCTAAAGAA	TTAAACTTAA	ATGGTGTAAC	TTCAACTGCT	AAAGTGCCAC	CAATTATGGC	2400
	TGGAGATCAA	GTATTGGCAA	ATGGTGTAAT	CGATAGTGAT	GGTAATGTTA	TTTATACATT	2460
25	TACAGACTAT	GTAAATACTA	AAGATGATGT	AAAAGCAACT	TTGACCATGC	CCGCTTATAT	2520
25	TGACCCTGAA	AATGTTAAAA	AGACAGGTAA	TGTGACATTG	GCTACTGGCA	TAGGTAGTAC	2580
	AACAGCAAAC	AAAACAGTAT	TAGTAGATTA	TGAAAAATAT	GGTAAGTTTT	ATAACTTATC	2640
30	TATTAAAGGT	ACAATTGACC	AAATCGATAA	AACAAATAAT	ACGTATCGTC	AGACAATTTA	2700
	TGTCAATCCA	AGTGGAGATA	ACGTTATTGC	GCCGGTTTTA	ACAGGTAATT	TAAAACCAAA	2760
	TACGGATAGT	AATGCATTAA	TAGATCAGCA	AAATACAAGT	ATTAAAGTAT	ATAAAGTAGA	2820
35	TAATGCAGCT	GATTTATCTG	AAAGTTACTT	TGTGAATCCA	GAAAACTTTG	AGGATGTCAC	2880
	TAATAGTGTG	AATATTACAT	TCCCAAATCC	AAATCAATAT	AAAGTAGAGT	TTAATACGCC	2940
	TGATGATCAA	ATTACAACAC	CGTATATAGT	AGTTGTTAAT	GGTCATATTG	ATCCGAATAG	3000
40	CAAAGGTGAT	TTAGCTTTAC	GTTCAACTTT	ATATGGGTAT	AACTCGAATA	TAATTTGGCG	3060
	CTCTATGTCA	TGGGACAACG	AAGTAGCATT	TAATAACGGA	TCAGGTTCTG	GTGACGGTAT	3120
45	CGATAAACCA	GTTGTTCCTG	AACAACCTGA	TGAGCCTGGT	GAAATTGAAC	CAATTCCAGA	3180
	GGATTCAGAT	TCTGACCCAG	GTTCAGATTC	TGGCAGCGAT	TCTAATTCAG	ATAGCGGTTC	3240
	AGATTCGGGT	AGTGATTCTA	CATCAGATAG	TGGTTCAGAT	TCAGCGAGTG	ATTCAGATTC	3300
50	AGCAAGTGAT	TCAGACTCAG	CGAGTGATTC	AGATTCAGCA	AGCGATTCCG	ACTCAGCGAG	3360
	CGATTCCGAC	TCAGACAATG	ACTCGGATTC	AGATAGCGAT	TCTGACTCAG	ACAGTGACTC	3420
	AGATTCCGAC	AGTGACTCAG	ATTCAGATAG	CGATTCTGAC	TCAGACAGTG	ACTCGGATTC	3480

1520

	CGATTCTGAC	TCCGACAGTG	ATTCCGACTC	AGACAGCGAT	TCAGATTCCG	ACAGTGATTC	3600
	CGACTCAGAT	AGCGATTCCG	ACTCAGATAG	CGACTCAGAT	TCAGACAGCG	ATTCAGATTC	3660
5	AGACAGCGAT	TCAGATTCAG	ATAGCGATTC	AGATTCCGAC	AGTGACTCAG	ATTCCGACAG	3720
	TGACTCGGAT	TCAGATAGCG	ATTCAGATTC	CGACAGTGAC	TCAGATTCCG	ACAGTGACTC	3780
	AGACTCAGAC	AGTGATTCGG	ATTCAGCGAG	TGATTCGGAT	TCAGATAGTG	ATTCCGACTC	3840
10	CGACAGTGAC	TCGGATTCAG	ATAGCGACTC	AGACTCGGAT	AGCGACTCGG	ATTCAGATAG	3900
	CGATTCGGAC	TCAGATAGCG	ATTCAGAATC	AGACAGCGAT	TCAGATTCAG	ACAGCGACTC	3960
15	AGACAGTGAC	TCAGATTCAG	ATAGTGACTC	GGATTCAGCG	AGTGATTCAG	ACTCAGGTAG	4020
	TGACTCCGAT	TCATCAAGTG	ATTCCGACTC	AGAAAGTGAT	TCAAATAGCG	ATTCCGAGTC	4080
	AGTTTCTAAC	AATAATGTAG	TTCCGCCTAA	TTCACCTAAA	AATGGTACTA	ATGCTTCTAA	4140
20	TAAAAATGAG	GCTAAAGATA	GTAAAGAACC	ATTACCAGAT	ACAGGTTCTG	AAGATGAAGC	4200
	AAATACGTCA	CTAATTTGGG	GATTATTAGC	ATCAATAGGT	TCATTACTAC	TTTTCAGAAG	4260
٠	AAAAAAAGAA	AATAAAGATA	AGAAATAAGT	AATAATGATA	TTAAATTAAT	CATATGATTC	4320
25	ATGAAgnAAc	rCCTTAAAAG	GTGGCTTTTT	TACTTGGATT	TTCCAAATAT	ATTGTTTGAA	4380
	TATAATTAAT	AATTAATTCA	TCAACAGTTA	ATTATTTAA	ÄAAGGTAGAT	GTTATATAAT	4440
22	TTGGCTTGGC	GAAAAAATAG	GGTGTAAGGT	AGGTTGTTAA	TTAGGGAAAA	TTAAGGAGAA	4500
30	AATACAGTTG	AAAAATAAAT	TGCTAGTTTT	ATCATTGGGA	GCATTATGTG	TATCACAAAT	4560
	TTGGGAAAGT	AATCGTGCGA	GTGCAGTGGT	TTCTGGGGAG	AAGAATCCAT	ATGTATCTAG	4620
35	TCGTTGAAAC	TGACTAATAA	TAAAAATAAA	TCTAGAACAG	TAGAAGAGTA	TAAGAAAAGA	4680
	TTGGATGATT	TCAATATGGT	CCnTTCCCA				4709

(2) INFORMATION FOR SEQ ID NO: 588:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1554 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

CTTTTTTAAL	TAwCgGaAtA	TTGtCaTgaT	tAcAcTTCGt	TAGGGTTTAC	gTCGtAATTT	60
CATTTaaTAA	`gCgCTTCAcC	ATTAAALGTG	gTAmCCTTTA	ATTCGCCAGT	AGAAACATCA	120
CAGTAACTAA	GCGCAATTTC	AGGTTGATTC	ATAACAAAAC	TTAAAATATA	GTTATTTTGT	180

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CGTCTAACCA	TACCTTTCGT	TTGTTTCGGA	TCTTCCATCT	GTTCACAAAT	AGCTACTTTA	300
TATCCATTAT	TAACAAGTGT	ATCTATATAA	CTATCTGCAG	AATGATACGG	AACACCACAC	360
ATCGGAATTG	GATTTTCTTT	TTTAGCATCT	CTTTTAGTTA	AAGTAATTTC	AAGTAYACGT	420
GATGCCTCCT	TGGCATCTTC	ATAAAACATT	TCATAGAAAT	CACCTAGTCT	TAATAAAAA	480
AAGCAATCTT	GGTATTCTGA	TTTTATTTTT	AAATATTGCT	GCATCATTGG	TGTAACATTA	540
GACATATTAT	TTCTTCACAA	CCCTTGTCTC	TTTTTTAAAAT	TTGTCTTTAC	AATATATTCG	600
TTTGTAAGyT	TTTTAATTAT	TAATTATTTA	ACTTATACAT	TTTAACATAC	TTACTTTTAC	660
AAACCTATTC	ATACCATATA	ATCACGAAGC	ATCTTAAATG	TATAAGAAAA	CGCCTCAAAC	720
СТААТААААТ	GTGTCAATAG	CATGTTTAGA	ATTAAATTAA	AATTCTAACA	TTCAAGACAT	780
TTAATTAAGT	AAGGCCGTTC	AATATTAAAA	TGAACAATGA	CTCTGTTTGA	AATCATATAT	840
CATAAAATTA	TTTTATAAAC	CTTTGAAGAA	TACCACGTTT	TTTTAGAGTA	ATTAATAAGA	900
AATAACTTAT	AATAGATCCG	ATAGCACTTG	aGACTATGaA	CGTAATCATT	AACGGTTTAA	960
TGAAGAAGTC	TTGAAGCCCA	AGGaAATATG	CTAATGGLAT	аСаААТТААА	cTTCCgATGA	1020
Caccagttcc	aAGTACTTCa	CCGACCGCGG	ССаталатат	ATGTTTACGA	TATnygTAAA	1080
ACATACTAGC	СААТААААСТ	CCAATCATAC	TACCCGGAAA	TGCAAAAGst	GTACCAGTAC	1140
CAAAAAGAAC	TCTTAAAATT	GATGATATAA	GCGCTTGAGC	TAATCCATAC	CAAGGACCTA	1200
CTATGACCGC	ACTTAATACA	TTTACAAAAT	GCTGTACTGG	TGCTGCCTTA	ACTGGTCCTA	1260
GAGGAATGAT	GATAATACTG	CTTAATACAA	CATTTATTGC	AATTAAAAGT	GCAGTTATAG	1320
CCAGTTTTCT	TGATTTCATA	TGATTGTTCT	CCTTTTTGTT	TGTAATTAAT	CACTATGCTT	1380
GGCTTTATTA	TGGTCATTTA	AACGTGTTTC	CATTGTTGAT	ACAAACATTT	TCAATAATTG	1440
ATTCGCTTCA	TATTGTGAAG	TTTGAAACTG	TTCAACTATG	GGCAATGTAT	TTATTTCTGC	
						1554
	TATCCATTAT ATCGGAATTG GATGCCTCCT AAGCAATCTT GACATATTAT TTTGTAAGYT AAACCTATTC CTAATAAAAT TTAATTAAGT CATAAAATTA TGAAGAAGTC CACCAGTTCC ACATACTAGC CAAAAAGAAC CTATGACCGC GAGGAATGAT CCAGTTTCT GGCTTTATTA ATTCGCTTCA	TATCCATTAT TAACAAGTGT ATCGGAATTG GATTTTCTTT GATGCCTCCT TGGCATCTTC AAGCAATCTT GGTATTCTGA GACATATTAT TTCTTCACAA TTTGTAAGYT TTTTAATTAT AAACCTATTC ATACCATATA CTAATAAAAT GTGTCAATAG TTAATTAAGT AAGGGCGTTC CATAAAATTA TTTTATAAAC AATAACTTAT AATAGATCCG TGAAGAAGTC TTGAAGCCCA CACCAGTTCC AAGTACTTCA ACATACTAGC CAATAAAACT CAAAAAAGAAC TCTTAAAATT CTATGACCGC ACTTAATACA GAGGAATGAT GATAATACTG CCAGTTTCT TGATTCATA ATTCGCTTCA TATTGTGAAG TTCTALACTC TGAATGGAAG	TATCCATTAT TAACAAGTGT ATCTATATAA ATCGGAATTG GATTTCTTT TTTAGCATCT GATGCCTCCT TGGCATCTTC ATAAAACATT AAGCAATCTT GGTATTCTGA TTTTATTTTTT GACATATTAT TTCTTCACAA CCCTTGTCTC TTTGTAAGYT TTTTAATTAT TAATTATTTA AAACCTATTC ATACCATATA ATCACGAAGC CTAATAAAAT GTGTCAATAG CATGTTTAGA TAATTAAGT AAGGGCGTTC AATATTAAAA CATAAAATTA TTTTATAAAC CTTTGAAGAA AATAACTTAT AATAGATCCG ATAGCACTTG TGAAGAAGTC TTGAAGCCCA AGGAAATATG CACAGTTCC AAGTACTTCA CCGACCGCGG ACATACAAAC TCTTAAAAAT GATGATATAA CTATGACCGC ACTTAATACA TTTACAAAAT CAAAAAGAAC TCTTAAAATT GATGATATAA CCAGTTTTCT TGATTTCATA TGATTGTTCT GGCTTTATTA TGGTCATTTA AACGTGTTTC ATTCGCTTCA TAATGGAAG TTTGAAACTG	TATCCATTAT TAACAAGTGT ATCTATATAA CTATCTGCAG ATCGGAATTG GATTTCTTT TTTAGCATCT CTTTTAGTTA GATGCCTCCT TGGCATCTTC ATAAAACATT TCATAGAAAT AAGCAATCTT GGTATTCTGA TTTTATTTTT AAATATTGCT GACATATTAT TTCTTCACAA CCCTTGTCTC TTTTTAAAAT TTTGTAAGYT TTTTAATTAT TAATTATTTA ACTTATACAT AAACCTATTC ATACCATATA ATCACGAAGC ATCTTAAATG CTAATAAAAT GTGTCAATAG CATGTTTAGA ATTAAATTAA	TATCCATTAT TAACAAGTGT ATCTATATAA CTATCTGCAG AATGATACGG ATCGGAATTG GATTTCTTT TTTAGCATCT CTTTTAGTTA AAGTAATTTC GATGCCTCCT TGGCATCTTC ATAAAACATT TCATAGAAAT CACCTAGTCT AAGCAATCTT GGTATTCTGA TTTTATTTTT AAATATTGCT GCATCATTGG GACATATTAT TTCTTCACAA CCCTTGTCTC TTTTTAAAAT TTGTCTTTAC TTTGTAAGGY TTTTAATTAT TAATTATTTA ACTTATACAT TTTAACATAC CTAATAAAAT GTGTCAATAG CATGTTAGA ATTAAAATTAA AATTCTAACA CTAATAAAAT GTGTCAATAG CATGTTAGAA TACCACGTTT TTTTAGAGTA AATAACTTAT AATAGATCCG ATAGCACTTG GGACATATGA CGTAATCATT TGAAGGAAGTC TTGAAGCCA AGGAAATATG CTAATGGAA CGTAATCATT TGAAGGAAGTC TTGAAGCCCA AGGAAATATG CTAATGGAA ACGAATTAAA CACCAGTTCC AAGTACTCA CCGACCGCGG CCATAAATAT ATGTTTACGA ACATACTAGC CAATAAAACT CCCAACCGCGG CCATAAATAT ATGTTTACGA CACAAAAGAAC TCTTAAAAAT GATGATATAA GCGCTTGAGC TAATCCATAC CTATGACCGC ACTTAAAACT CCAATCATAC TACCCGGAAA TGCAAAAGGSE CAAAAAGAAC TCTTAAAAATT GATGATATAA GCGCTTGAGC TAATCCATAC CTATGACCGC ACTTAATACA TTTACAAAAT GCTGTACTGG TGCTGCCTTA CAGGGAATGAT GATAATACA TTTACAAAAT GCTGTTACTG TGTAATAAAT CCAGTTTTCT TGATTCATA TGATTGTTCT CCTTTTTGTT TGTAAATTAAT CCAGTTTTCT TGATTCATA TAGATGTTCT CCTTTTTGTT TGTAAATTAAT ATTCGCTTCA TATTGTGAAG TTTGAAACTG TTCAACTATG GGCAATGTAT ATTCGCTTCA TATTGTGAAG TTTGAAACTG TTCAACTATG GGCAATGTAT	CGTCTAACCA TACCTTCGT TTGTTCGGA TCTTCCATCT GTTCACAAAT AGCTACTTTA TAACCATTAT TAACAAGTGT ATCTATATAA CTATCTGCAG AATGATACGG AACACCACCA ATCGGAATTG GATTTCTTT TTTAGCATCT CTTTTAGTTA AAGTAATTC AAGTAYACGT GATGCCTCCT TGGCATCTC ATAAAACATT TCATAGAAAT CACCTAGTCT AAAAAATAAT AAGCAATCTT GGTATTCTGA TTTTATTTTT AAATATTGCT GCATCATTGG TGTAACATTA GACATATTAT TTCTTCACAA CCCTTGTCTC TTTTTAAAAT TTGTCTTTAC AATATATCG GTATTAATTAT TAATTATAT TAATTATTTA ACTTATACAT TTTAACATAC TTACCTTTTAC AAACCTATC ATACCATATA ATCACGAAGC ATCTTAAATG TATAAGAAAA CGCCTCAAAC CTAATAAAAT GTGTCAATAG CATGTTTAGA ATTAAATTAA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 638 base pairs (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

TTTTGACGAA AAAAGTTGAT TTACAAATAT ATAAACGTTG TGATTTCAAT GTTTGTATAG 60

TATATACATG	ACAGCAACTT	GGGAAAAAAA	GGAAGGTAAC	GAAGGTTTAT	TAACTGTTAC	180
TGTTCCTGCA	GAAAAAGTAA	ACAAAGCTCT	GAGAGATCCC	CTCATAATTT	CCCCAAAGCG	240
TAACCATGTG	TGAATAAATT	TTGAGCTAGT	AGGGTTGCAG	CCACGAGTAA	GTCTTCCCTT	300
GTTATTGTGT	AGCCAGAATG	CCGCAAAACT	TCCATGCCTA	AGCGAACTGT	TGAGAGTACG	36
TTTCGATTTC	TGACTGTGTT	AGCCTGGAAG	TGCTTGTCCC	AACCTTGTTT	CTGAGCATGA	42
ACGSCCGCAA	GCCAACATGT	TAGTTGAAGC	ATCAGGGCGA	TTAGCAGCAT	GmTATCAAAA	48
CGCTCTGAGC	TGCTCGTTCG	GCTATGGCGT	AGGCCTAGTC	CGTAGGCAGG	ACTTTTCAAG	54
TCTCGGAAGG	YTTCTTCAAT	CTGCATTCGC	TTCGAATAGA	TATTAACAAG	TTGTTTGGGT	60
GTTcGAATTk	CAACArGTaA	GTtAGtTGCT	AGAnccca			63

(2) INFORMATION FOR SEQ ID NO: 590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

. 60	ATTTGTCATT	TGACTTTAGG	GGGGCTTTTT	GATGTCTGTA	CGTACATTTT	AAAATATTCC
120	TAACATTTGA	CACGTAAAAG	AATGAATCAG	ACGAACGAAA	ATAAAGGGAG	TTTTCAATTC
180	TACCGATAAA	CCAGCATATT	CTTAGCAGTA	GCACATATGA	TATAATTACG	TTTTACTAAT
240	TCAATACACA	ATATTTGATG	GGACATTTCA	TGGATAGTTT	GCTTTAGTAT	AAACTTAATA
300	TTGATTATCA	GATCGACTCA	TGTTGAAAAT	GTCAATTACT	ATGACGAAAG	AATTAAAGTG
360	TTAAAAATCA	AAATAGATGG	ATAGGAGGGA	TGAAGTTACT	GGAGATATTT	AATCGCTGAT
420	AAGCAGCTAA	GATGCTGAAG	AACGCCTTTA	aA GATATGTT	AATGAAATGC	TAACCCTAAA
480	CAGAACATTT	TCAATTAAAC	TCCTAAGTCT	TGAGAGAGAT	CGCTTAGATA	AACAAAATTA
540	AATTAACTGA	ATAGATGCTG	TCCATATTTT	AACAACATTC	TACTTATTAG	TCATTTAATG
600	CTTTTGATAA	AATCATACAC	CATTAATGAC	TACATLATGA	aGTTTCCaAA	ACTACGTGAC
660	AAAATTTAGA	CTCAATATCA	ACGTTACTTA	ATGAAAAATT	TTTACTAAAA	TATTAAATCA
720	TTTTCACAAG	GATGAATTAT	GTTGGCACCA	ACACATTTGT	CGTACACGCT	AGAAGTAAAT
780	CATTACCTGT	GTTGTTGATC	GTTACAAAAT	AAACAAGAGG	CCCATTGCTA	AGATGGATTA
840	TCAATGAGAA	ATCTGTGCAT	AGCGCTGGTT	CAAGATATAA	GAATTTTTAA	GTCAGAAGCT

	AACTAAAGTT ATTGAAGCGG CAACGTTAGA TTTACTAACG GCATTTTTAG ATGAACAGTA	960
_	TCAGAAACAA GAACAAGATT ATAGTCAAAA TTATGCATAT GTACGCAAAG TAGGACATAC	1020
5	CGTTTTCAAA TGGGTTGCTA TCGGTATGAC AACGTTAAGT GTTTTATTAA TTGCATTCTT	1080
	AGCCTTTTTA TATTTTTCAG TAATGAAGCA TAATGAGCGC ATTGAAAAAG GATACCAAGC	1140
10	ATTTGTAAAG GATGETATAC GCAAGTACTA AATACGTATG ATGATTTAGA TGGTAAAAAt	1200
	TGATAAAGAG GCACTTTACA TTTATGCCAA AAGTTATATC CA	1242
	(2) INFORMATION FOR SEQ ID NO: 591:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 744 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:	
05	TTCCAGATAG AGCCTTAGTT GCTGCCGCTG AATTGTCTGA TCGTTACATC ACTGATCGTT	6'0
25	TTTTTACCAG ATAAAGCGAT TGATTTAGTT GACCAAGCAT GTGCAACAAT TCGTACGGAA	120
	ATGGGATCAA ATCCAACTGA ATTGGATCAA GTTAATAGAC GTGTCATGCA ATTAGAAATT	180
30	GAAGAAAGCG CACTTAAAAA TGAATCTGAC AATGCGAGCA AACAGAGATT ACAAGAACTA	240
	CAAGAAGAGC TTGCCAATGA AAAAGAGAAA CAAGCAGCAC TTCAATCTCG TGTAGAATCA	300
	GAAAAAGAAA AAATAGCAAA TTTACAAGAA AAACGTGCGC AACTAGATGA AAGTAGACAA	360
35	GCGTTGGAAG ATGCACAAAC AAATAACAAT TTAGAAAAAG CTGCTGAACT ACAATATGGA	420
	ACAATTCCTC AATTGGAAAA AGAACTTAGA GAATTAGAGG ATAATTTCCA AGATGAGCAA	480
	GGTGAAGATA CAGATCGAAT GATTCGTGAA GTTGTAACAG ACGAAGAAAT TGGCGATATT	540
40	GTCAGCCAAT GGACAGGCAT ACCAGTTTCA AAATTAGTTG AAACAGAACG TGAAAAATTA	600
	CTTCACTTAA GTGACATCTT GCATAAACGT GTTGTAGGTC AAGATAAAGC GGTTGACCTG	660
45	GTTTCAGATG CAGTAGTTAG AGCAAGAGCA GGTATTAAAG TnCAAACAGA CCTATTGGTA	720
	GTTTCTnATT CCTAGGTCCn ACTG	744
	(2) INFORMATION FOR SEQ ID NO: 592:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1449 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

	TTGTTATAGT	GTCTGAATCT	GTGTAACTCT	TGCCCATGTG	TTCTGAGTAA	AGCACCCACT	60
5	GTTTATTTAC	TTTTCGTTGT	AGTCTAGCTT	CGTGTAGTAG	TTTGTTTAAC	TTTTGTGCTG	120
	ATATACCGTA	GTCTGCCGCG	ATTTGAGTTG	TGGCTAATGT	GCCAGTTGAT	TTTAAGATTT	180
10	CATCAACATA	ATCTGCTTTG	GGTTTTAGCT	CTCCAATTTC	TTGTTGTAAA	AGTAAGTTTT	240
10	GCTCTTTTTC	TTTCTTATAC	TCAGTCAACA	CTGTAATGAT	GTAGTCTGGA	TCTTTTAATG	300
	TTTGTTCAAT	TACATTGTCT	GTTGCGTATA	TACCGTGTTT	GCGAATAGCT	GGTaGGACAT	360
15	CTGATGTTAC	CCAGCGTTTG	AATTTTCTAG	CGGTTTCTCT	AATTTTTTCG	TTTTTGCTTT	420
	GTTTAGAAGC	ATCGAAGATT	AGACTGTATA	ATCCTGATTC	GTTGATAATG	ATCATATTTC	480
	TGTTTTGACC	TGATGCACTA	AATTGGTGCG	TCAGTTTGTC	CTCGCTATCA	ACATGATTTC	540
20	TAATGGCATT	GTCTGATCTT	GCATATCCTA	AAATCTCAGC	AATATCTTTT	CCTACAAAAT	600
	AAGGTTCGTT	TTCAATTTCT	ACTGTTCTTA	CTGGTAGCTC	TTTAAAATTA	AATGTTTGTA	660
	ATGCTTGCAT	TTGAGTATCC	TCCTTTTTCC	TCAACACCCA	CATTCAGCAG	ACGGTTATCG	720
25	CAATGACTAT	CGAATGTATT	TAAACGCGGC	TCATATCATC	GCCAGcTCTC	GCTCACATCT	780
	GCTCAATGTG	GATGTTGATA	AGCGTGGTTA	TATTAAGAAG	TGAATGTTAC	TGATTCACTT	840
	TCCGCCACTC	TGTTAAATCA	СТААСТТТСТ	TATCCCTTTC	AACACCGTTA	ACCTTCTCTA	900

ACGCTTTCAC TACTTTTTGG AACTCTTTGA TAGCACTLCG TAGCTTTTTA GTAATTTCAT

CTTCTACCAT TTCCAAACCA GCAAATGCGT CTTCGTTATT CATGCTTAGA TGTTTGTTGA

AAAGATCTCG AGTGTATCTT ATTTCTTTAA GTGATTTATC ATAAGCTTCA ATTTGTCCTG

AAAGGTTATG ATATTTTAGT TGTAGTTTTA CTAATTTTAA TGATTGGTCT TGCATTTGTT

ATGTCTCCTT TAAGATGTTT GTTTGCGTTT CGTGTACTTT GTGGGTAAAA AAATATCTCC

AATATTTTCG TCAAAAAAAT CAGCGATAAT AAACATCTCA TCATTCTTAA ATTGATGCTT

TCCTAATTCT TTTAAACGAT AACCTTCAGT TGATATATTC AAGAGGTTTG CTAAATCTTC

TTGAGTACAC TTTCTTTCTT TTCTCAACTT TATTAAATTC CATTGCATGT TGTCACCTCC

CGCTTTACAA AACCTACTAT ACACGATACG GTACTTGnGT CAACATAAAA GTTTGCTTTT

960

1020

1080

1140

1200

1260

1320

1380

1440

1449

(2) INFORMATION FOR SEQ ID NO: 593:

(i) SEQUENCE CHARACTERISTICS:

CGTGTATTT

- (A) LENGTH: 1170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:	
5	ACCAAAAACA CTTTCTAAAG AAATTGTTTC AGAACCATTT GCTAAAAACC AATTACGTGA	60
	AAAAGCTCGT CTAACTAACA TTAAAGGTTT AGAGATTCCA AGAGTTTCAT ACACTTTAGA	120
	CGATGATGAT TTCATTACAG ACGTAGAAAC AGCAAAAGAA TTAAAAGCAA AAGGTGATAC	180
10	AGTCAAGTTC ACTACTAATA AATTCAAAGT ATTTGCTGCA ATTTCAGATA CTGTAATTCA	240
	TGGATCAGAT GTAGATTTAG TAAACTGGGT TGAAAACGCA CTACAATCAG GATTAGCAGC	300
15	TAAAGAGCGT AAAGATGCCT TAGCAGTAAG TCCTAAATCT GGATTAGAAC ACATGTCATT	360
	TTATAATGGA TCTGTTAAAG AAGTTGAYGG AGCAGACATG TATGATGCTA TTATTAACGC	420
	TTTAGCAGAT TTACATGAAG ATTATCGTGA TAACGCAACA ATTTATATGC GATATGCAGA	480
20	TTATGTCAAA ATTATTAGTG TTCTTTCAAA TGGAACAACA AATTTCTTTG ACACACCAGC	540
	AGAAAAAGTA TTTGGCAAAC CAGTAGTATT TACAGATGCA GCAGTTAAAC CTATTGTGGG	600
	AGATTTCAAT TATTTTGGAA TTAACTATGA TGGAACAACT TATGACACTG ATAAAGATGT	660
25	TAAAAAAGGC GAATATTTGT TTGTATTAAC AGCATGGTAT GATCAGCAAC GTACATTAGA	720
	CAGTGCATTC AGAATTGCAA AAGCAAAAGA AAATACAGGE CCATTACCCA GCTAAGCCCC	780
	AAAAGGTTAA TGTAACAGCT AAGGCTAAAT CAGCTGTAAT ATCAGCCGAA TAGGGGTGAT	840
30	GAAATGAGTT TAGAAGAAAK TAAATTGTGG TTGAGAATTG ACTATAATTT CGAAAATGAT	900
	TTAATTGAAG GTCTCATTCA ATCGGCTAAG TCTGAATTAC TATTAAGTGG GGTnCCAGAT	960
35	TATGACAAAG ATGACTTGGA ATACCCGCTT TTTTGTACAG CGATTAAATA TATCATTGCA	1020
	AGAGATTATG AAAGTCGTGG ATACTCAAAT GACCAATCTA GAAGCAAGGT GTTTAATGAA	1080
	AAAGGATTGC AAAAAATGAn TTTGAAATTA AAAAAGTGGT AGGTGATTTT TAAATGGAAT	1140
40	TTAATGAATT TAAAGATCGC GCGTATnTTT	1170
•	(2) INFORMATION FOR SEQ ID NO: 594:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1393 base pairs	
45	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:

TGAAGGGTGT TTTGTTTATG GCCAATTGCT GTGTTATTAA AnCGAATGTT TCGAATGGAA 60

	ATCATTCCGG	AAGAGGACAT	GTCTTCAGCT	TCTGATTTGA	AAGCACAGTT	TTATCGCGGT	180
	ACTTTGCAGC	GCTTTTACCA	At CnTTGCAC	GCAGAAAAGC	TTACACCTTA	TGTTATGTCT	240
5	TATGACGATA	TCATTTCATT	TTGTAAAGAA	AACAATATCT	CTGAAGTAGT	GACTGCGGGT	300
	GATATTATGA	GTTATCATCT	TGAAGAATAT	GATATTTTAC	ATCAACGTTC	TTTATTCAAT	360
10	GAAGCACGCA	TTGCCGTTAC	TTTGATACGT	GGGAATCATT	ACTTTAAAGC	GAGTAAAACA	420
10	ATGAATCAAC	AAGGGGAGCC	ATACAATGTT	TTTACTAGTT	ТСТАТАААА	ATGGCGACCT	480
	TACTTGAGGC	ATAGAGACGT	ATATCACTAT	GATTTAAAAT	CATTCGAAAA	CTTTGTCATT	540
15	GCATCACCTG	ATGATTTAGT	GTTTGATGAC	ATAGCATTTG	GATCCTCACA	aataattgaa	600
	CAGatAAATG	GCAACATTTT	TTAGATCAAG	ATATACAGAA	TTACGAAAGC	GGAAGAGACT	660
	ATTTACCTGA	AGTATTAACA	AGTCAGCTAA	GTGTTGCTTT	AGCATATGGA	TTATTAGATA	720
20	TTATTGAAAT	TTTTAATGAT	TTATTGGCGC	GTTATGATGA	AGATGAGGCA	AACTATGAAG	780
	CATTTATACG	TGAACTCATT	TTTAGAGAAT	TTTATTATGT	GTTAATGACA	CAGTATCCTG	840
	AAACCTCATA	CCAAGCTTTC	AAACCTAAAT	ATCGACAGAT	AAAATGGTCG	CAAAATGAAG	900
25	CGGATTTTAA	TGCATGGTGC	GAAGGGCAAA	CAGGATTTCC	AATCATTGAT	GCAGCAATAA	960
	TGGAATTGAC	ACAAACTGGT	TTTATGCATA	ATCGAATGAG	AATGGTTGTG	TCGCAATTTT	1020
20	TAACCAAAGA	TTTATTTATA	GATTGGACAT	GGGGAGAAAA	ATTCTTTAGA	AAGCACCTTA	1080
30	TTGACTATGA	TGCAGCATCA	AATATTCATG	GATGGCAATG	GTCTGCTTCT	ACAGGTACGG	1140
	ATGCAGTGCC	GTATTTTAGA	ATGTTTAATC	CAATAAGACA	GAGTGAACGC	TTTGATGCTA	1200
35	AAGCTTTGTA	TATCAAAACA	TATCTTCCGA	TTTTTAATCA	AATTGATGCA	AAATATTTGC	1260
	ATGATACACA	ACGCAATGAG	TCCAACCTTT	TTGAACAGGG	GATTGAATTA	GGTAGTCATT	1320
	ATCCAAGACA	AATGGTAGAT	CATCAAGAAA	AACGTACACA	AGTTTTAGCT	ACATTTAAAG	1380
40	CGCTAGACTA	ATT					1393

(2) INFORMATION FOR SEQ ID NO: 595:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1484 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:

TTAACTTGAA AGATTTCCCC GACATCTATA ACTTGTATAA TGTGTATATG TCGTTTTTAG

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	AAAAATTAAA	AAAAGAATAT	CTTGATTGGT	ATAATCAGAC	CTTAGAGTTT	TCTAATTTAT	180
	CAAACAATGT	AGTAAGWATA	GATACTCCTT	TTAAAGATAA	TTCTTTAGAT	AATTTAATAA	240
5	TTTACGCTTT	ATACGATCAG	TCCAGAGACA	TGATTACACT	GACAGATGAC	GGCTATACTA	300
	TATETGATTT	AGAAAATAAT	GGTATTTCTT	TAAATAAATC	AAAAAAACGT	AAAAAGATTT	360
10	TTGAAGAGCA	CCTTTCAGCT	TACGGTATTA	AATATAACGA	TAAAACTCAC	GAAATTTTTG	420
10	TTCAAACTAA	CTTTAAAAAT	TTTAATAAAT	CGAAACATAA	TTTATTACAG	TGCCTTATAT	480
	TTGTTAATGA	TATGTACTTA	CTTTCTAATC	CTAAGTCACA	GAACATATTT	ACAGAAGATG	540
15	TTGCAAACAA	ATTGGATGAA	CATAACATTT	ATTACGGAAG	AGATTTACCT	ATTATAGGAA	600
	GCAGTGGTGT	TGTTCATAAT	TTCGACTTTT	TTATTAGCGC	TAAGAAAAAT	CAAAAAGAAA	660
	AATTTATCAA	TGCTATTTCT	AACCCTAATA	ATTCTATGAT	TATTAAGTCG	AAAATAACGG	720
20	ATGCTATGCA	AGCAAAAAAA	ATAAAAAGAC	ACAGGCAAAA	TGAGTTTATT	TTTATTTTAA	780
	ATGACTCAAA	AAAAGAAATA	AATGAACATA	ATAAAAATCT	TCTTCATGAA	AACTATATTA	840
	GTACAATAGA	TTATAGCGAA	TTAGATGAAA	AGATAGGTTT	ATTGATTTAA	TATATATAGA	900
25	CGTGATAATA	TCAATGTTTA	TATTAAATGA	AACGAATTTG	AAAATTTCGA	AACAGCTTAA	960
	GATAGCAAAT	TGAATAGCCT	TATTGATAAT	GCAGAATCGT	CTACACTTAG	TTGAACAAAT	1020
	TCTATGAGAA	TAGATATTGT	TAAACTATTT	GGGTAGGCGA	TTTTATTTTG	ACAAGAGTCA	1080
30	GAAGATTATT	TAGTTCATAG	TTTAAGTTAC	AAATGGCTAA	ACTTTATGAA	aatggtatga	1140
	CTAGAATCGA	AATTATACTC	GAATACGATT	TAACACTCTC	AATCTTCTCG	AACTGAATAA	1200
35	ATACTGGGTC	ATTCAATCAT	CAAGACAACT	TAATAAGTGA	TGATAAATGT	TCATACCATT	1260
	TTGCAAATAT	AACCAGATAC	TCTCAACAAA	ATGTAGAGTT	CAAAATTAAA	AATGTCCCTA	1320
	ATTGGCACAT	TGCTGTATGA	TAATAAATTC	AACTTAGATT	TCAACAATAT	AACTAATGAT	1380
40	GCTTATATTT	ACCGCGATAT	CAAACCAAAC	AGCCCATCCA	CAAACAAATT	AGAATATATC	1440
	mTGTTAATAA	TAGTAAATGA	TATATCTTCC	AAAGACCGCA	AACT		1484

(2) INFORMATION FOR SEQ ID NO: 596:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1435 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

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	CTTTATCaTT	AAATGCCaTT	TTGaATCCTT	CTTGAATTTG	TTTGATTTCC	TTTTCAGTAT	120
	TATTAACCTT	GTTCAAGACA	GTGCCATTAA	TTTTCTTCTT	GAGTGGACCA	ACCTCATCTT	180
5	TATTAGTTGA	TTCATGAATC	GTTAATCCAA	TGTGTGGCTG	TATTCTATAA	CCATCATTCG	240
	CTATAGTTGA	AACATATTGT	Gataattgta	ATGGTGTATA	GGTATCATAT	TGACCAATTG	300
0	ATAAATCTAG	ATAATTACCT	GGATTATTTG	TTAATGGTTC	GATTTGACCT	CTTGTTTCAT	360
· ·	TTGGTAAATC	TATCCCTGTT	TTCACACCTA	AGCCTACTTG	ATTTAATCCT	CTTCTTAGCT	420
	TTTGGGCAGG	TGAACTTATG	TCTGAAGGTA	AAGCCATACC	AGAATAATAA	GGGTCTCCCG	480
5	CTAATTTTAA	TGCTGTTTTA	AACATATATA	CGTTTGATGA	ATGCATCAAA	GCTTGCTTAT	. 540
	CATTAATAGT	TACATGCCCG	TTTTTTTGA	AGTATGATCG	TTTTGTCAAA	CCACCTTGGA	600
	AATGTAATGG	TTCATCGACC	ATTGTTTCTC	CAACTTTGAT	AGCTTTATTC	TGATAACCGG	660
20	CTAATAATGT	TCCACCTTTT	ACAGAAGATC	CAACCGCAAA	TTGAGAAGTA	AACGTACCAA	720
	TGTCATAATC	AGTCATTTTA	CCACTCTTAT	TAATCTGCTT	TCCGGCAAGC	GCAAGAATGT	780
	CTCCATTTTT	AGGATTTTGT	ACAACCATCA	TTGCATTATC	CATATCTTTG	GCACCTTGAC	840
25	TGCGASTTCT	TAATTTGTTT	ATCTAATAAT	GCTTCTACTT	CTTTTTGAAG	ATCTATATCG	900
	ATCGTTAATT	TCAAATCTTG	ACCGCGAGCG	CCAGGrTTTA	ACACTTCTGA	AGATGTAACT	960
٠	TTACCAGATT	TGTCCGTTGT	GTATTTCATT	TCTTTCTTCT	TACCACGCAA	TACATCTTCA	1020
30	TATTGATATT	CTAGGTAAGA	TTTTCCAACA	CGATCATTGC	GTGAATATCC	TTTGGATAAG	1080
	TAATGTTCTG	TCAATTCTTT	TGGaATACCT	TCAGCAGGTG	TCGATACATC	TCCGAATATA	1140
35	CCTCTTAAAG	TATCGCCATA	TGGATATTTT	CTATCCCAAT	CCATAGACGT	GTTAACACCT	1200
-	GGTAATTTGG	AAAGTTGCTG	AGAAACTGCT	GCATACTCTT	TTTCACTGAC	ATCTTCATTT	1260
	TITATCATIT	GTGGATCTAA	AACTGTTCCT	GGCATTCATC	TCTCGAAAAA	TAGCTAAAAC	1320
10	TTGGTAAATC	TTTAGAAGAC	AATTCATCTA	ATTGTGGATT	TTCCGGATTT	CGGATAACAG	1380
	TTGGTnTATC	CATAATGGAT	CCTGGTTTAA	TACCTTCCAn	CnGGCGAACA	TAGCC	1435

(2) INFORMATION FOR SEQ ID NO: 597:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 516 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

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	AGAAAAAGAT TTAGAAAAGA TTACCATTCG CGACATAACA ACACGCGCTG ATATCAATAG	120
5	AGGGACATTT TACTTACATT ACGAGGATAA ATATATGTTA CTCGCAGATA TGGAAGATGA	180
5	GTATATTTCA GAACTAACGA CATATACTCA ATTTGATTTG	240
	AGACATTGCG AATACTTTTG TAAATAATAT ACTCAAAAAT ATTTTCCAAC ATATTCATGA	300
10	TAATTTAGAG TTTTATCATA CTATTTTACA ATTGGAACGC ACGAGTCAAT TAGAATTGAA	360
	AATCAACGAA CATATTAAAA ATAATATGCA ACGTTACATT AGTATCAATC ATTCTATCGG	420
	AGGCGTTCCA GAGATGTATT TTTACAGTTA CGTTTCCGGA GCAACAATTT CAATTANNTA	480
15	AATACTGGGG TAATGGACAA ACAGCCCATT TTCAGT	516
	(2) INFORMATION FOR SEQ ID NO: 598:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1955 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
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23	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:	
	AGTACTTTAC CATGAGGTAA GACTTTATTC CCTGCTTTTA TAGATTGTGC TTTTATTTGT	60
30	GTGCCAGAAC CAATAGLACE GGTCTAATGA TTTTGCACTC ACATTATCAA TAGCTTTTTG	120
	TTTGTCTTGA CCTTCAACAT CTGGCACTTT ACTATACTCT GCATTAGATG TGTCATCTTT	180
	TGATTTACCT ACATTTAAAT ATTTCAAAGT ATTTTCCATT ATTGGTTTAA ACGCTTTACT	240
35	AACACCTAAT TCATAAGCTT CTTGGTCATT TTTTTGTGCC AAGCTCATAC CAGCGTATAC	300
	AATAACTTTA GGATTTTTCT TCGGCGCGTC ACCCATAAAA CTTACAAAAT ATGGGTTTGG	360
	ACCTTTAACG TATCCACCAC CATTAGGTGC AGCGACTTGT GCTGTACCAG TCTTACCTTC	420
40	GACCTCATAA CCATCAATAC GATAGTTTGC AGCGTGACTC TTCTTACTAT TCACAACTAA	480
	ATCCAATTGC TTTTCAACTT TTTCAGCAGT ATCTTTTGTT ATTGGTTTGC CTGCGATTTG	540
45	TTTTTGCCCT TTATAAAATT GTCTTTTACT AACAGGATTT TCAACGCTAT TCACAAACCA	600
45	TGGTTTTAAC ATATTACCAT CATTAAAGAA CGCTGATTGC GCTTGTAACA TTTGAACAGG	660
	TGTTACTGTT GTCGATTGAC CAAATGATGA CGTTTTTTGt TGCAACTCAT TACTCCATCC	720
50	AATTTGACCA GGTGCTTCTC CATCAAACAT ACCTTTAGTT GATTTTCCAA ATCCAAATCG	780
	TTCATACCAA GATTTCATTT TGTCTGCACC AACTAAATCT TGTAAATGCA TCATCAATGT	840
	ATTAGATGAA TAAGTAAATC CGAGTGACAT TGGGATTTCA CCCCAACCGA CTCTATTCCA	900

	AAAAGCACCT	TCTTGAATAG	CAGCTGCTAA	CCCATATGAT	TTAAATGTTG	ATCCAGGCTC	1020
5	GTATGTGTTT	TGATAAAGGT	CATTTGCCCA	CTTTTTACCA	AAGTCTTTAC	CAGTTTCAGG	1080
3	ATTAAATGTT	GGTCGCTGAC	TGTATGCTAA	AATTTCTCCA	GTTTTGGCAT	CCATGACAAC	1140
	CGCAAATAAA	TCTTTCGGCT	GGTATCTTTC	AACCATGCCA	TCTAAAGCTT	CTTCAACAAA	1200
10	TACTTGAATA	TTTGAATCGA	TTGTTAAATG	GACATCATCA	CCACGTTTAG	GCTGCTTCTC	1260
	TTTTTTAGTA	TTTGGTGCGA	TATATCCCCA	AATATCATGA	ATATATCTCA	ATGATCCTTT	1320
	AGATCCACTT	AAATAACTAT	CAAAAATCTT	TTCAACTCCA	AGTGCACCTT	TAAGTTCACC	1380
15	AGTATCCGGA	TTTTTCTGAG	CTCTACCAAT	TAAGTGTGAT	GCAAAATTGC	CATTTGGATA	1440
	AAAGCGTTCT	GTTTCAGGCA	ATAAAGAAAT	ACCAGGCAAA	TTCATTTTCT	CTATTTTCAA	1500
	TTTGTCCTGA	TACGTTAAAT	TTGTTCCTTT	GCGTCCAAAT	TCAATTTGGA	AAGCTTTCTT	1560
20	TTGACTAAGT	CTCTTTTCAA	TTTCCTCTGG	CTTCATATTA	ATGACTGTAG	ATAATTTCTT	1620
	TGCAGTCTCT	TTTTTATCAA	CTACATGCCT	AGGTTTTTTA	GAATTGGCAC	TCGCCTTTTT	1680
	ATCTATTACT	GCAACAAGTT	TATATCTTTC	TACATCTTCT	GCTAGCACTT	TACCATKACG	1740
25	ATCATATATC	TTTCCTCGTT	CTGGTTGTTG	TGCATTCTTA	ACTAAATACT	TTTCATTTGC	1800
	CTTCATGACT	AAATCTTGAC	CATTAGAATG	TCCAGTAATC	ATGATATATG	AAATTCTTAA	1860
30	AACCAATATA	AAAAAGAGCA	GTCCGAATAA	ACCAACAAGT	AGGACTGCCC	CTATTTTATT	1920
••	TTTTTTTAATT	TTAATTTTTT	TGGTCGCCAT	TACTA			1955

(2) INFORMATION FOR SEQ ID NO: 599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 base pairs (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

TAGCAAGAGT	AGGTGATAAC	AGPTCTTTTA	ACGIGITIGE	TGCTTGCTCA	TITCITGGCT	60
CATTGTAGAC	TAAAATATAA	TAAGCGTTTT	CAAATAAGTG	CTTTTTAGCA	TTTAGTACAC	120
CAGATTTATG	ACTACCAGCC	ATTGGATGAC	CACTGACTAA	ATGAATATTA	TGCTTTAATA	180
AATTGCATTC	GTGTTGCTGT	ATCATTGCTT	TAGTACTACC	AGTATCAGAA	ACAATAACAC	240
CAGGTTTAGT	TGGCATATCT	ATAAGCTCGC	TAAGATATTT	ATTTGTGATA	GCAACAGGTG	300
ттаатааат	AATTACATCC	CCALALALALA V	тассттеаст	44477444	CATTTTCAT	360

TATTAGTATT	AGGGTTATGG	TATTTTATAT	TGCTAGCAAG	ACTTCCACCA	ATTAATCCAA	480
GCCCAACAAA	TAAAACTGTT	GTCATATAAA	TCACCTTATT	TCGAAATTTT	CAGAATAATA	540
ACATTGTAAA	TGAGCTGTTG	ACACAGTGCA	ATAGTAAATA	AAAATCGATA	ATAGCATTAA	600
TAGATAAACG	GAGATAAATC	ATCTACAATA	AAGAGTATAG	TAACACAATG	GCAACGGAGG	660
GGTAAATCAA	TGGAACCAAT	ATTAGAAATG	ATTAAAACAT	TAAC		704
(2) INFORMA	ATION FOR SE	EQ ID NO: 60	00:			

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1158 base pairs

(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

60	TTAAACCTAT	TATAATACCC	TGACTAAGCC	TTTTTCATCG	ATCACGAACC	CCTCTAAAGG
120	TGACGTTTAT	GCGACGCCAG	TATCAATTAG	GTGTATTCCC	TTTTACCTCT	TATTATTAAC
180	ACTACATAAA	ATTATATAAA	CCTTGTCATT	GTCACCAACT	TACTTTCACA	CTATATACTT
240	TATTTATTAT	CATATGAAAA	TTTTGTTAAT	GTTTTATAGT	TCATGATACA	TGATGTCATG
300	GATAGTACAC	ATATTAATTA	AAAATAGACA	CAATTTACTT	CAACTCGCTT	TATTTTACTA
360	TCGTTTTCAA	CACACTCTTA	ATATAAATAA	TTTTTCAAAA	ATAAAAGTGA	ACATTTCTTC
420	CTGATTCAAT	CAAATCTATT	GCTGAAGCAT	ATTAAAAACA	TGCTATTTTC	AATCATTTAA
480	AAACCACTTC	AACAACCTTC	AAGGTTTATT	AAGTGACTCA	TATAAAAATG	CAAGAATACA
540	CGGATATTGC	ATTTAAGATG	TCGATTACTG	AGCATATTTT	TTTATTTTAA	ATTGATCACT
600	CGGTTGACAC	ACTCAAATGC	AACTGCTTAA	AAACAATTCA	CAGATTGCTT	GTAATTAATT
660	AATTGTTCCT	AAGAAGCAAA	ATTTCGATTG	AGTATTTGAT	CTAAACTAAA	ATACAACCTA
720	TGTTGCAGTC	CAGTACCCAA	TTTTGGATAT	TACATCTCCA	CATATTGCAA	TTAGGCACTA
780	ATGATAGTAC	AATCGCCAGC	ATTGTTAGAG	TATCATATGA	CATCCGGATT	GTATATTCCC
840	AAGTAAAAA	TGTCATCTGT	TGCGAAATAT	TCGATGAAAA	CAGCATCAAT	CATACTTCAT
900	TGTCTCTCTA	CTTCTCGAAT	TCTTTCAATA	TCTGCGTCCA	TAAACGGCGC	TAAATACTAC
960	TTCTGCTGAT	CaATCCATTG	TGCAATTCAT	TGATTCAAGT	CTTCAGGATG	TAGAAACCAC
1020	TCTTCTAATG	ATCTTCTAAA	CGTTTTGTAC	TTATGGAATA	CAAATCCACA	TTCATTATTT
3000	TCTCTTTTTTT	AACTTCAATA	ССССТТСВСВ	CTTACTTCCT	TTTTTTCAAAT	CATCGATTAA

	GAACGACTGC AAATTGAT	1158
	(2) INFORMATION FOR SEQ ID NO: 601:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 827 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:	
	TGATACTTAT TTTTCAATAT TATTTGGAAT AAAnTCTTnT AATTGTGGTG TGAAATAAAC	60
15	ACCGAAATTC TTTTCAGATT CATCTTTTCC ACTACCTGCA TATAAAATAC CAATCAGTYC	120
	ATGTTTAGAA TTCAATACAG GAGATCCTGA ATTACCTGGT TGTGCATACG CATCAAATTC	180
20	CATAAACGTT CCACTGATAT GGTTAATCGT TCCTGTCGAT TCAAACATTT TATATTTTGT	240
	TTGTGCACCC TTTGGATAAC CAATAACAGA AATTCTATCT TTCACTTTTG CTCCGTCTGC	300
	AAATTTTGTA TAACTAACGT TCTTATTAAA ATTCAAACCT TCTGTACTTG TTTCATGAAC	360
25	ATGAACTATC GCAAGGTCTT CTTTTCCGGG ATATTCTACA ATGTCTTTAA CGTCGTAGTT	420
	TCCTCCGCCT TTACCTTTAC TCGAATGATG TGCTGATACT CTATTTTTAA AAATATCATT	480
	ACTITIAGCG ATATGTTTGT TAGTTACGAT TGTATTTTTA CCAACAACTA CACCAGTACC	540
30	ACCCACAAAT GCTACCACTG AATTGTATGG TTCCTTAGTT GCATCGGTAA TTTCTTTGAC	600
	ATTCTTTCT GCTTTGGCAA TTGAATGAYG CTGATTAGAA ATATTTTCAG CAAAACCAAG	660
	AGATGTTAAA ATAGTTAAAG CAGTTAAACC TTTAACCATT ACATTTTTAT TCATATTTTA	720
35	CCTCCTTCCA AATTTATTTT NATAGTTAAT GTATCTAGAT ACACATTTAC TATATACATT	780
	TTAAATAAAA ATATTAATTAATT AACCACTTAT NAACGTT	827
40	(2) INFORMATION FOR SEQ ID NO: 602:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 796 base pairs (B) TYPE: nucleic acid	
45	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:	
50	nggnacgtaa agtatttatg ttaaatggca naaatatatg aatgatgagt tacctggatt	60
	ACCAATGTTC CAAGGTAAAT CGATAACTAT TGTTAACGAT AAAGTACGAA ACTTAGACAT	120

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CGACGATTTT	GTCGAGGTTT	ACTTATATGG	GGGGATGTTA	TGAATAATGT	ATTGTTAGAG	240
GTTAAAGATT	TAGAAACATC	ATTAAAAATA	AATAATGAAT	GGTTAGCAAC	TGTTGAAAAT	300
ATTTCTTTTG	AATTATCTAA	AGGAGAAGTT	TTGGGTATAG	TAGGGGAATC	TGGTTGCGGT	360
AAGTCCATAT	TAAGTAAGTC	AATTATTAAA	TTATTACCAG	AAAAGATATC	TAAACTAAGT	420
AATGGAGAAG	TTATATTTGA	TGGTAAACGA	ATCGATACGC	TCAATGAGAA	GCAATTGCTA	480
GATATTCGAG	GAAATGATAT	TGCTATGATT	TTTCAAGAAC	CTATGACTGC	TTTAAATCCT	540
GTATTTACCA	TAAAAAATCA	ACTTGTGGAA	TCTATAAAAT	CACATAAAAA	AATTTCTAAA	600
AAAGAAGCAA	ATAAATTAGC	AAAAGATTTA	CTAAAAAAAG	TTGGAATTGC	TAGACAAGAT	660
GAAATATTAA	ATAGCTATCC	TCATCAATTA	TCTGGTGGTA	TGAGACAAAG	AGTAATGATT	720
GCAATGGCCA	TTTCATGTTC	TCCTAAATTA	TTAATTGCTG	aTGAACCTAC	AACAGCATTG	780
GATGTCACGA	TTCAAG					796
(2) INFORM	ATION FOR SE	EQ ID NO: 60)3:			
1		ACTERISTICS 1618 base p cleic acid		•		

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GGATGTGTTC ATCCCAAATT GAAACAGAAA TTTATGATCA AAtGATGTGG ATTGGTTTTA 60 AACCATTCAA AATTACCAAT ATTAMACAAG AATCTGAAGA CATTAAATCA TITLACAGTT 120 GAAACTGAAG AATATGACTT TAGTGAATTT ACACCAGGCC AATACATCAC AGTTGATGTT 180 TCTAGTGATA AACTTCCATA TAGAGCTAAA CGTCACTATT CTATCGTATC AGGTGAAAAA 240 AACCATTTAA CTTTTGGCGT TAAACGTGAT GTCACAACAG AACATGAAGG CGAAGTTTCA 300 ACAATTTTAC ACGATGAGAT TAAAGAAGGC GATATGATTA ATTTASTGCG CCTGTAGGTG 360 GATTCGTATT AGAGAATACG ACTGAACCAC AACTTTTCTT AGGTTCAGGT ATTGGTGTTA 420 CACCTTTAGT AGCTATGTAT GAAGCTGCCT CTGCCAAAGG TTTAGATACA CAGATGGTTC 480 AAGTTGCTGA AAATGAACAA CATTTACCTT TCAAAGACAA CTTCAACAGT ATCGCAAGCC 540 ATCATGACAA CGCTAAATTA TATACACACT TANAGATAAA CAAGGCTATA TTGGTGCTGA 600 AGAATTACAA GTATTTTTAG CAAATAAACC TGAAATTTAT ATCTGTGGTG GTACAAAATT 660 CTTACASTCT ATGATCGAAG CACTTAAATC TTTAAATTAC GATATGGATC GCGTACACTA 720

	ATATGAAACT	TAATCAACGT	TACGTAAAAG	TATTTGCATT	ATATTTCGTA	AGTATTGTTA	840
	CTGCAAATAT	TATTGTTAAA	AATAATAATT	TAATTAAAAC	Attgatacaa	ACCATAGCCG	900
5	GGTACACGGT	CTTTGCAGTT	GGTTTGAAGT	ATTTAACTAA	ACGTAAAAAT	AAATGACATC	960
	TATACCAAAA	CAGCTATGAC	TTTACTTTGT	CATGGCTGTT	TTTTAATTGG	GAGTAGGACA	1020
10	GAGATGATAT	TTTCGCAAAA	TTTATTTGGT	CGTCCCACCA	CAACATGCAT	TGATGTATGC	1080
	TCACTGAATT	TCATAAGAAA	GGAGTTCACA	AGATGACCGT	AGATATTGGA	CGGATTTATG	1140
	ACAATAAAGA	TAATACCGAC	GCTATTCGTA	TCCTAGTCGA	TAGAGTCTGG	CCGAGAGGTA	1200
15	TTTCGAAAAG	AACTGCTAAC	CTAGATTATT	GGTTAAAAGA	CATTGCCCCT	TCTACTGAGT	1260
	TGCGACAATG	GTTCCAACAT	GATCCTAAAC	TTTTTGGAGC	TTTTAAAGAA	AAATATGAAA	1320
	AAGAATTACG	TGATCAGGAT	GCGCAAAAAG	ATGCTTTTGA	AAAATTAAAG	GATATTGTAA	1380
20	ATCAGCATAA	TCATGTTCTA	TTGTTATATG	CAGCAAAAGA	TACTAAACAT	AACCAAGCTG	1440
	TAGTACTACA	GCAGTTGCTC	AATACTTAGT	TATATATGTT	TATCGTGAAT	CACTATAAAT	1500
25	GTCGCTAACT	TCATTTCTAA	TATTTATTTT	TAAAAAGCAT	AATTACTACA	ATTAATTGGA	1560
	ACTITAATAA	TTACTAAACT	TGGAACAATA	TTTTACTTTA	ACAAAATAAA	GTTTTAAA	1618
	(2) INFORM	ATION FOR S	EQ ID NO: 6	04:			

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

ATTATAATGC AAATATTGAA GCATTTAAAA CAGTCGCTAA AGCAGTAGGC AAAGAGAAAG 60 AAGGCGAGAA GCGTCTGGAA AAGCATGATA AAATATTAGC GGAGATTAGA AAGAAAATTG 120 AACAGAGTAC GTTAAAATCT GCATTTGCAT TCGGTATCTC AAGAGCAGGT ATGTTTATTA 180 ATAATGAAGA TACATTTATG GGACAATTCT TAATTAAAAT GGGTATTCAA CCTGAAGLCA 240 MAAAArAMAA AACTACGCAT GTTGGTGAAC GCAAGGGTGG TCCTTATATA TATTTAAATA 300 360 ATGAAGAACT TGCCAATATC AATCCAAAAG TTATGATTTT AGCCACTGAC GGAAAAACGG ACAAAAATAG AACGAAATTC ATTGATCCTG CAGTTTGGAA ATCATTAAAA GCTGTGAAAG 420 ATAACAAAGT TTATGACGTT GACCGAAATA AGTGGTTGAA ATCAAGGGGG ATTATCGCAA 480 GTGAAAGTAT GGCAGAAGAT TTAGAAAAAA TTGCAGAAAA AGCAAAATAA AAATACAGCG 540

	TGTGATGATT	TACCTGAAAG	TTTATTTCGA	ATAAATTAA	TTACATAACC	GACAAGGATT	660
	GTTTTAACAG	TTCTTTTAAT	GAATTGGCGC	ATCGTTACAT	ACCTCATTTC	TCTATATCTT	720
5	ACGAACTATA	TACCCATTCA	TATATGCTTT	TTAAACGTCA	TTGTCACAAT	TTAATTTTTA	780
	GGGAATATAA	TATAACCATC	TTTATCTGCT	TTTTTAGTAA	AAATGACAAA	AATTGCATGT	840
10	ATTATTGaGA	TGATGGTAGG	GATACCTGTC	CAGAAAAATA	ATAAGTGAAA	AAGACCTTGT	900
	CCAAATTTAT	CAGCATAAAA	TTTATGaATA	CCTAAACCTC	CAAGAAATAA	TGCAACmATa	960
	ACATAAATGG	CTTTATTGAC	TTTCATTTGT	AALCCTCCTT	AACTATAATT	CTACTTAAAT	1020
15	TCGTTGTGAA	AACCAATATT	TCTAACTTTA	GAATTTTCAA	ACTTTCTAAA	ATTATAAGTA	1080
	TATCTTTTTA	AAATAAGCTA	GAATTTCTAT	ATAATAAATG	TTAATAACGT	AAAAGGGAAT	1140
	GATGACATAG	TGATACGTCA	AGCACGTCCA	GAGGACCGAT	TTGATATTGC	GAAGTTAGTT	1200
20	TATATGGTTT	GGGATGATAT	GGAATTAGAA	TTGGTAAAGC	ATCTACCTAA	AGACATGGTA	1260
	TTAGATGCAA	TTGAAAAAAG	CTGTGTTGAT	GCAACATATC	GAACTTTTTA	TCAGCATATT	1320
25	TTAGTTTATG	AAGTAGAAAA	TAAAGTAGCA	GGTTGTATTA	TTAGCTATAG	TGGTGAAAAT	1380
	GAATTGAAAT	ACGAAAAAGC	ATGGGAACTA	CTTGACTTGC	CAGAAAAAAT	AAAACAATAT	1440
	GGCACGCCAT	TACCTGTAAA	AGAAGCTAAA	GACGATGAGT	ATTATATAGA	AACAATTGCG	1500
30	ACATTIGCAG	CATATAGAGG	TAGAGGCATC	GCGACAAAGT	TATTAACGTC	ATTACTTGAA	1560
	TCAAATACAC	ATGTTAAATG	GAGTTTGAAT	TGCGATATTA	ATAATGAAGC	AGCATTAAAG	1620
	TTATATAAAA	AAGTAGGCTT	TATATCTGAT	GGACAGATTG	AATTATACAA	GCACATGTAT	1680
35	CATCATTTAA	TTGTTAAATA	AAATACTCGA	CAGTTCGATG	TAAGTCGATT	GCCGAGTAGT	1740
	ATCATTTTCT	ATTAAATGCC	TGCAAATAAT	GCACTAATAT	AAATACCTAA	TGCATATAAT	1800
40	AAACCGAAAA	ATGTATTTGT	TTTACCAGCA	GCAGCCATTG	CTGGCATCAT	TGTAGGCGGT	1860
	GTATCATTCT	TCTTGAAACG	TCTGATAACT	TTAACAGGCA	TTGGGAATGA	TAACAACGCA	1920
	AGTAAGTAAA	ATAATGAGCC	ACCAGGTTTA	ATAATGATCG	TAAGTACAAT	AAAGGCATAA	1980
45	GCGATAAAGT	ACATGATTGC	CATAAATGTT	AAAGAAGCAT	TTTTACCTAA	TAGAATGGGT	2040
	AAAGTTTTGC	GACCACTTGC	TTTATCTTTG	ACACGGTCGC	GAATATTGTT	AGCCATATTA	2100
	ATTAAACCGA	TAGTG				•	2115
50	(2) THEODM	ATTON DOD C	EO TD NO. C	۸۴.			

(2) INFORMATION FOR SEQ ID NO: 605:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1003 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:	
5	TATGTCTCAA ACTCAAATTA ATCAAATGTT CCAGCAGAAA AACATGTCTA CTGAATTAAA	60
	ACGTCGTTAT GCACAACGTT TATTACAGTT TCCACATGTA CACAATAAAG AATACTTGAA	120
	ATCTTATGCT AAAAACCCTA AAGAAACTAA AGATAGTTAT ATTTCTGGTT TTAAAGAGAA	180
10	TCAATTGATT AAAATAGAAG CGATTAAATC ATTGTTTGCA ATGGATAAAT CTCCATTAGA	240
	ACATGTTAAA CCTGCTACAA AACCAGACGC TTCTTGGGAT GAGATGAAAC AAAAAGCAGT	300
15	TGAAATTGGT AAAGCTGATA CTACATCGAA TAAATTTGGT ATTAGAGATC AATACTGGAA	360
	ATTAATTCAA GAAAGTAAGC GTAAAGTTAG ACGTGACTAC GAATTCAATG TTAATTCTCC	420
	AGAATTCCAA GATTTAGAAT TACTTGTAAA AACAATGCGT GCTGCTGGTG CAGATGTTCA	480
20	ATATGTAAGT ATTCCATCAA ACGGTGTATG GTATGACCAC ATTGGTATCG ATAAAGAACG	540
	TCGTCAAGCA GTTTATAAAA AAATCCATTC TACTGTTGTA GATAATGGTG GTAAAATTTA	600
	CGATATGACT GATAAAGATT ATGAAAAATA TGTTATCAGT GATGCCGTAC ACATCGGTTG	660
25	GAAaGGTtGG GTTTATATGG ATGAGCMAAT TGCGAAACAT ATGAAAGGTG AACCACAACC	720
	TGAAGTAGAT AAACCTAAAA nTTAAAATAC AAATAGCACA TAACTCAACG ATTTTGATTG	780
30	AGCGTATGTG CTATTTTAT ATTTTAAATT TCATAGAATA GAATAGTAAT ATGTGCTTGG	840
	ATATGTGGCA ATAATAAAT AATTAATCAG ATAAATAGTA TAAAATAACT TTCCCATCAG	900
	TCCAATTTGA CAGCGAAAAA AGACAGGTAA TAACTGATTA TAAATAATTC AGTATTCCTG	960
35	TCTTTGTTGT TATTCATAAT ATGTTCTGTT AACTTAATAT CTT	1003
	(2) INFORMATION FOR SEQ ID NO: 606:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1097 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	·
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:	
	GCTnTTATAT TTAAAAAATT TATTnGCGGA TAATTACCTT TATTAAATCC CACCCATTAG	60
50	GAWTACGAGT AATAGGACTA ATACTGGAAT CACATAATGT AACATAACGT CCCTCCTTTA	120
	ACTTAATTTT AATTGTAATC AAATTTGACA ATAAGTCAAA MCATTAATAC CTATGATATG	180

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TATCATTTAT TAACATATGT ATCATATTTT TAATCTTGCG TAATTTTTAT CGTTAACTAT

	CTTTTGTCAT	TTTAATTATG	TTAAGATAAT	AGTAGTTATA	GAAGTTCAAT	CTATAGGAGG	360
5	CATAGCATGG	ATATTCCAAA	AATCACGACA	TTTTTAATGT	TTAATAACCA	AGCTGAAGAA	420
3	GCTGTTAAAC	TATACACAAG	CTTATTTGAA	GATAGTGAGA	TTATAACAAT	GGCTAAGTAT	480
	GGTGAAAATG	GACCTGGTGA	TCCCGGGACT	GTACAACACT	CAATATTTAC	ATTAAATGGA	540
10	CAAGTATTCA	TGGCGATTGA	TGCTAATAGT	GGCACAGAAT	TACCAATGAA	TCCTGCGATT	600
	TCATTATTTG	TTACAGTAAA	AGATACTATT	GAAATGGAAC	GACTATTTAA	TGGATTAAAA	660
	GATGAAGGTG	CCATTTTAAT	GCCAAAAACG	AATATGCCAC	CATACAGAGA	GTTTGCTTGG	720
15	GTTCAAGATA	AGTTTGGAGT	AAGTTTTCAA	TTAGCATTAC	CTGaGTAAAA	GGATTCGCAC	780
	AGCtTGgAAT	GATAAAGAAA	CACTTTTTCT	TATGCATGCG	TTTTACCTAT	GTATTTCTAT	840
20	TITAAGTACA	CATTAGCATT	TTAGTTTCGC	TCATTTTTAA	AATCACAAAG	ATAATTTGTA	900
20	ACTTAAATGA	TGATACGTTA	TTTAAAAAACA	CGATACTTCG	TTTCAATGAA	CGCATTAAAT	960
	AATAAATAAA	CACCTCACCA	TAAGAAAGGA	CTACTTTCTT	TTGTGAGGTG	TTTatTTGTC	1020
25	GACAACTTGA	TTATGATTGT	TTCATTTTTT	GAATAAGTTC	ATAATCAGGT	GTAGCATACA	1080
	AAGTTTTTTG	ATTGTCA	1		•		1097

(2) INFORMATION FOR SEQ ID NO: 607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2031 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

GAGGTCTAGC ATGTCTCGTT CAAAAAAATA CTTTTACTTA TCTAGCTTAA TGATTATTTT 60 AAGCTTTTTC TITAATACAA ATAACGTTTT CCTAAGTGGA CTTTTTAATT CTTTTATTAA 120 ATTAATACTT TTCTGCAGTG TTATTAACTC AATTGTACTA ATTTTGTCTA TAATTTTTGC 180 AGATCGTTCA ATTAAATCAC TAAAGCCTGA TGCAGATTGG ATTAGAATTG CGAGTAAAAG 240 TTTGCCTTGG ATTATTCTAA TTGTTATTTT AGTACATATC TTTTCAATTG TTCGTACATT 300 CGGTTTTATT TAAAAAAGTT AATATGTCAT TGTAGCCTTA ATACAAAACA ATACAATGTA 360 TCATGCTATA ATGAGTAAAA CAATTTGATA ACGTTGTTGC GTATAAAAAA TATTAGATTT 420 TCGAAATCAT AACTATGCAT CTAATCGCTA TAGTTATACA ACAAGATATA ACATATAATG 480 AGGTTTGATA ATGCATCGAC AATTTTTGTC GTCGCGTTGC CAAAACCTCT TTTTTAAATT 540

	TTTAGGCGCT	TTATTACGTT	ACCTCATTTC	TTTTCTGAAT	ACTGACGGAG	GTTTTCCAAT	660
	CGGAACACTG	ATAGCCAATT	TGACTGGTGC	CTTTGTAATG	GGATTGCTAA	CAGCCTTAAC	720
5	AATTGCATTT	TTTTCAAACC	ATCCGACCCT	AAAAAAAGCT	ATTACGACTG	GTTTTCTTGG	780
	TGCTTTAACG	ACTITITCAA	CATTTCAATT	AGAATTAATA	CATATGTTTG	ATCATCAACA	840
10	ATTTATAACT	TTACTACTAT	ATGCTGTAAC	AAGTTATGTC	TTTGGTATTT	TGTTATGTTA	900
	CGTCGGTATA	AAACTAGGTG	GTGGTTTATC	ATGATATCAA	TCATTTTAGT	CATGATTGGC	960
	GGCGGTTTTG	GCGCAATTGC	TAGAAGTGCC	ATTACTGATT	ATTTTAATCA	TAAATTTACT	1020
15	TCAAAGTTAC	CTATCGCAAC	ATTGATAGTA	AATCTAGTTG	GTAGTTTTTT	AATTGGATTA	1080
	ACTATAGGCT	TATCAATTTC	AATCTCATGG	TTCCCTGCGT	TCTTTGTTAC	CGGTTTTTTA	1140
	GGTGGCTTAA	CAACTTTCTC	AACGTTAGCC	AAAGAACTTA	CACTAATGAT	GACGCCAAAA	1200
20	TTTAATATTA	ACCTTTTTCT	CAATTATTCA	CTTTTACAAT	TCATCATTGG	ATTTATAGCT	1260
	TGTTATATTG	GCTATCATAT	TTAAAAATAA	AATGCTTCAT	TCAGCAAATA	GGTAAATTAC	1320
25	GACACCTTCC	TGAACGAAGC	ATTTTTTAAT	TTTCATGCAA	ATTTTTAAGC	ACCATATAAT	1380
	GCCTACCAAA	TTTCAATAAT	CTTTGTTGCC	GTTTAAATAA	TGTGAATGTC	AATAAATTCT	1440
	CCAAACTAGT	CGAAAATAAA	GGGAGTGGGA	CATAAATCCC	TAAAAAAAACA	GCAGTAAGAT	1500
30	AATTTTCAAT	TAGAAAATAT	CTTACTGCTG	TTCTCTATTT	ATACAATACT	TCGTATTGAa	1560
	TGGcTTCGCT	TTCCTAGGGT	GCCGTCTCAG	CCTCGGcTTC	GACTGGCACT	GCTCCCTCAG	1620
	GAGTCTCGCC	ATTAATACTA	CGTATTAACA	TGTAATTTTA	CTTTTACATA	СТТТААААА	1680
35	TAAGACACTT	TGCCCAACTT	ACACTACCAA	TAGAAACCTC	TGTTAGAATT	CCTCAAAATG	1740
	ATATTTCGCG	ATATGTTAAT	GAAATTGTTG	AAACGATACC	TGATAGCGAA	TTCGATGAAT	1800
40	TCAGACATCA	TCGTGGCGCA	ACATCCTATC	ATCCAAAAAT	GATGTTAAAA	ATCATCTTAT	1860
	ATGCATATAC	TCAATCTGTA	TTTTCTGGTC	GAAGAATAGA	GAAATTACTT	CATGACAGTA	1920
	TTCGAATGAT	GTGGTTAGCT	CAAAATCAAA	CACCTTCTTA	TAAAACTATT	AATCGTTTTA	198
45	GAGTGAATCC	TAATACTGAT	GCGTTAATTG	AATCTTTATT	TATTCAGTTC	С	203

(2) INFORMATION FOR SEQ ID NO: 608:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 687 base pairs

 - (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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TCCCCGGGAA	TCGAACCCGC	GAnCTCCTGC	GTGACATGCA	GGCGTGTTAA	CCGCTACACT	60
ACGAGACCTA	TTANATTAAA	AACTATGTAT	TGCGGGAGGC	GGATTTGAAC	CACCGACCTT	120
CGGGTTATGA	GCCCGACGAG	CTACCGAACT	GCTCCATCCC	GCGCTAATAT	TATTTTGAAT	180
TACCTAATTA	ATATACCATA	ATCAAAAACC	TAAAGTsrrG	AACTTTTTGA	ATTTAATTTA	240
AATGTTATCT	CTTAAATAAT	TACTTAAATA	TCGTAGCAAC	ATGTTCTCTG	TTGAACACAA	300
ATATTAGTAT	ATTCATTTTT	GTAGTGTACG	TCAACGACAT	TTTCAAAGTT	TTTTGTGTAA	360
AAAAACGCTT	CTTATTCCCT	TTTATCATAT	AAGTGTCTAA	TAGTTGTCAT	AAATAGTGKT	420
AAAGCATTTA	AAAAGGTATA	GGAGTTATAA	AGTTTACAAC	GCCTATACCT	TCTGAAAAAG	480
AAATTATAAA	AGCTTGTTAC	ACCGCATATT	CTTTCAGTCA	GCGACTACCA	ATATAACATT	540
GTAGCCCtAA	GACATTGCTT	GACGCCTCAn	TTACAACAAT	TTTTCAAAAT	CAGCAGCTAC	600
CTACTGACAC	AACATAACAC	AACCCnTACA	CTAnCTATCG	TGTCATGTAA	TCTTGCATCC	660
GATCTTGCAA	CGCTGTAAAT	GTTTCGA				687

(2) INFORMATION FOR SEQ ID NO: 609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

GTGTTGAATA	CTTTGACAAA	ATGAAATCAT	TIGITCITTC	GTTTCAAATT	TAACTGTTTG	60
AATTAAATCA	GTTCGTTTTT	CGTAGTACTT	CGGCGTTGTG	TTCATATTCA	TTTTTTCTAA	120
AAATAAACTA	GTAAACAATG	CACCTTTAAG	ACTCTGACTG	ACAACGTGTG	GTGCTAAAAA	180
GAAACCTTGA	TACATTTCAA	GCAATGCATT	TAATGATGCA	CCCGCTTCTT	TACCAATACC	240
AGGTGCTGTC	AATCTATAAC	CACATCGTTC	AATTAAATCT	TTTCTACCAG	CAATGTATCC	300
ACCAATCTTA	GCTAAACCAC	CGCCAGGGTT	TTTAATTAAT	GATCCTGCTA	TTAAATCGGC	360
ACCACATTCT	ATAGGTTCAC	GTCTTTCAAC	AAATTCCCCA	TAACAGTTAT	CCACAAATAT	420
TAAAATATTA	GGATGCACGT	TTTTCAACCT	AGTAATTACC	TTTTCAATTT	CATCTAGCGG	480
AATTGAAGGT	CTTTGATCAT	AGCCTTTCGA	ACGTTGAATC	GCTATTACTT	TGGTGCGCTC	540
AGAAACCCCa	TCTAACACAC	TTTCAATATC	GATCTTACCT	TCTTTAAGTG	CAATATCTTT	600
ATACGATmCG	CCATGCTCCA	TTAAACTTTC	AATACCATTT	CCGTTTACGC	CAATGACTTC	660

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	ACTITGTAAT GCAATAGTAA TCGCATGCGT ACCTGAAATA ATTTGCGGAC GAACAATTGC	780
	ATCTTCTGCT TTAAATGCCT GCGCATATAT TTCTTAATTG AACGAATTTA GAACTAATCG	840
5	TAA	843
	(2) INFORMATION FOR SEQ ID NO: 610:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 775 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:	
	GATTATTATA AACCGAATGA AACAAAAAAG TTTTTACATA TTTTCAACAA CTTTATTTCA	60
20	ATAAAGCATC AAGTTGATCT AAAGTTTGAT TCATACCTTG TTCAACACCC ATGTTTATGA	120
	CTTGTTGAGC GGCTTCTTTT GTTGGAAATA CCGATGTTGA TGTCACTGTC GTTTTCGTTG	180
25	TATTGCTCTT GGAAAATGAC AAAGTAATTT TCATGCTTGG CATTTTTGTA TCTTTTGCAC	240
	CTTGAGGTGT CGCAAATGAG TCAATATATT CAATTAAATA TGGACGCTTA ACCGTTTTAT	300
	ATTCTGCTAA TGTATAGCTG GTCATTGTAG GTGTTTTAAT CGCATAAAAT GCATCACCGC	360
30	CTGAAACAGC ATTAAAGCGA AACACTTTGG TACTAGCGTC TTTTGGALGA AACCATTTTT	420
	CAAATAATGC TTTKGTCGTA TAGGCATCAA ACACCTTTTC AATCGGTGCT TCTATCGTTC	480
	TTGAAAAAT AATTITATTA TCTTCAACTT TAATCGTCAT CTTCCCACTC CCTATCTTTT	540
35	ATATTTACTC ATCTTAACAT GCATTGAGTA ACATATGTTA CCAAATCATT TGTTATAAAC	600
	TATAGTAATA TTAATCATTC CCTCTGTnGA AATTGATAAC TACGAAATAA AAAACACACT	660
40	CTATTCAGCT ATTAACAGTT GAGTAGAGTG TGCAAACCTG TTGAATTAAT GCGCTAACAT	720
	TTCTTCTTTG ATTTGGTCTT NATNTAATTT TGAAGGATAA TATGTTGGCC AGTTA	775
	(2) INFORMATION FOR SEQ ID NO: 611:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 728 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:	
•	ATCAAAATTT GATACTAAAG GGCTCACGCT ATTTTATGTA TTTATTGGAT TGATTATGTT	60

TGTGGCAATG	TGTTTATTTA	AAGTAGAAAA	ACATGTTTCT	TCACCATTTT	TACCTGTGGT	180
TGAATTTAAT	CGTTCGATTA	CTTTAGTTTT	TATAACTGAC	CTTCTAACAG	CTATTTGTTT	240
AATGGGATTC	AATTTATATA	TTCCAGTCTA	CCTTCAAGAA	CAACTAGGAT	TATCTCCATT	300
GCAAAGTGGA	TTGGTTATTT	TTCCTTTATC	TGTAGCTTGG	ATTACATTGA	ATTTTAATTT	360
ACATCGAATT	GAAGCAAAAC	TATCAAGGAA	AGTTATTTAC	TTACTATCAT	TTACATTGCT	420
ACTAGTAAGT	AGTATTATCA	TTTCATTTGG	TATTAAATTG	CCGGTACTTA	TAGCATTTGT	480
GTTAATTTTG	GCAGGATTAA	GTTTTGGATA	TATTTATACG	AAAGATAGTG	TGATTGTCCA	540
AGAGGAAACT	AGCCCATTAC	AAATGAAGAA	AATGATGTCA	TTTTATGGAT	ТААСТАААА	600
TCTTGGGGCA	TCAATAGGTT	CAACAATAAT	GGGATATCTT	TATGCGATAC	AATCAGGAAT	660
CTTTGGTCCA	AACTTACACA	nTGTGTTAAG	TGCTGTTGCT	GTAATTAGCA	TGGGCTTATn	720
GTTTTATG						728
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(2) INFORMATION FOR SEQ ID NO: 612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 913 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

TATCAGAGCA AATAAGCAAG TTAGATAAAA AGATTTCTGA CTTACAATTA ATTAGACGCT 60 CTGTATGTGA ATTTATTAAA GGACTCTCTC TAATAGATAC CAGCATTTTA AACAAGACAC 120 TACAGTCACA ATATGATAAA GAAGCATCTA TAAAATATGG TCATACGAAA GCATATCANT 180 CATTTATTAG ACGTAAAGAC AGCTTACAAT CGCAGGATAT CAGACATAAA TTGACAACTA 240 TCTTCAATAA ATTTAATCAT ATGTCTTTGA GTCATTATCC AATCCAAGAT TGTAGTGATC 300 TCGTATTTGA GTGGAAGGCA TTTATGAACA CTATCGCTGA TTTTGmTGAT GAAACATTAT 360 GCTGTATTGC TAAAACATAT GAAGATGATA CGCGTTTCAA AGATTACTTT AATTCATATG 420 ATAATCAAAA TTTAGCATCA TACATTTCAG AAGCTGTTAA TTATTTTTTG AGCAATGTGA 480 ATAAGAGCGA CAATTTTTAA TCCTCATACA GATGCTACAA CACTGAATAC ACCAACTAAA 540 ATAATTGTTC AAAGTAGAAA ACTAATCATT TATTCTCTAA ATCAATAACT ATATTAAAAG 600 TTATACCTTT GCAAAGCGAA TTAGTATAGG TTACCGAAAG GAGAAAGGAT TAGGTTCCAT 660 TCGATTTATA AAAAAATATA TTTCGAAACA TACAAAAGCG CCAGAAGATA ATCATTCCT 720

	TCAATGCATA TTCAACTAGC TCAGGTTTAC TCTTTAAGCC AAGCTTTGTC ATAATATGCG	840
	TCTTATGTGC TTCTACTGTT TTCACAGATA CAAATAATTT CTCTGCAATT tCTTTATTCC	900
5	CGTAACCTIT GGC	913
	(2) INFORMATION FOR SEQ ID NO: 613:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 654 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:	
20	ACAAGTGTTG ATGTCATAGT AGCGTCAAWT GTGCTTTATT TCTGGGACAC ATTTAAATTT	60
20	TTCCACCCA TTACTTGGAG CTTAATCTTT ATTACAATTT TACTATTATT AAACATTTTT	120
	TCTGTAAAAT CATTTGGAGA AACTGAGTTT TGGTTATCAT TGATTAAAGT GTTAACAATT	180
25	ATCGTATTCG TTATTTTTGG CTTTTTAATG ATTTTCGGTA TCTTAGGTGG TCATACATAT	240
	GGATTTGAAA ACTATACAAA AGGCCAAGCA CCGTTTGTTG GTGGTATCTC TGGTTTCTTA	300
	GGCGTATTAT TAGTCGCCGG ATTTTCGGTT GGTGGTACAG AAGTAGTAGC AGTAACTGCT	360
30	GGTGAATCAG ATGACCCTAA AAAGTCTATG CCTAAGGCAA TTAAACAAGT ATTTTGGCGT	420
	ATTCTTTTAT TCTATGTCTT ATCAATTGCA GTAATTGGTG CAATTATTCC GTACACAGAT	480
	CCATCATTAT TAAGAGCAAG TAGTTCAATA AGTCAAAGCC CATTTACAAT TGTATTCGAT	540
35	AGAGLAGGCA TAGCCTTTGC AGCATCAGTA ATCAACGCGG TTATTTTAAC TTCATTATTA	600
	TCCGCTGCAA ATTCAGGTGT TTATACAACA GGCAGAATGT TGTATTCCTT AAGT	654
	(2) INFORMATION FOR SEQ ID NO: 614:	
40 45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 642 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:	
50	TCGATCTTTA TTGATAATAA TTAAATTGTC GCCTTTAAAA TGTGATATTA ATCCTGCGGC	60
	AGGNTGTACA ACGAGTGATG AACCTAGTAC AACAAGGGTG TCAGCATGTT CAATTTTATT	120
<i>55</i>	TAATGCCCTT ATGATGGTAG GTTGATCTAA CATTTCACCG TATAATACGA TGTCCGGTCG	180
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ATAAC	SATTTA	TGACATACAT	TACAATAAAA	ACGATTTAAC	GTGCCATGTA	ATTCATCAAC	300
ATGT	IGACTT	CCAGCGTCTG	AGTGCAAACC	ATCGATATTT	TGCGTGATGA	CACCTAAAGA	360
TTGT	rgatta	CGTTCTAATT	TTGCAATCCA	ATCATGAACG	ATATTGGGCA	TCGTATCGAC	420
AAAT	AGTAAG	CGCTTATGGC	AGAAATTGAT	AAAACCTTCA	GGATCATCTT	CTAAATAATC	480
ACGG	CTTAAC	AAGTATTCTG	GCGAAAGCCC	ATCTTTTGaA	ATTTCATCAA	ATAAGCCACC	540
CATTO	Gaacgg	AAATCTGGAA	CGCCACTTGC	GACAGATACA	CCAGCACCTG	TAAAAAATGT	600
AATAG	CGATTC	GAACTATCTA	TAATATGTTT	TAGTGTCTCT	AA		642

(2) INFORMATION FOR SEQ ID NO: 615:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

Trrecedence	CCTCCAAATA	TCCAAnGGAA	CTTTAATAGT	CCAATTGGCA	CAGTAAAACT	60
ATGGCATTTT	ATAAGTATAA	TATATCTGTA	ATTTATGGTC	AATTAGTAAA	TTGTTTTTTA	120
TTTGAAACAT	ATTTCACATC	AAAATCACAA	AGACTTTTAG	ATTTTGtTCT	AAAAATCTCT	180
TAATAATTTA	TTTAATGAGA	AGAGTTGCTT	ATATAGTAAA	TTGTGAAGCC	GTTAAAACAA	240
CGTTACAAAA	CCTATATCTT	TAATACGGAA	CCATATGGTA	TGAATCAAGG	AATACTTAAA	300
CTAAAACTTC	TCTATCAGAT	TTATTTGTTG	CGAAATCAAC	AACTTTAATT	GCTTGCCCTT	360
CATTTAATGG	ATAATTTGCT	TGCGTAATTT	TAACTTTTAC	AATTTGACCT	ATGAGTGATT	420
CGTCACCTTC	AAATTGTACT	TTCATATAAT	TATCTGCATA	TCCAACTAAT	GTACCTTCTG	480
TGLCACCCTG	TTCCTCAGGA	ATTACTTCAA	GCACATCTTG	ATCAAATTTA	GACGCATATA	540
ACTTTCCGAG	TTGATTGCTT	AGCGTAATTA	ACTTATGCAC	CCGTTCATTT	TTAATTTCTT	600
CATCAATTTG	GTCATCCATT	CTTGCAGCTG	GCGTGCCAAT	TCTAGGAGAA	TAAGGGAAAA	660
CATGCAGTTC	AGAGAACTTA	TGCTTTACGA	TAAAATCATA	TGTTTCTTGG	AACTCAGCTT	720
CAGTTTCACC	TGGGAAACCA	ACAATTACAT	CACTCGTAAy	TGCCAAGTCT	GGTAAAGCTT	780
TATGCAATTT	TGTTAATCGT	TCTGAAAATC	TATCCATTGT	ATACTTACGT	CTCATACGTT	840
TTAATACTGT	ATCTGAACCA	GATTGTAATG	GAATATGCAA	ATGACGCACA	ACTITIGITG	900
AACCTTCTAA	AACGTCAATT	ACTTCATCTG	таасттсаст	TCCTTCAATT	GAAGAAATTC	960

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	CTTTTAAATC TTGACCATAT CCACCTGTAT GAATTCCCGT CAATACAATT TCCTTATATC	1080
	CTGAATTCAC TAGTTGCGTC GCTTGTTCAA CTACTTTTTC CGGATCTCTT GAACGCATTA	1140
5	AGCCACGAGC CCATGGAATA ATACAGAATG TGCAGAAGTT GTTACAACCT TCTTGAATTT	1200
	TTAATGACGC	1210
10	(2) INFORMATION FOR SEQ ID NO: 616:	
15 ⁻	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 652 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:	
20	TAATAAAATA CAATACTTTT CAATACAGAG AATCGCGCAA TGTCGGGATT CTTATTTATG	60
	CTGATTTGT TTTTGTCTAT GATCAGGGAC TTtCAGGGAC TCAATTAATT ATCACATTCA	1,20
25	TATTTTCTTA TGACCAAATT GATACATATG ATGCTATTTA ATGAGAAAAT TAGGCATCAC	180
	TTGGTTATTG AATTTCCTTC ATTAAACTTT CCAGCTCAAT TTAATAGTTA GTCGACTATT	240
	ATTCATTAAA CACTTTTTAA TCATAAAAAA GTGTTTTTGa TAATTCACTA CCAAAAACAC	300
30	CTTCTTACTT ATAATTCTAT TTGTTCACCA TTTCTAATCT TATCGGCTAA ATCATTCAGT	360
	TTTCTTAATC GGTGATTTAC ACCTGATTTT GAAATTGGAC CAGTTGATAC CATTTCTCCA	420
	AGCTCTTTCA ACGAAATTTC TTGATGTTCT ACTCGAATTC TAGCAATCTC TCTCAACCTG	480
35	TCTGGTAAAT TTTCAATACC AATTTCTTTA TCAATCAATT TAATGCTCTC AACTTGTTTC	540
	ATCGCAGCAC TAACTGTTTT ATTTAGATTG GCCGTTTCAC AATTAACGAG TCGGTTAACA	600
40	GAATTACGCA TATCTCTTAC AATACGTACG TCTTCAAATT TTAATAACGC TT	652
	(2) INFORMATION FOR SEQ ID NO: 617:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 798 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:	
	THACCACTTT AAAATAGCGC TTAATAAALG AAGGGGGCAA GTCTTATGAC GLTTTACAAT	60
	TTCATCATGG GTTTTCAAAA TGTTAACACA CCATTTGGTA TATTGGCCGA ACACGTTAGT	120

TCTAATTACA	CAGATCATCA	ATTAATTGAA	ACTACAAATA	GAGCTATTAG	CTTATATATG	240
GCAAATTAAT	TTGAGTAGTA	CCAATTATGA	TGTATTAGTG	CATCCCAAAT	ATCTTTTGTT	300
TTAAAGTTTA	TTTCATCATT	TCTTATCGAA	AATGGTGTAA	TAATGTCTTT	ATCTAACCAA	360
GTGTTGATAA	GTTCATTTGG	TACACCATCT	AACAACATTT	CACTTTTACT	AAATTATAAA	420
CATTCCCAGT	CAAGTGAAAC	ATTTTGTGGA	TTCACATAAT	TACATTGATT	ATGATTATCC	480
ATAAACACTC	ACTCCTTTAA	AATTCTGTAC	TCTTCATTGC	GTTTTACCCC	GTCACATTAT	540
CTTTTAAACT	AAAATCATCA	TTACTTATGA	AAAAAATGTA	CATCAAAAGC	AAAGGTTTTC	600
GCTACCGAAA	AAGTTTAAAT	AATGGTttAA	TATATLLGGT	ACTCATTTTA	ATAAAAAGAG	660
AATACATTTT	GAGCTATCAA	TACTTTTTAT	TGAAGAGGTG	TTATTSYTGG	CTAAAACGTT	720
ATATTTAATG	CGCCACGGAC	AAACTTTGTT	TAATTTTAAG	GGACTAATTC	AGGGATTTGG	780
AGATTCGCCG	CTAACAGA					798

(2) INFORMATION FOR SEQ ID NO: 618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

MIM	CICAA	IIGAIAAAA	IIIAAIAICI	GCCATTIGIA	IACGCAICGC	IICGAAIGII	60
TCC	STTGCAA	TATCAAATGA	TAATTGTGAC	TGGAACCTTA	AACATCGAAT	CATACGTAAA	120
GCA?	CTTCTT	GGAATCGTTC	CTCAGCTATA	CCTACAGTTC	TTATTATTCG	ATTATTAATA	180
TCT	IGTTGAC	CATCAAAATA	ATCATACAAT	TTGTATGCTG	TATCCATTGC	TATCGCATTC	240
ATC	STGAAAT	CTCGTCGTTG	CAAATCTTCG	TATAAATCAC	GAACAAATGT	AACACCÁCTT	300
GGT	CTACGGT	GATCGACATA	ATCTTCTTCA	GCCCGGAATG	TTGTCACTTC	ATAATTTECA	360
TCA:	ItAAAaa	CTACATTLAT	CGTGCCAtGT	yCTTnACCTA	CAGGTATCGT	ATGACTAAAG	420
ATA	GATTCTA	TTTCATCCGG	CGTTGCACTT	GTTGTGATAT	CTATATCATG	AATATTTCTT	480
cca	ATGACAT	AATCTCTTAC	AGAGCCACCT	ACATAATATG	CTTCAAAACC	ATTGTCTTGA	540
ATT:	IGTTCTA	ATATAGGCCT	TGCCTGTTCA	AATAATGATT	TATCCATATT	ATTACTCGCC	600
TTT	ACTTTTG	TTATGCTCAT	TTAGCATTTT	TTGATAATAA	TACTCATATT	GATCTGTAAT	660
AAG'	TTCTGAT	CCAAAACGTT	CAGCAATATC	TGCTAGCATG	TTTTTCTGAA	GTTTGTTGTA	720

ATCTACGACA	AATCCAGTTT	CACCATGTTT	AATAACCTCT	TTAATTCCAC	CGGCATTTGA	840
ACCAATTGGA	ACGACGCCTG	TWTTCATAGC	CTCAAGTAAA	GTTAGTCCAA	AGCTTTCTTT	900
TTCACTTAAT	AATAATACTA	AGTCAGATAA	TTGGTAAAAT	TCACTTACGC	AATCTTGTTT	960
CCCTAAAAAT	AAAACATCCT	CTTCTACGTT	TAACTCTTTC	GTCAATTGAC	GCATTGGCAC	1020
TAATTCAGGA	CCATCTCCAA	GTAAAATTAA	TTTACTAGGT	ATCTTTTCAC	GTACTTTTGC	1080
AAATGTTTCT	ATAATAGTAT	CTATGCGTTT	TACTTGTCTA	AAATTCGATA	CATGTATTAA	1140
CACTTTTTCA	TCTGGTGCTA	TACCAAATTG	TGATTTTAAT	GCTGTGTTAT	GTTTAGTTGG	1200
AAACTCATTT	TCACGTACAA	AATTATAAAT	CGGTATAATT	TCTTTGTTAG	TTTCAATAAT	1260
TTCATGTGTT	TCTTGTGCTA	AAGATTTACT	CACACTTGTC	ACAATATCAC	TTTTTTCAAT	1320
GCCAAATTTA	ATTGCACCTT	GGAGTGAATG	ATCATAGCCC	AAAACAGTAA	TATCAGTACC	1380
GTGTAGCGTT	GTCATAATTT	TTATATCTTT	ACCTGAGATC	TCACGAGCTA	AAATCCCACA	1440
AATTGCATGA	GGTACAGCAT	AGTGCATATG	CAACAAATCA	AGATCATATT	CTTTAATAAC	1500
TTCAGCGATT	TTAGTACTTA	ACGTAATATC	ATACGGTGGA	TACTGAAATA	CTGCATATTG	1560
ATTCACTTCA	ACTTGATGAA	AAATCATATT	CGGTAATGGT	TTTCTTATTC	TAAACGGGAT	1620
ATTTGAAGTG	ATAAAATGTA	CTTCGTGACC	TCGCTCTGCT	AATTTAATTC	CTAATTCTGT	1680
GGCAATAATT	CCAGAACCAC	CCATGGACGG	GTAACATGTT	ATACCTATCA	TCATTCGCTT	1740
GCCCATCCTT	TCTTTCTATT	TCTCnCTATG	ATNCTCGATG	CGTAGA		1786

(2) INFORMATION FOR SEQ ID NO: 619:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 844 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

ACAGGTATGG ACTTMGCTCA AATGACACGA CATTATTTAT CAAGACCTAT TGCTATAATC 60

TTTTGGATCA TTGCAGAACT AGCAATTATC GCTACAGATA TTGCTGAGGT TATTGGTAGT 120

GCTATTGCTC TTAATCTCCT ATTTAACATA CCTTTAATCG TCGGTGCACT AATAACTGTA 180

CTTGATGTAT TTTTACTACT TTTTATAATG AAATATGGTT TTAGAAAAAAT TGAAGCTATT 240

GTTGGTACAT TAATTTTCAC AGTGTTATTC ATCTTTATAT TTGAAGTCTA TATTTCATCA 300

CCACAGTTGA ATGCTGTGTT AAATGGATTT ATACCACATA GTGAAATCAT TACAAATAAC 360

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	TTACATTCAT CAATTGTACA ATCTAGAACA TACTCAAGAC ATAACAATGA AGAAAAAGCG	480
	CAAGGATTAA ATTTGCTACG ATAGATTCGA ACATTCAGTT ATCAATCGCA TTTGTAGTCA	540
5	ATTGCTTATT ATTAGTGETA GGAGCATCAC TATTTTKCAA CTCAAATGCT GACGATTTAG	600
	GTGGTTTCTA TGATTTATAT CACGCCTTAA AAACTGAACC TGTACTAGGT GCAACAATGG	660
10	GTGCAATCAT GAGTACATTA TTTGCAGTTG CATTATTAGC GTCAGGTCAA AATTCAACGA	720
.•	TTACTGGTAC TTTAGCAGGA CAAATTGTAA TGGAAGGATT TTTAAGATTA CACATACCAA	780
	ATTGGTTAAG ACGTTTAATT ACACGTTCTC TTGCTGTCAT TCCTGTTATC GTATGCTTAA	840
15	TCAT	844
	(2) INFORMATION FOR SEQ ID NO: 620:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 574 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
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25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:	
	TGTATTGCAG TCATGCCATA AATTTTTTGA ATAATAAACG GAGACGCAGA AATATAAGTA	60
30	AATAATATTA CAAATGTCAT ACCTTGGAAT GAGCATTGGT AATACAAAAC GTGGCGTCTT	120
	CANTAATATT TTGAAGTTTT TAAACATTGT CTTTAATCCA CTACTTGACT CACGATTTGT	180
	CACTGTTAAT GATTCAGGTA CTTTTAATAA AGAACCTATG ACCATGACGA AGCCAAAGAT	240
35	AGTCAGAATG ACAAAGACCA TACGCCAGAC AGAATAATTT AAAATTATGC CCCCTATTGT	300
	TGGCGCAACA ACTGGTGCAA TACCATTAAC AAGCATCAAT AATGCCATAA ACTTAGTTAG	360
40	TTCATTACCA CTATACATAT CACTTGCTAT AGCTCTTGAA ATAACTGCTG EGCGCCACCT	420
40	GTCACTCCTT GAAGAATCT TAATGCAACC ATCAGCCAAA TATTATGTAC AAAAACAATA	480
	CCTAAACTTG CTAATGTAAA AATAATCATA GCTATAATAA GCGGCTTTCT GCGCCCAGTT	540
45	GAATCTGAAA TTGGAChAGC AACCAAATTA CCAA	574
	(2) INFORMATION FOR SEQ ID NO: 621:	
50	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 523 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	

1548

(D) TOPOLOGY: linear

AAGCAAGAGA	GAGTACAACA	TTTATATGAT	ATTAAAGACT	TACATCGATA	CTACTCATCA	60
GAAAGTTTTG	AATTCAGTAA	TATTAGTGGT	AAGGTTGAAA	ATTATAACGG	TTCTAACGTT	120
GTACGCTTTA	ACCAAGAAAA	TCAAAATCAC	CAATTATTCT	TATTAGGTAA	AGATAAAGAG	180
AAATATAAAG	AAGGCATTGA	AGGCAAAGAT	GTCTTTGTGG	TAAAAGAATT	AATTGATCCA	240
AACGGTAGAT	TATCTACTGT	TGGTGGTGTG	ACTAAGAAAA	ATAACAAATC	TTCTGAAACT	300
AATACACATT	TATTTGTTAA	TAAAGTGTAT	GGCGGAAATT	TAGATGCATC	AATTGACTCA	360
TTTTCAATTA	ATAAAGAAGA	AGTTTCACTG	AAAGAACTTG	aTTTCAAAAT	TAGACAACAT	420
TTAGTTAAAA	ATTATGGTTT	ATATAAAGGT	ACGACTAAAT	ACGGTAAGaT	CACTATCAAT	480
TTGAAAGATG	GAGAAAAGCA	AGAAATTGAT	TTAGGTGATA	AAT		523

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(2) INFORMATION FOR SEQ ID NO: 622:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1871 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

AGAAGTGTGA NAAAAATTTA ANAGAGATAT GCACATAGAT GACGCATTGC TATATCCAAG	60
CAATTGAGAA AGCTGCTGAT GCTCCAAATC aCGGAATGAG GGAACCATGG AGAGTTGTGC	120 [.]
ATGTTCCGAA AGACAGATTA GGAGATATGA GTAAGGATAT TTCTAAATTT GCATTTCCTA	180
ATGAATTAGA TAAGCAACAA TGTCATTATG ATGCAGTTAC GAAACTAGGT GGCATGTTAT	240
TGCTTATTTT AAAAACAGAT CCAAGACAAC GTCAAAATGA TGAAAACTAC TTTGCATTTG	300
EGCATATGCA CAAAATCTTA TGTTGTTACT TTATGAAGCG GGAATAGGTA CATGTTGGAA	360
aTCGCCATTA TATATCTATG ATCCTAAAGT AAGNAAACAC TTGGTATAAA GNAAGATGAA	420
GTTCTTGCTG GATTCTTATA TTTAACGGAT TTAGAAGNAG ATATGCCTAA AGCACCACGT	480
AAAAATAGAA ACTTAATTAC ATTATATTAA TATGTATAAT TATAGAAACA TTAATAAAAG	540
CTGAGTCATG AATTGATGGA CATCTATCGA GTTAGAGATT TAATCTAACT TACTAGAGTC	600
GGTACAATAA CAGTCTCAGC TTTTTATTGT GCAGTATATA CACATTTTTA TTTTAGTATT	660
TATTLAAAAG TTLCTGCTAA AAATGATTCA ACTTGTTCAG GTGACTTAGC ATTTGCTGAA	720
TGAAGGTGTG CAATTTTATC GCCGTTTTTA AATACTAGCA AGCTAGGGAT ACCCATAACT	780
TCATTTCAA CAACTACATC TTCTAATTCA TCACGATTAA CAGTATACCA TTGGTAATCA	840

	CCTGCCTCAA	ATTTAACAAT	TACAGGTGTA	TCGCTATTAA	TTACAGATTT	AAATGATTCA	960
_	TTACTTTTGA	TTGATTGCAT	TGTAACAACT	CCTCTAGATA	GTTTAATAAT	TTTTATTATA	1020
5	GCTAAATTTA	TATCATAATA	AAAAATTTTA	GCTTCAAAAT	GAAAGCCTTT	TGCTTTGGAA	1080
	AATGATATAT	TTATTTTAAA	TACATAAAGG	AGGTTGCAGT	CGTATGATTA	AATTTTACCA	1140
10	ATATAAGAAT	TGTACAACTT	GTAAAAAGGC	AGCAAAGTTT	TTAGATGAAT	aTGGCGTAAG	1200
	TTATGAACCA	ATTGATATCG	TTCAACATAC	ACCTACAATA	AATGAATTTA	AAACAATAAT	1260
	TGCAAATACA	GGCGTAGAAA	TTAATAAATT	GTTTAATACA	CACGGCGCGA	AATATCGTGA	1320
15	GCTTGATTTG	AAAAATAAAT	TACAAACTTT	ATCAGATGAT	GAAAAGTTAG	AGTTGTTATC	1380
	ATCTGATGGT	ATGTTAGTAA	AGCGTCCTCT	AGCAGTAATG	GGCGATAAGA	TAACATTAGG	1440
	ATTTAAAGAA	GATCAATATA	AAGAGACTTG	GTTAGCGTAA	GTGaAATGTA	AGCGTTTACT	1500
20	AAATATCTCG	ATATTTAGAT	TCATTACATG	TAAAATGAAA	TAAGCTATAC	AATTGTTAAT	1560
	TTTTATAAAT	ATAGTTGAAT	AGCATCTAGC	CTTATGGCAT	CATTAATGAT	GTAAAGATTA	1620
25	ATTAGGAGGG	GATTCTCTTG	GCAGTACCAA	ATGAAYTGAA	ATATTCAAAA	GAGCATGAAT	1680
	GGGTTAAAGT	TGAAGGTAAT	GTAGCAATAA	TTGGAATCAC	AGAATACGCA	CAAAGCGAGT	1740
	TAGGTGATAT	TGTTTTCGTT	GAATTACCAG	AAACAGATGA	TGAAATTAAT	GAAGGGGATA	1800
30	CGTTTGGTAG	CGTAGAATCA	GTTAAAACTG	TATCAGAATI	ATATGCACCA	ATCTCTGGTA	1860
	AAGTAGTTnA	. A				·	1871

(2) INFORMATION FOR SEQ ID NO: 623:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

TTGCTGTAGA AGATAAAGAG TCCCATCAAT GGATAGGCTT TATAGGTTTG AATTATATTC 60 CAGAAACAAG CGATTATCCA TTTAAAGAAT TACCGCTTTA TGAAATAGGT TGGCGCTTGT 120 TGCCAGAATT TTGGGGAAAA GGATTAGCAA CTGAAGGCGC AAAGGCAACA TTGAAGTTAG 180 CAGAAGAACA TCAAATATAC GATGTCTATA GTTTTACAGC AGAAGCAAAT AAAGCTTCAC 240 AACGTGTAAT GGAAAAAATT GGCATGACAG TGTATGATCA TTTCGAATTA CCCAATCTAA 300 GTAAGTATCA TTTATTAAAA AGGCAAGTGC GCTATTACAT TAATCTTCCG AAAGTGGAAA 360

	ATTAGGGGT GtTTnGTkTn ATTTTTTAA n	451
	(2) INFORMATION FOR SEQ ID NO: 624:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 665 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:	
15	CGATAGTTAT CTAAAGCCAT TTTnGATTGT GTTATGAAAT CTAATGATGC GTGATAATTT	60
	AATGCTACAT AACGTTAATA TAAAATATCA ATAGTGAACA TTTGAGCAAA TAATGAAGTT	120
	GTTGCTCCCA TATGCATCTC ATTTTCATCA GTTTTCCCAT AAGTTAAAAC AATATTTGAT	180
20	GCCTGTGCTA CGGGATTATC CCTTGTACTA GTAATTGTAA TTATAGGTAT ATGGTAGTCA	240
	TCAATAACTT TAACCATTGA TTGCATTTCA CTTTGCGTAC CATTGTTAGT AATAAGAATA	300
	aCACTGTCGT TCGAATTGTG AGTTGCTAAT AATGTAGCAA AAATATGTGT TTCTTGAACA	360
25	AGTTGAATAT TAAGACCTAT TCTTGATAAC TTTTGGTATA AGTCGGTAGC AACTACAAAA	420
	GATGCGCCAA AACCATATAT AAAAATCGTC TCAGAACGTT TTAAACAATG ACATATTTGA	480
30	TCAATAGTTT TATCATTTAA TTCGTTATTT GCATGATTAA GTGCGCGTGT AGTACGTGTA	540
	TGGAGTTTAG TTCTTAAAGA TTCTGTGCTT TCGTTATTCA TTAATTCAAC ATTGTAAATT	600
	GATGATGCTT TAGGAACATA TTTAGATATA TTTATTTTCA AGTCGTGAAA ACCGCCATCA	660
35	GTAAT	665
	(2) INFORMATION FOR SEQ ID NO: 625:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2549 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:	
	GATGCCAATT AACCGTGCAT ATAATGTTGA GAAGTTAATC GAAGCAATTC AATATTATCA	60
50	AGAAAAACA AATCGTCGTG TTACTTTTGA ATATGGTCTG TTTGGTGGTG TGAATGACCA	120
	ACTAGAACAT GCAAGAGAAT TAGCACATTT AWTAAAAGGC TTAAACTGCC ATGTTAACTT	180
	AATTCCLGTC AACCATGTTC CAGAAAGAAA TTATGTGAAA ACGGCTAAAA ATGATATCTT	240

	TTCGGATATT	GACGCAGCTT	GTGGTCAATT	AAGAGCAAAG	GAACGACAAG	TAGAAACGAG	360
	GTAAAGACAA	ATGCTAGAGG	CACAATTTTT	TACTGATACT	GGACAACATA	GAGATAAGAA	420
5	TGAAGATGCG	GGTGGTATTT	TTTATAATCA	AACTAATCAA	CAACTTTTAG	TTCTGTGTGA	480
	TGGTATGGGT	GGCCATAAAG	CAGGAGAAGT	TGCAAGTAAA	TTTGTTACAG	ATGAGTTGAA	540
	ATCYCGTTTT	GAAGCGGAAA	ATCTTATAGA	ACAACATCAA	GCTGAAAATT	GGTTGCGTAA	600
10	ТААТАТАААА	GATATAAATT	TTCAGTTATA	TCACTATGCA	CAAGAAAATG	CAGAATATAA	660
	AGGTATGGGT	ACAACATGTG	TTTGTGCACT	TGTTTTTGAA	AAATCAGTTG	TGATAGCAAA	720
15	TGTCGGTGAT	TCTAGAGCCT	ATGTTATTAA	TAGTCGACAA	ATTGAACAAA	TTACTAGTGA	780
	TCACTCATTT	GTTAATCATC	TTGTTTTAAC	GGGTCAAATT	ACGCCGGAAG	AAGCATTTAC	840
	ACATCCACAA	CGTAATATTA	TTACGAAGGT	GATGGGCACA	GATAAACGTG	TGAGTCCAGA	900
20	TTTGTTTATT	AAGCGATTAA	ATTTTTATGA	TTATTTATTA	TTAAATTCAG	ATGGATTAAC	960
	TGATTATGTT	AAAGACAATG	AAATTAAGCG	TTTGTTAGTA	AAAGAAGGTA	CAATAGAAGA	1020
	TCATGGTGAT	CAATTAATGC	AATTGGCATT	AGATAACCAT	TCGAAAGATA	ACGTTACTTT	1080
25	CATACTCGCG	GCTATTGAAG	GTGATAAAGT	ATGATAGGTA	AAATAATAAA	TGAACGATAT	1140
	AAAATTGTAG	ATAAGCTTGG	CGGCGGTGGC	ATGAGTACCG	TTTATCTTGC	TGAAGATACG	1200
30	ATACTTAACA	TTAAAGTTGC	AATTAAGGCG	ATTTTTATAC	CACCTAGAGA	AAAAGAAGAA	1260
	ACATTAAAAC	GTTTTGAACG	AGAAGTACAT	AACTCATCAC	AGCTATCACA	TCAAAATATA	1320
	GTAAGTATGA	TCGATGTTGA	TGAAGAAGAT	GACTGTTACT	ACTTAGTAAT	GGAATATATC	1380
35	GAAGGTCCGA	CTTTGTCTGA	GTATATTGAA	AGTCATGGGC	CATTAAGTGT	TGACACAGCG	1440
	ATTAATTTTA	CGAATCAAAT	ATTGGATGGC	ATTAAACATG	CGCATGATAT	GCGTATTGTA	1500
	CATAGAGATA	TTAAGCCACA	AAATATATTA	ATTGACAGCA	ATAAAACGTT	GAAAATATTT	1560
40	GATTTTGGAA	TTGCTAAAGC	TTTAAGTGAG	ACGTCTTTAA	CTCAGACTAA	TCATGTGTTA	1620
	GGTACTGTGC	AGTACTTTTC	GCCAGAACAA	GCAAAAGGTG	AGGCAACGGA	TGAATGTACA	1680
45	GATATTTATT	CTATAGGTAT	kGTGTTATAT	GAAaTGCTTG	TTGGTGAACC	ACCCTTTAAT	1740
43	GGAGAAACTG	CAGTTAGCAT	TGCGATTAAA	CATATTCAGG	ATTCTGTGCC	AAATGTGACA	1800
	ACAGATGTAC	GTAAGGATAT	TCCGCAATCT	TTAAGTAATG	TCATTTTACG	CGCTACAGAA	1860
50	AAAGACnAAG	CGAATCGTTA	CAAAACAATT	CAAGAAATGA	AAGATGATTT	GAGTAGTGTT	1920
	TTACATGAAA	ATCGAGCGAA	TGAAGATGTC	TATGAACTCG	ATAAAATGAA	AACGATAGCG	1980
	GTACCTTTGA	AAAAAGAAGA	TCTAGCAAAG	CATATTAGTG	AACATAAGTC	GAATCAACCT	2040

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AGCCAGAAGG	TACGGTGTAC	GAACCAAAAC	CTAAAAAGAA	ATCAACACGA	AAGATTGTGC	2160
TCTTATCACT	AATCTTTTCG	TTGTTAATGA	TTGCACTTGT	TTCTTTTGTG	GCAATGGCAA	2220
TGTTTGGTAA	TAAATACGAA	GAGaCACCTG	ATGTAATCGG	GAAATCTGTA	AAAGAAGCAG	2280
AGCAAATATT	CAATAAAAAC	AACCTGAAAT	TGGGTAAAAT	TTCTAGAAGT	TATAGTGATA	2340
AATATCCTGA	AAATGAAATT	ATTAAGACAA	CTCCTAATAC	TGGTGAACGT	GTTGAACGTG	2400
GTGACAGTGT	TGATGTTGTT	ATATCAAAGG	GCCCTGAAAA	GGTTAAAATG	CCAAATGTCA	2460
TTGGTTTACC	·TAAGGAGGAA	GCCTTGCAGA	AATTAAAATC	GTTAGGTCTT	AAAGATGTTA	2520
CGATTGAAAA	AGTATATAAT	AATCAAGCG				2549

(2) INFORMATION FOR SEQ ID NO: 626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

TGCTTACTTC	GCCTTCAATA	CGTACTAATT	CATGTCCACA	ACTTGGACAA	TGGGTTGGCA	60
TATGATATGT	GACAGCATCC	TCAGGTCTAC	GTTCTGGAAT	ACTACGTACA	ACTTCAGGTA	120
TGATGTCACC	TGCTTTTTTC	ACTACAACAC	TATCACCAAT	TCGAATATCT	CTGTCATGAA	180
TTAAATCCTC	ATTGTGCAAA	GATGCTCTTG	aTACAGTTGT	ACCAGCTACT	TTTACTGGTT	240
CTAAAATAGC	AGTAGGTGTG	ACTACACCTG	TTCGTCCAAT	ACTTAATTCA	ATATCTAATA	300
ATTTAGTTAC	TACTTCCTCA	GCTGGAAATT	TATAAGCAAT	GGCCCATCTA	GGAGATTTTT	360
GTGTGAATCC	CATCTCATCC	TGTTGATCTA	AATCATTAAC	CTTAATAACA	ATCCCATCAA	420
TATCATAAGG	TAATGACTCT	CTTTGGCTTG	TCCATTTTTC	AATATACTCT	AAAACACCAT	480
CGATATTATT	TACACGCGCT	CTATTTTTAT	TCGTTGTAAA	ACCTAATTTA	TCTAACTCAT	540
CTAATGCTTC	ACTTTGCGAA	CGCGCATTGA	AATCAGTGAA	ATCATTGACA	СТАТАТАТАА	600
ATACGCTTAG	CTTTCGTTTT	GCCGTTAATT	TAGAATCTAA	CTGTCTTAAT	GATCCCGCAG	660
CAGCGTTTCT	TGGATTnGCA	AATAACTGCT	CATCATTTTT	TTCTTTTCT	TCATTTAATC	720
GTAAAAATGA	ACGTCTCGGC	ATATATGCTT	CACCACGAAC	TTCTACATTT	AATGGETCTT	780
TCATTTTCAA	AGGTATCGCA	TGAATTGTTI	TTAAATTTTC	GGTAATATCI	TCACCTGTTG	840
TTCCATCACC	ACGTGTTAAA	CCTTGaACGA	AGTATCCATC	AACATATTTC	AATGATACTG	900

	GIIGGICGAA	TTTTCTCAAA	TCATCCTCAT	TAAATGCATT	CCCTAAACTT	AACATTGGCG	1020
						ACTGTTGGAG	1080
5						TGAAGTAATT	1140
						TAACTGTATT	1200
10				GAGACGATAA			1260
	CCTTTTTTEC	AATTGGTGCA	AATTGCGCTA	ACAAACGTTT	TGGCCCTTGT	GATTTAAAGA	1320
				CGTTTACATT			1380
15				TCCAATCAGA			1440
				TAGCAAAAGG			1500
				ATAGTGATTC			1560
20				ATAACATTCT			1620
				CATAACAAAT			1680
25				TATGTGGGAA			1740
				TAGCCGAGTG			1800
				CTACTAACGA			1860
30				CCTCATAGTC			1920
				CTAATGTATT	•	•	1980
				CTATTTCATG			2040
35				AATTAAGACA			2100
	aCAATCCGAT	AAAATCAGCT	TCTCCAAGTG	CATCAAACAT	ACTGATATTG	TTTTGAAGTG	2160
40				GACCTACACC			2220
40	TACGTTGCAA	ACTAATGTCA	TCATTACTAT	TGGCAATTAT	ACGCAAATAA	CTTAATAAAT	2280
	CTTTGA						2286

(2) INFORMATION FOR SEQ ID NO: 627:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

	TGACATTAAA AGTTGGGTGA ANAAACAAGG CATACTTTAG TTAAGCTTGA TGAAAATAAC	120
	AATGGAATTA ATGCGATTAT TCAAAAAGAA AAAGCAAAAG ATTTAGATAT AAATTATTCT	180
5	GCTAAAGGTA CTACCAATTG TATTATTTAG TGGAGAATTA GACAAGCTGT AGCAGCGTTG	240
	ATTATTGCCA ATGGTGCTAG AGCTGCTGGA AAAGATGTAA CTACCTCCTT ACTTTTTGGG	300
	GGCTTATGCC nTTAAAAAAG TGCCACCGTT AATGTTAAAA GCAGTTGCCA AAATGTTTGA	360
10	TTMATGTTGC CCCAAAAGAT TTACGATGCC CCTTCCCAAA	400
	(2) INFORMATION FOR SEQ ID NO: 628:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 453 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:	
	AATAATTTGG GCGCTnTTTG CGTCGGGATA TTATACCGCT TCCTTAATTG TTCAACATTG	60
25	TAATCACTGT TTTTCAATTG ATATTTTGCA GAGTAAATTG GTACTTCTGG GTTATATGAC	120
	ACTTCGTCCT CTTTATAGTT TTCCAATTCT TTGAAATTCC CGTATTGTAC AAAGAAGTTA	180
30	AATTCTTCGA TTTCTTTTTT TACTTTTTCG TCATCGATTG GTTTTAATGG AATCATTTTA	240
	TTAKTTTCCA TTTTCACAGG ATATCTTTTT GTATGATTGT GTGTCATTCC ATCGCTATCT	300
	TCAACAACTT CTCTAACAAT ATAATGCCCT TTAGCCGTTC TAGTATTTCT GTTAATTTCT	360
35	AAAACTGCTC CTCTrGATTC CAGATTTTCT CCTTTTAATT GGATTTTCAT TTCAGATCTA	420
	ATTAGECAAG TACCTTTATC ATCTETTTTA AAT	453
	(2) INFORMATION FOR SEQ ID NO: 629:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1221 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:	
50	TCATATGCAT TTGCAAAATA AACGCCAGAA GCAAGGTTTA GAATTGGGCC GTCCGTTTTG	60
- -	CTCARTTCAC TTGCATTCAA TAATTCATGC TGATCATGAT CAATTTGCTT ATCTAATTCT	120
	GCAATTITCT TCATTTGCTT ATCTGATTTG TTTTCTTTCG CCATCATTTG ATCACGACGA	180
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	GCTAATGGTA	CTAATACTTT	ATCTCCATAT	GTGTCAATAA	AGTTATAAAA	ATAATCATCT	300
	GTTTTTGATA	CAAATCCAGC	ACGCTCTTCA	GTTTCACGAT	ATAAATCTAA	GAAAAGATTG	360
5	AACTCATCAC	GTTCAAGGAA	TCTGACTTTA	ACACCATAGT	TTATCGCTTT	ATTAATATTA	420
	CGTTTACGTT	GACTATCAAA	TGTCTTTTTC	AATGTTTCGG	GTGTTTTACC	TTCAAGGTTT	480
10	AATACGCCCA	TCCATCGTAC	TTGGCTCGAT	GTATCATACT	CAGTTGTAAA	GCCATGATGC	540
	TCGTAACCAT	GTGATTTAAA	CAAGTTTACT	AGGGCATCAT	TTTTCTCGCG	ACCTTCAAAT	600
	GGCACGATAT	CTTTATCATA	TAGATGATAT	AACCAATACG	GATCTAATTT	AACATATAAA	660
15	CATTGATGTT	GCTGTAAATA	TTTATCTAAC	TCTTTTAAAT	AATAATCAAC	TAATCCTAAA	720
	TCTGAAAAAT	CCATTACTGG	ACCACGATTC	GAATAGTAAA	CATAACTTCC	CATAGTAGGA	780
	ATTTTAGAGA	AAAGGCTTGC	TGCAATTACT	TTGTTATTGT	CGTCTTTAAT	ACCTAATAAA	840
20	ACTACTTCAA	AGCCATCATT	CTCACGGGTA	ACTATATTT	CTTTTACTTG	GAAATAATGA	900
	CTTTCCAATG	ATGGATTTTG	TACAAAGTTG	TCAAATTCGG	TAACAGTTAA	CTCTGTAAAT	960
	TTCATGTTTT	GATAATTCCt	TCCTAAAAAA	TTCTGTCTTT	AACTTTTTTA	AGTGCGGTAT	1020
25	ATGCTGCGTA	AACAGGTTTA	TTAATTGGTT	TAATAAAGTC	ACCAACATAT	TCmATAATTT	1080
	CAGCATTGTA	ACCTTTTTTG	AATTTAACTA	CACCAGCATC	TTCAGCATCT	TCTGTAAATT	1140
30	Trccactaac	ACCATAGAAA	TTATAACGGT	CAATGCATGA	TTTAATGCAT	AATTAATCAT	1200
	TTCCCATTGC	ACTGCATAAC	т				1221

(2) INFORMATION FOR SEQ ID NO: 630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

TGGCCCAANT AACACAAGTA ATTGCTGCTA ATGGTAACAT CACAAAAAAT GAAATCGTAA 60
CTACAAATGT TAAACCTTGG AATACACCAA CCATTTCTGG TAATCGTTTA CTATAGTATC 120
TATTGTGAAT CCAAGTAATA ATAGCTGAAA TAATAATACC ACCTAGAATA TTCGTATCCA 180
ATGTGGCAAT ACCTGCAATT GATTTTAAAC CAGGTACATT TTCAACGCCT TTTTCTAAAT 240
TAGCGCCAAA CGTATGTGGC CATTGTGTTA AAATGGCATT TATAAATGTA TTAAACATTA 300
AGTAACCCAT CAATGCTGCA AGTGCTGCAT GACCTGGTGC TTTTTTAGCT AAAGAAAGTG 360

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Lord Caller . T. C.

TT	ACTGACCA	AAATTTAAAC	CAAAACGTAT	GTTGATCTGC	TAAACTCCCC	ATGATTGTAG	480
GA:	AAATTTT	TAATGTCGCA	AAGCCAAGCA	CTATCCCAAA	GAAAGCGAAC	ATTAATACCG	540
GT	ACAATCAT	TGCACTACCG	AAACGCTTTA	TCGCATTCAT	CTTCTATTCC	CTCCATATCA	600
TC	ITTCCTAA	CAATACATCT	AATTAGATTC	ATTTATAAAT	AGATGTCTTA	CTATTTAAAT	660
AT	ATATATA	GTAAACGCTT	ACACACCTAC	AACGACATTG	ACGTATTTTG	AAAGTATTTT	720
GT	ATAATCAG	ATTATCTTTT	CATATAGTGA	AAATTTTTTC	ACGACCTTAT	ATATGACATC	780
GT	TGTATTTG	TAATACATTC	GTTTTAAACG	CATAATCAAA	CCTATATCAA	TACACAAATA	840
TA'	TATAATGA	CATACAAGAT	TTTAATGTAA	TAACGATCTA	TTACACATTT	ATTTTCAAGG	900
AG	GTTGAATA	TGTTTTTAGA	TGAACACATT	AATCGAAACT	TTGATAAACT	TAATGATAAT	960
GA'	TTTACATA	TCGCTCACTT	TATCAATACA	CATATAGATG	AATGTAAAAA	TATGAAAATA	1020
CA	AGATTTA G	CGCAATTCAC	ACATGCCTCG	AATGCAACCA	TTCACAGATT	TACACGCAAA	1080
Tn	AGGTT TTG	ACGGTnATAG	TGGATŤŤĀAA	TCGTACCTTA	A		1121

(2) INFORMATION FOR SEQ ID NO: 631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4005 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

AACCTTCCAT TTTACTTGAT CGATAACATC AGTTCTGCTT TACAAATCTC TTCATTAATA 60 TGCGTCTTAA AACCATGAAA TTTAACATGT TCCGATAAAT GATAATCTTC TACAAGTTGT 120 CGATATTCTG ACAAACCATT TCCATGTCCA TAAATATTCA ATTGAATATT GGGATGTTTT 180 GTTACTAATT GCTTGATTAC TTCAATTTGA TGTTTAATTT GTTTATTTTC AACGAGGCGA 240 GCAATTGATA TGATATGATT TTTCTCCTTT TGATTGATGT CAAATTGATA CTTTAAATTT 300 GCCACGTAGC CAACCGGAAT ATTGATAACT GGTATTTTAT TTTCAATATA TTGTGAAATA 360 420 TCTTGGCATT GCTTTTCTGT TGATACAACA ATCGCTTTAT AACGTGTTAA ATTATTAAAC ACTGTTTTAT AAAAACTTTT TATACCATTA CCGGCACCGG ATAAATGTGT ACTATGGAGC 480 ACAACAATAA CTGGAATACT TTGATTTAAT CCCGCTATAA CATTTCCTAA TTCATGAGGA 540 CGATCTAATA TGATTTGATC ATTATTTTTA CATAATTGAT GGAGAAAATA TTGAACTAAT 600 TCATCTTCTG TATCAAAAA TTGTTGATGC TGGTCTTCAT TTAAGATAAC CTTTGTGAGC 660

	TAGTAATTTT	CGAGTACAAT	CCGTTGTCCT	TCACCTAAAA	TTCGAGAACA	ACTTAAAAAG	780
_	CCTCTTCCAT	CATACAATTC	GCGTTTTACT	TTTCTTCTTT	TATGATCAAA	ATAATTCACA	840
5	TAATTTAATT	GATGATACTG	TTTATCTAAA	AAATGAGCAT	ACATTACAAA	TTGCTCTTCA	900
	TCATATATTC	TGACATCATT	TGAATTTTCC	ACAAATTTCA	ATGTGTACCT	ACATGACTTT	960
10	TCCCAATACT	GTATCCAGTT	AACTTGCTTT	GTCTTTTTAT	AATTGATTGC	TTTTTGAAAA	1020
	TAGTCATACA	TTGTAAATAC	ATCATTTTCA	ATCTGATGTT	GCTTCGCATA	TGTGTATGAA	1080
	TAAGGATTCC	ATTTAACATA	TACACATTTT	GAAGATATGC	CGTGTTGTTT	GAACAACTTC	1140
15	AATCTATTTA	TTTGCGCTTT	TTCTACACCT	GTAATTTTAC	TTTCTAAAAT	TGTTCCTAĄA	1200
	ATGTAATTCA	TATTATCGCC	TCATATAAGT	TTTATTCCGT	ATCTTTATTG	TTTATTTTAT	1260
	ATGAAAAATA	CATCTATTGC	ATGTGTAATT	ATAAAAAAAC	CAGGCCACAA	GGACCTGGGT	1320
20	CATATTGTAT	TATTTGTTTT	GTTTTTTGCG	ACGACCGAAT	AACAATAATG	AACCTAATGC	1380
	TGCAAATAAT	CCACCAAATA	ACGTTGCGTT	ATTTGAGCCG	TTATTTTCAC	TACCTGTTTC	1440
	TGGTAATGCT	TTTGCTTTAT	TGTGATGGTC	TTTAGTAGTA	CTCATTGGTT	TAACAGGTGT	1500
25	ATGTTTTCCT	GCATCCGAGT	CTGAATCGCT	GTCTGAATCA	CTGTCTGAGT	CTGAGTCGCT	1560
	ATCAGAGTCT	GAGTCGCTGT	CCGAATCTGA	GTCGCTATCT	GAGTCTGAGT	CGCTGTCTGA	1620
30	ATCTGAATCA	CTGTCTGAGT	CTGAGTCGCT	ATCTGAGTCT	GAATCGCTGT	CTGAATCTGA	1680
	GTCGCTATCT	GAGTCTGAAT	CGCTGTCTGA	ATCTGAGTCG	CTATCTGAGT	CCGAATCGCT	1740
	ATCTGAATCT	GAGTCGCTGT	CTGAGTCTGA	GTCGCTATCT	GAGTCTGAAT	CGCTGTCTGA	1800
35	GTCCGAATCG	CTATCTGAAT	CTGAGTCGCT	GTCTGAGTCT	GAATCGCTAT	CTGAATCTGA	1860
	GTCGCTATCT	GAGTCTGAAT	CGCTGTCCGA	ATCTGAGTCG	CTATCTGAAT	CTGAGTCGCT	1920
	GTCTGAATCT	GAATCACTGT	CTGAGTCTGA	GTCGCTGTCT	GAGTCTGAGT	CGCTGTCTGA	1980
40	GTCACTATCT	GAGTCTGAAT	CGCTGTCTGA	TGTATCTTCT	TCGAAGTATC	CGTTATCAAG	2040
	TGTGAAATCA	TCATGATCCG	TAATTGTTAC	GTCAACTTCG	CCACCATCTG	CATCTTTATC	2100
45	ATCTTCAGTT	GTATTTGTAA	CTGTTTGTGT	TAAGCCAGCA	GGCTTTTCAA	AAATAACTTT	2160
45	GTATTTACCG	CTATCTAAAT	TATCAAAGCA	GTATTTACCA	TTTTCATCTG	TTTTAGTTGT	2220
	TCCAATTACT	TCGCCTTTTT	CATTTAATAA	AGTAACTTTA	ACATCTTTGA	TACCTTTTTC	2280
50	AGTTGAATCT	TGTTTGCCGT	CTTTATTACT	GTCGTACCAA	ACATAATCAC	CTAAACTATA	2340
	TTTTGGTGTT	TTATAGAAAC	CACTGTCTAA	TGTCATGTTA	TCTGCATCTT	TAATGACACC	2400
	TGTTGTTGTT	AAACCATTAG	AATCTTTTTC	AGTATCATTT	CCAGAAGTTA	CTGAAGTTGG	2460

AND THE CONTRACTOR

	TTGATATTTA	CCATTTTCAT	CTGTTGTAAC	TGTTTTTAAA	ACTITGTCGT	TTTCATCTTT	2580
	TAACGTAACT	GTTACACCTG	AAATGCCCTT	TTCATCTTTA	TCTTGAACAC	CGTTTTTATT	2640
5	TGTATCTTCC	CATACATAGT	CACCTAAGTT	GTAAGTCGGT	TTGTAGAAAC	CAGAGTCAAT	2700
	AGTATCGTTA	TCTTTATCTT	TAATGACACC	TGTTGTTGAT	GTACCATTIG	AATCTATACC	2760
10	TTCATCAGTT	CCTGAACCTA	CTTGTGTTGG	TGTGTAACCT	GATGGTGTTT	CGAATTCAAC	2820
10	TTTATAAGTT	CCATTTTCTA	ATCCAGTAAA	TTGATATTTA	CCATCTTTAT	CTGTTTTAGT	2880
	TGTTTGTAAA	ACTTCACCGT	TTTCATTTTT	CAATGTAACT	GTTACGCCTG	AAATACCTTT	2940
15	TTCAGTTGAA	TCCTGCTTAC	CATCTTTATT	TGTATCTTCC	CATACATAAT	TACCTAAATT	3000
	ATATTTTGGT	GTTTTGTAGA	ATCCACTATC	TAATGTCATG	TTATCAGCAC	CATTAATAAC	3060
	ACCTGTTGTT	GTTAAACCAT	TAGAGTCTTT	TTCAATGTCG	CTACCAGATG	TTACTGTAGT	3120
20	CGGTGTATAG	CCTTCTGGTG	TAGTAAATTC	AACTTTATAA	TTACCATTAT	CTAAATCAGT	3180
	TATATTTAAA	TTGCCATCAG	CGTCTGTTGT	AACTGTTTTT	AaCAgTTACC	GTTTTCATCT	3240
	TTTAATGTTA	CCGTTACGCC	AGATATACCT	TTTTCATCTT	GGTCTTGGAT	ACCATTTTTA	3300
25	TITGTATCTT	CCCAGACATA	GTCACCTAAG	TTGTATTTAG	GTTTGTAAAT	ACCTAAGTCT	3360
	GCAGATAAGT	TATCTTTGCC	ATTAACTGTA	ATAACTGAAG	ATAAGCCGTT	TGAATCTAAT	3420
30	TCTTCGTTAT	TACCTTGTTT	TGAAGGGGTT	ACTTCATAAC	CTTTTGGTAA	GTTTGAAAAT	3480
30	TCTACACGGT	AATCTCCATT	AGGTAAGTTT	GGAATCAAGT	ATGACCCATC	TTCTTTAGTA	3540
	ACTGCTTCTC	CTACTTTTGT	ATTTGTATTA	TTATCAAATA	CAGTTACAGT	TACATTGCCA	3600
35	ACGCCTTTTT	CTCCTAATTC	TTGAACACCG	TTTTTATTAG	TATCTTCCCA	TACGTAGTTA	3660
	CCAATTTTAT	ATACTTCTTG	ACCAGCTCCG	CCACTTTGGT	TATTAGTAAA	TCCTAAAGCA	3720
	TTGCCAGTAG	AAACGGATTT	ATTACCTGTT	GAAGATAAAG	TAGCCATTTG	AACAAGTGTT	3780
40	GGGCTTTCGC	TATTTGTATA	TTGGAATTTT	GTATTAACCA	TTACAACATA	AGCAGAATCT	3840
	GCATTTCCAA	AATCAATAAC	AGCGCTATTG	TEGTCGCCAT	ATGTAATTTT	CTGCAAGTAT	3900
	TGATTTGTTA	CATCTGTAAG	CTCTTTAGTA	TTCACATCGT	ATCCTTTATI	TAATGTATAA	3960
45	CCTTTAGGAA	CTTGATATAT	TTTTATATCT	GTTACATCTT	TATTT		4009

(2) INFORMATION FOR SEQ ID NO: 632:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

	TATTAGGTTA	CTCTAGTTTC	CAAAGCGGGA	ATTTTAATGT	TATTAACAGC	AAGGACAGCA	60
5	AAAGCAATAT	CGGCGCATTG	ATTGAAAATC	CAGGAATATA	TCCTTTTATG	TCTGGATATG	120
	AAAACTTGAA	GTTATTGAAT	GAATCAAAAA	ACACTCAAGA	TATCGATAAA	ATTGTCTCAC	180
10	AACTTCATAT	GGATGAATAC	ATTCATAAAA	AAGCTAAAAC	GTATTCTCTT	GGTATGAAAC	240
	AAAAATTAGG	AATTGCTATA	GCATTTTTAA	ATAAACCTCA	ATTCATTATC	TTAGATGAAC	300
	CAATGAATGG	CTTAGATCCA	AAAGCTGTGC	GAGATGTACG	TGAATTGATT	GTCCAAAAAG	360
15	CGCAAGAAGG	TGTTACTTTC	TTAATTTCGA	GTCATATTTT	AAGTGAATTA	GTTAAAATCA	420
	CAAACTCTAT	CCTTATTATT	AACAAAGGTA	AAATTGTTAC	AGAAACATCG	GAAGAAGAAC	480
	TTAAACAATT	TAAAGATAAT	GATTTAGAAA	ATGTATTACT	AGAAATCATA	GAAAGGGAGG	540
20	ACCAAGCATA	AAATGGGAAC	AAATTAATTT	CAAGAATGTT	TCAAATTATT	TAAAAAGAAA	600
	TCAACTTTTA	TCGCACCTAT	TGTCTTTATT	CTACTAATGG	TTGCTCAAGG	TTATATTGCT	660
	ACAAAATACA	ATGAAATTTT	TACGCCACAG	GAATCTTTCA	CATCTGCTTA	TAATGGTTTT	720
25	TCATGGTTTG	CATTTTTATT	AATTATTCAA	GCAAGTACAA	TCATTTCAAT	GGAATTTCAT	780
	TACGGTACGA	TTAAAAATTT	ACTCTATCGT	GAATATTCAA	GAACAACTAT	GATTGTTAGC	840
30	AAAATCATCA	CATTATTTAT	TATTTCTTTA	ATTTATTTTG	TTATTACAAT	TATTGCTTCA	900
	ATTGTTATTG	GGTCTTTATT	CTTTAATGAT	TAAATATAT	TTGAAAGTAG	CGGTAATCAA	960
	TTATCTTTAT	TGAATCAATT	ATTATTAGTT	AGTTTAGGCA	CATTTGTTGG	CGTTTGGTTA	1020
35	GTTTTAAGCT	TAACGTTGCT	ATTATCATCT	GCAACAAATT	CAACGGGAGT	AGCCATTGCT	1080
	GTAGGTATTG	TTTTTTATTT	TGCAAGTTCT	ATTTTAGCAG	TTATTCAAAC	GGCACTTTTA	1140
	GAAAAAATAG	ACTGGCTAAA	GTGGAATCCT	ATTAATATGA	TGAATATTAT	GCTTCAAACA	1200
40	GTTGAAAAAG	GCTTTAGTAA	GTCGACAAAA	TTAGAACTTC	ATGAATTGTT	TATTGGTAAT	1260
	ATTGCTTATA	TTTCTATTTT	CTTAATACTT	GTAGTATTTA	TTTTCAAGAA	GAAAAATATT	1320
	TAGTAACTTA	AAGTATTAAA	TGTCTAAATA	A CACACATATT	CCATCGTAAT	TCAAAATCAT	1380
45	TTTCAAATCC	CTTCACCCAA	ATAATGGTG	GGGGATTTT	TCATCCAAA	TTTGGAAATT	1440

(2) INFORMATION FOR SEQ ID NO: 633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1323 base pairs(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:	633:
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	GCTGACATAA	TTGCATCAAA	TTTCACATCC	CCATAAAAAT	CGCTACCACA	TAACCTACGA	60
5	TAATACCTAC	AAGAACTGGA	ATTAAAGATA	GGAATCCTTT	AAAAAATCCT	TGAACGACTA	120
	TTGTTACAAG	CAAGGTTATC	ATTGCAACAA	TTAAGAAACT	GATATTGTAA	CCTTTCATAT	180
	CTCCAGGATT	TTCATACATT	GCCATATTGA	CTGCAGTAGG	CGCTAAGCTT	AAACCAATTA	240
10	CCATGATGAC	TGGTCCAACA	ACAACTGGTG	GTAATAATTT	CATTAACCAT	GCTGTCCCAC	300
	TTAATTTGAT	TAGAATCCCG	ATGATGACGT	ACATAACACC	ACTCATGAAT	AATGCTACAA	360
15	GCATGTCTCC	TAAGCTATGC	GTACTTAATC	CCGTGATAAT	TGGCGTGATA	AATGCAAAGC	420
	TAGATCCCAA	GTATGCTGGT	ATTTGCGCCT	TCGTTATTAA	GATATAAAGT	AATGTACCGA	480
	TTCCCGAAGC	TAGTAACGCT	GCTGATATTG	GTAGTCCTGT	TAAGAATGGT	ACTAGTACTG	540
20	TTGCGCCAAA	CATCGCAAAT	AAATGTTGTA	AGCTTAAAAA	TGCCCATTGC	GCTGGTTGTG	600
	GTTTTTCATT	TACATCTAGT	ACGGGTTTTA	CTGTTCGTTC	AAACATTTCA	TCATTTTGCA	660
	TAATATTCAT	TTCCTCCGAT	AAAAAAAAA	TCTCTTTACA	TCAGTATATG	TAAAGAGACA	720
25	AAAAGTGTGA	CAAGTTGCTA	CAAGTCATTT	TCGTCCATAG	AAATTGACTT	ATAGTTGTCG	780
	AACATGAGGG	TATTATTAGA	TAAACAAGCA	TATGAAAACT	TATTTATCAT	TCAACTCCCC	840
	CACCTTTTTC	AGTCTCTCGT	ACTGAATTAA	AAGGGGTATT	ATTTAATTAT	AACTGCATTT	900
30	CTTTGATCcA	TTtCTTCyAA	ATAGACACTT	ACCGTTTCCT	CTTTAGAAGT	AGGTAWATTT	960
,	TTACCAACAA	AATCTGCTCG	AATTGGTAAC	TCACGATGTC	CTCGATCAAC	CAAAGCAGCT	1020
3 5	AAACCAATTT	TAATAGGTCT	AGCATTTAGC	AAAATAGCAT	CAAGTGAAGO	ACGAACCGTT	1080
	CGACCAGTAT	ACAGCACATO	GTCAATAATC	ATGACTACTI	TATCTGTAAT	ATCTGTGTCG	1140
	ATGTCTATTG	CGTCTTTTGT	CGTAAGTGAT	GACATGTGCT	CTATATCATO	TCTAAAGTAT	1200
40	GTAATATCAA	TTGTTCCAGT	AGGTATACGT	TGTTGCTCA	TTTGATGAA	TTEATCTTGT	126
	ATACGATTCG	CTAAATATT	ACCTCTTGT	TTGATACCTA	AAAGATTAA	A TTATCAGTAC	132
	CTT						132

(2) INFORMATION FOR SEQ ID NO: 634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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	ACCCATCTCA	TCGTATTTTG	AATTTAATAG	ACGAGATCGA	TGTATATCTG	AATTCATCCC	60
	AACTATGGAT	TAATGTTGGT	ACATCATLAA	CGCATAACCA	ACATTTTGAG	CAGTTGTTTT	120
5	ATAAGTAACG	TGATTTTTAT	CTAATTGCCC	TCTTAATGCG	TCCTCTGTAA	ATTCAACACT	180
	ATCAGAACCA	TTAGAGGTCG	CTTCATATAA	GTTATTAGAT	GCAATATGTG	CTAAATCGCT	240
10	ATTGATTTTC	AATGGTTTTA	ATCCTTTTAA	TTTTCTCATT	TCATTCGTTA	CTTCATAAAG	300
10	AGAAATTAAT	TGATTTGGAT	TTTGCTCAAC	TGGACGCTTA	TTATGCTCTT	CTGACGTAGA	360
	ATTAGAATTT	AATTGATAAG	GTTCAATATC	TGCTAACATT	TCTTTTGTTA	AAAATCGTAC	420
15	ACTTAGCACC	TTTTTCGATT	GTTGATCAGA	ATACACTTGT	GCATATATGT	CGCCATATTT	480
	AATCaGTGTT	TGTGTTTTTA	AATCTTCATC	TGAAAGTTCA	AATTCATATT	TTTTACCATC	540
	AACTTTAAAG	GACGGTTCTG	GATTAATACT	TGTATGATTA	AAAATTTCTG	CAGAATGTTG	600
20	TCCTATTTTT	AACGGACTAA	CATTGACTTT	CTCACCTGTA	GCATACACTG	AAACGATTTC	660
	TTCACGTTTA	GTTGAAACAA	TGTAATAACT	GTTTTTGTCT	TTAAACACAT	AATTTTTGTA	720
	rCCATCTCTA	AAAGGGTAGA	CrCGATCTGC	TTGTCCAAAT	Т		761
25	(2) INFORM	בס מכם מחודע	O ID NO. 63	a s .			

(2) INFORMATION FOR SEQ ID NO: 635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

TATATATAT	TTATATATTA	TAGAATAGAA	AGACCTGAAG	ATTGAATATC	TTTCGCAAAG	60
CCTTTAACTG	TATCTACTGA	TAATTCGTTA	ATATCGCGAC	CTAAGTTTGT	ATTCACTTTT	120
TTCACAACAT	CTGCTGGGCA	TGTAATAATA	TCTGCACCAA	TTTCATCAGC	TTGAATCACA	180
TTGAATAATT	CGCGGCAACT	TGCCCATAAT	AATTTAACGC	CGTCTTTACT	ATGCGTAACT	240
TTnACAGCCT	CTRTCATTAA	TGGTaATGGA	TCTACGCCTG	TATCTGCAAT	ACGTCCTGCA	300
AATACTGAAA	CATATGTTGG	CACACCTTCA	GTTACTGCTT	CAGTTATTTC	TTTAACTTGT	366
TCAATTGTGT	AAACAGCCGT	AACGTTTAAT	CTCACATTGT	CAGCTGAAAG	TTTTTTAATT	420
AAAGGAATCG	TTGATTCACC	TTTTGTATTT	ACAATAGGAA	TTTTAACAAA	TACATTTTCG	48
CCATATTGTT	TTAAAATTGC	TGCTTCTTTK	TCCATAGTTT	CTAAATCGTC	TGCAAATACT	54
TCAAATGArA	TTGAAGCATC	TGGAATTTCT	TTCACAGCTT	CTTCAGCAAA	AGCTTTGTAA	60

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TTTTTATAAG	CTGCTTTCAT	TnCTTCAATA	TCTGCACCGk	CCGCAAATAC	TTCTACATTT	720
AGTTTAGCCA	TATAAYATAG	CCTCCTTGAT	TCTTATTAAA	ATTTTAACAA	CATCTGCATG	780
kCTTTTTCTT	ACAACCATTT	GTAAAAAATG	ATTTTTATTT	CTTtGTT		827

(2) INFORMATION FOR SEQ ID NO: 636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

TTAGTCGGTA TAACCATCGG CTAGGTGGTT TTTGTATTAA AAAAGTGGAT aCCAAAATTT	60
ATTAATAATT ATTTTAATGT TAGAAAAAA CTAAATAAAA ACTCGCTAAT GATATCCAAT	120
AATATGTATA CAAAACGAGA CATATATTGC ATATGATTAA CGAGATACTG AAAATATTTT	180
ATCACCCCTA AAATGATTAT TCATTTTCAG CGGTAATTCG ACCTAAAGTC AAACTTACAA	240
TAAAACCGAT GATAAATACT ACTAATGAAA CGAACCACAT CACGATATTA GTTGGTAAAC	300
CTGGAAATAC TGCAAAGAGG GAGCCAACAA CAAAACCAAT GATTAATGCA AAAGTCATTA	360
GTTTATGATG TGTTAGGAAA TACTGGATAA TTTTGCTTGA AATAATGAAT CCAGCAAGCA	420
CGCCAAATCC GACTGCAAGT AATATAGGAA GACCTGCAAA GTTAAGTTTA ACAACTTCAG	480
ATATTGCTAG CATGACCGTA CCATAGACGC CAAATACTAA TAACATAAAT GACCCTGAAA	540
TACCTGGGAG TAACATAGCA CTAGATGCAC ACATACCTGC AATAAAATAT TTAATAATAA	600
GACTAGTTGA TAGAGTAAGT GTTTCTCCAG CATGTTTATC ACCATTATTC ATTAATGTAA	660
TAACAATTAA GATAGCGATA CCAGCTATAA CCATCATGTA ATGTYTAGTT GTAAATGACG	720
TTTTATAGTT AGAAATTTTC AATAAATATG GAACGATACC AATGATTAAT CCACCAAAGA	780
AAAACATAGT TGGAATATGG TGTTGGCTTA ATAAATAATT AAAAAGATTA CTTAGTGATC	840
CCATTGCCAG TAACATTCCA ATTATAATGG GGATTAAAAA TGTAAAACTT GGCCAAAAAC	900
GTCGTGAGAA TATGCCGCTA ATTGAAGCGA TAAATTGATT GTAAATACCT AACAATAATG	960
CGATAGTCCC ACCGCTAACA CCAGGTACCA AGTCACTCGT TCCCATAGCA AAACCTTTTA	1020
GAATATTAAT CCATTTAAAT TGTTGCATGA ATAACTCCTT TCAAACGATT GGAATAAAAT	1080
CATAAATAGC ATCATACCAT ATTACAAATG TCCTAGTGAA ATGATAACAT ATTTTAAATT	1140
CATAAAATCC ATTGAGAAAT TATGTGCACT TATTATCATT TATATTTTTA AAGAGAGCGG	1200

AGGTATAAGT	AAGTTATAAT	TAACTGAACG	CATTATTACA	AAGTCTTTTT	GACTACAAAT	1320
TAAAATTATT	ATAAACTAGT	TAAGAAAACT	TTATATTTTA	CGGAGGGAAT	ATAAAATGGC	1380
ATCAACATTA	GAAATYAAAG	ACCTACATGT	GTCTATTGAG	GATAAAGAAA	TCTTAAAAGG	1440
TGTTAACTTG	ACAATTAACA	CTGATGAAAT	ACATGCGA			1478

(2) INFORMATION FOR SEQ ID NO: 637:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1995 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

ATTACAGCAT	CTTCTCTAGG	TAGATTATTA	AAAGATAGAG	GTCTAAATGT	AACAATTCAA	60
AAATTCGATC	CATACTTAAA	TGTTGACCCA	GGTACAATGA	GTCCTTATCA	ACATGGTGAA	120
GTATTCGTAA	nGGATGATGG	TGCAGAAACT	GACCTAGACT	TAGGACATTA	CGAAAGATTT	180
ATTGATATTA	ATTTAAACAA	GTTTTCAAAT	GTGACAGCCG	GTAAAGTGTA	TTCACACGTA	240
TTGAAAAAAG	AACGTCGTGG	TGATTACTTA	GGCGGAACAG	TTCAAGTTAT	TCCGCATATT	300
ACAAATGAAA	TTAAAGAACG	TTTATTACTT	GCAGGGGAAA	GTACGAATGC	AGACGTTGTT	360
ATCACTGAAA	TTGGCGGTAC	AACAGGTGAT	ATTGAGTCAT	TACCGTTTAT	TGAAGCGATT	420
CGTCAAATTC	GTAGCGATTT	AGGTAGAGAA	AATGTTATGT	ATGTTCACTG	TACATTACTG	480
CCTTATATTA	AAGCTGCTGG	AGAAATGAAA	ACGAAGCCAA	CACAACATAG	TGTTAAAGAA	540
TTACGAGGCT	TAGGTATTCA	ACCAGACTTA	ATCGTTGTAA	GAACTGAATA	TGAAATGACA	600
CAAGATTTAA	AAGATAAAAT	TGCATTATTC	TGTGACATTA	ATAAAGAAAG	TGTTATTGAA	660
TGTCGTGATG	CAGACTCTTT	ATACGAAATT	CCATTACAAT	TAAGCCAACA	AAATATGGAT	720
GATATCGTTA	TTAAACGTTT	ACAATTAAAC	GCGAAATATG	AAACACAGCT	TGATGAATGG	780
AAACAGTTGT	TAGATATCGT	TAATAATTTA	GATGGTAAAA	TTACAATTGG	TTTAGTAGGT	840
AAATATGTTA	GCTTACAAGA	TGCATATTTA	TCAGTTGTTG	AATCATTGAA	ACATGCTGGA	900
TATCCTTTTG	CCAAAGATAT	TGACATTAGA	TGGATTGATT	CAAGTGAAGT	AACAGATGAA	960
AATGCAGCCG	AATACCTTGC	AGATGTCGAC	GGTATTTTAG	TACCAGGTGG	ATTTGGTTTC	1020
CGTGCAAGTG	AAGGTAAAAT	TAGTGCAATT	AAGTATGCTA	GAGAAAACAA	TGTACCATTC	1080
TTTGGTATTT	GTTTAGGAAT	GCAACTTGCA	ACAGTTGAAT	TTTCAAGAAA	CGTATTAGGC	1140

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TTACCAGAAC AAAAAGATA	T CGAAGATTTA	GGTGGTACAT	TACGCTTAGG	CTTATATTCA	1260
TGTTCAATTA AAGAAGGCA	C ATTGGCACAA	GATGTTTATG	GTAAAGCGGA	AATTGAAGAA	1320
AGACATCGTC ATCGTTATG	A ATTTAATAAT	GACTATAGAG	AACAATTAGA	AGCAAATGGT	1380
ATGGTGATTT CTGGTACAA	G tCCAGATGGA	CGTTTAGTAG	AAATGGTAGA	GATTCCGACA	1440
AATGETTCTT TATTGCTTG	T CAATTCCACC	CAGAATTCTT	ATCTAGACCA	AATCGTCCGC	1500
ACCCGATTTT TAAATCATT	T ATTGAAGCTT	CATTAAAATA	TCAACAAAAT	TTTAAATAAA	1560
GCTAATAAAA CCGGTACTT	T CATTGTTAAA	CATTGAAAGT	ACCGGTTTnT	CGTATAATTT	1620
TAATATTATG TTAGTGACA	A GGTATGAAAT	AACAATAGTG	ACTTTTATAA	TTCTAAGTCT	1680
CTTGTCATTT CAATCATTT	G TGTATAAATG	TCATAGTATA	CATAATTCAA	TGCCATCGCA	1740
TGTGGTYGGA CAATCTTAT	C GTAATCTTCA	GTGTAGACTA	TAGGTCTTGG	TGTAGATAAA	1800
TCGATAAAAT GTACGAGAT	G ATCAGGGAAA	CATCTGTTT	TAGGTTTGTT	GCTTATTAAG	1860
ACCACATCGA TATCTAAGT	C GATAAGTTTT	TGAATATCTA	ATGCAACTTG	ATYATTATAA	1920
AATGGTGCGA ATAATAATA	AC ACGATCAGTT	GAGTCAATTT	CTTTAAwkTC	TTTAATAGCG	1980
TaAGTTTnCG GCTAG					1999

(2) INFORMATION FOR SEQ ID NO: 638:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1107 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

60 ATTAGTGATG AAAGTCAGAT TGAAGCTTTA TTAACAGCTG AAAAATATTC AGAAATGATT GGTGAATAAT CACCGTGTAA CTCCTTAATC TAAGATTGAG GAGTTTATTT TTAGTCTGAG 120 AAAATAAATG ATATGAAAGA AAAATTATTA GGTACTATTA TTTGGAGTAT TGCTACATTT 180 TATTATTCAA GAATGATGGA AATAATGAAT TTAGCTATTT TAAAAATAAA AATTGGGGGA 240 AGTTAATATG CTAAACATTC AAGACGTTAn CATnCTTTCT AAAAAGGAGC AAAAAGCATA 300 TAACCGTTTC GTAGAATCTG TAGAAAACGG TAATTTACCA GTACTACCAT GTATTGAAAT 360 GGATCTAAAA GAGATGCAAG AAGAAACATT AAACCAGAGT AAGATTGGTG GAATGCCATT 420 TTTAAAATCT TTTAAAGATA TACCATTAGA TGAAAATAAT GTACCAATGG TATTGCTAGC 480 ACAGATTAAT TTGGATGATC TTCCAGAACA ACAAGAATTA TTTCCTGTAA AAGAAGGGAT 540

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AAACAATATA	AACTCAAGGC	TTGTTTATAT	AAAAGAGCCA	ATTACAGATT	TATCACTCGA	660
AAATATTCAA	GCGCATTTGA	AGTCATTAGA	TGCTGATAAT	GAGGATATCC	CGTTCAGTGG	720
AGCATTTTCT	ATAGAATTTA	GATTGTCGAA	ACAAACTATT	ACATGTACTG	ATTATAAGTA	780
CGATGAGGAC	GTGCTTGCAT	TGTGGAATAA	AGTCAATCCA	TCCTTCGCGC	TAAAATCAAT	840
GTTTGGTGGT	TATGATGAAT	TGATGGAACC	TGTGTGTAmC	AywTTTACTG	CTAAGGAACC	900
ATTTAATCAA	CTTGGTGGTT	ATCCATATTT	TGACCAAATA	GATCCAAGAA	CGAACGATCA	960
AGAACTGAAA	ATGTATGATA	GAGTCTTACT	GCAAATTGaT	TCTACAAGAG	ATGGTAATTC	1020
TTCGATTATa	TGGGGTGaTT	TAGGTATTGC	CAATATCLTA	GTGaAATCTA	CTGrACCTTG	1080
aGGcTAtGaa	GTTTTGAATG	ATTACCT				1107

(2) INFORMATION FOR SEQ ID NO: 639:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 904 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:

ATTCATATTA TTATAAATTA TTTCTACACC ATCCCAATTG AGTTGTTTTT CATAATTTAA 60 ATGTAATTCC ACTAACTCCC TACCAATTTC AACAAATCCA TATACATCCT TTAATATCGG 120 TATTCGCGGA AAACCTTTAC TCAAATCACT TGAATATTTG TTCACATAAT ATTTATGATG 180 CAAAATTGCA TATATATAAT ATACTATCTC TTCTGAATTA AGATTTATTT TCTTTTTAAA 240 AGAATTAGGA AATATTATCT ACAYGCCTCA AACTATCTTT ACCTTTGtAT GTAGCAAAGC 300 CTTKGCCATT ACCAATAAAL TGGAAATTAG GTAATATGTC CGTGATCATA GCCGAGAATT 360 420 AATATCTACT TGGCATTTCC ATAATATTTT TGTCGTACAC TATCCATTTT TTTGTAAATG 480 GTCTATGCAT AAATTTAACA ATTCTCTCTG GATTAATTGA AATATTTTTT CCTTTAGAAA 540 ATTTTTGGGT AAGTCCTCGT GTCCAACTAA TAAATGTTTC ATCTTTGTTC ACTAAATTTA 600 TACGTTCTCT TGAATCTAAG ATATCAATTA ATCTATCTAT TTCAGAATTA TAGTTATCTA 660 CAAGTAATTT TGCATTTACT AATGCTTTTT CATTCGAAAA ATTTGTTACC CAATTATCTC 720 TTGCTGaATT TACTCCATTA AATKGAKCTA AATATATAGA ATTTTCAATA TCCTTGGAAT 780 CATACATTGG TAAATAATTC CCCATAGTTT ATGTCTCGGT GATTAATCCA ATCATTGGGG 840

	AAAG	904
	(2) INFORMATION FOR SEQ ID NO: 640:	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 436 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:	
15	CGATGTCTTT ACTATTAGAC TTAGCCATTG GTTTCACCTC TCCAAAAATT GTAAATGTGT	60
	ATCATCAATA TGAAAGTTAC ATAAAACTGA CATATTTCTT TAAAATATCA ACGCCATTGA	120
	TAACTTCCTG TTTTAATTGA TACGCTGTAA CAAAATACTA TAGTTAGTGC TTACATGTAT	180
20	ATGTTAAAGC AAGCAGTGGT AAATGTAAAT TATAATTATT CATTAACTTT GCAATATATT	240
	AAATCTTTTA TTCATAGAAG ATAAATATCA AATCAATCAT AATTATTTGA CAACAAATAG	300
	CTAACGATTG TTTTAATCTA CATTTGGCTT ATAGCATTTT AAACCTATAC TCTATTTTGA	360
25	TACAATATAA GTGTAAAATC AATCATAAAA AGGATATTCA ATATCTGCAT CCAAGAAAAA	420
	CATTACAATT ACCTTT	436
30	(2) INFORMATION FOR SEQ ID NO: 641:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 442 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:	
40	GTTATTAAAT TCAGAGTGGT AGCAAATTAA AGTTANTCAA GAGTTAAGAT GAATTTAATT	60
	CATGAACACG TCTATTATTT TTATAATTGT AGCAAATAAA GCTTTACATC AAGGAGGTAA	120
45	TTARATATGT TCARARATA TGACTCARAR RATTCARTCG TATTRARATC TATTCTATCG	180
10	CTAGGTATCA TCTATGGGGG AACATTTGGA ATATATCCAA AAGCAGACGC GTCAACACAA	240
	AATTCCTCAA GTGTACAAGA TAAACAATTA CAAAAAGTTG AAGAAGTACC AAATAATTCA	300
50	GAAAAAGCTT TGGTTAAAAA ACTTTACGAT AGATACAGCA AGGATACAAT AAATGGAAAA	360
	TCTAATAAAT CTAGGAATTG GGTTTATTCA GAGAGACCTT TAAATGAAAA CCAAGTTCGT	420
	ATACATTTAG AAGGAACATA CA	442
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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2472 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

	CCAATTTTGG	TATGAATTAT	ACAGATAATT	CnGCGCCCGG	AGGATCATTT	GCTTATTTAA	60
	ATCAATTCGG	TGTGGATAAA	TGGATGAATG	AAGGGTATAT	GGCATAAGGA	GAACATTTTA	120
5	ACTACTGCCA	ATAACGGAAG	ATATATTAT	CAAGCTGGAA	CTTCATTAGC	CACACCTAAA	180
	GTTTCGGGAG	CACTAGCTTT	AATCATTGAT	AAATATCATC	TTGAAAAACA	TCCAGATAAA	240
	GCGATTGAAT	TGTTATATCA	GCATGGGACA	TCTAAGAATA	ATAAACCATT	TAGTAGATAT	300
20	GGGCATGGTG	AGCTTGATGT	GTATAAAGCA	TTAAATGTAG	CAAATCAAAA	AGCAAGTTAA	360
	TAAATCAAAG	GAGTTTTTGA	TTATGGCAAA	ATTAGTTACT	GAAAACATTT	CGAAGCGGTT	420
	TAAAAATCAA	GATGTATTAA	AGCATATTAA	TATCACTTTA	GAAAATAACG	AAGTTTATGG	480
25	ATTACTTGGT	ATTAATGGAG	CCGGTAAAAC	GACACTTATG	TATATTAAAA	GTGGCATACT	540
	TCAACAAGAT	TCAGGGGAAA	TTAAATTAGA	TAATAGACCA	ATGACACGAA	ATGATTTGCA	600
30	CAAAGTTGGT	TCGCTTATTG	AAACACCTGC	GACATATAAT	CATTTAAGTG	CACAAGATAA	660
	TTTGAAAATT	GTGTGTTTAA	ATGAAAGCGT	TGATTTCaGC	GAAATTAATA	GTGTTTTAAG	720
	CTTAGTCAAT	TTAAATGTCG	ATAAAAAGAA	AAAGGTTAAG	GACTTTTCTT	TAGGTATGAA	780
15	ACAAAGACTT	GGAATTGCAA	TGGCaTTAAT	TAAAAaGCCA	GAAATTTTAG	TATTAGACGA	840
	ACCATCTAAT	GGTTTAGACC	CATATGGAAT	CCAAGAACTT	AGAGAACTTC	TTATTAAAAT	900
	AACAGAACAA	GGTACTAGTA	TTATTATTTC	AAGTCACATT	TTATCTGAAA	TCCAAGTTTT	960
ю	AGCAGATCAT	ATCGGTATTA	TTCATGAGGG	TGAGCTAAAA	TATCAGCAAA	GAAATAACAA	1020
	AGATGAAAAC	TTAGAAGAGA	TATTCTTCAA	·AATAACGAAA	GGTGATTACA	AATGATACAT	1080
	TTAAAGATaG	AAGGTATCAA	ATTTAAAAAt	TCTTTCAGTA	TGTATGTTTT	ATTAATAAGT	1140
15	CcGcTGGTAT	TTCTTTGTTT	TGCTATTTTC	ACAGTCTTAT	TCGCCAAAAG	TAATACGGGA	1200
	ACAGCGAATA	GTGTGTCACC	ATATATAACT	TTACTATTTA	ATATTTGGCC	AATTGCTTTC	1260
50	ATCCCGATTG	TATTATGTAT	GGCTTGTAAT	TCGTTATTTA	AAATTGAAAT	GAGAAATAAA	1320
	TCATTTAATT	ATTACTTAAG	TAATAATTGG	TCGATTACAA	AAGAAATAAG	AGCAAAGATT	1380
	TTCATTTTAT	CAATAGCATT	TTTGGTACAT	TGCTTTTTAG	ТАТТТАТТАТ	тасттатата	1441

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TTGATGTATG	TAGTATCTCT	ACCATTGATA	CCGCTCAACT	TTTTATTAAC	TCGATACTTT	1560
GGTGTGTTCG	TATCAATATT	AATAAACTTA	GTATTATCAG	TCATTTGTGT	CTTGTTTTTA	1620
ACATTGAAGA	GTTTATTTTG	GGTGTTGCCG	TGGGGGATAA	TGCAGAGAAT	CCCGCTTATT	1680
ACGCTTGGTA	TACTACCTAA	TGGtTTAGTT	GTAAACCATA	ATTCAAAATA	CTTTAATGAT	1740
CTCAATGCCT	TATATATTC	GATTATTGTT	AGCATCATTA	TTTTCGCGAT	AGTAACATTT	1800
TTAAATAATA	AGAAAAGTTG	GCGATTAAAA	TGATAATTAA	CGAATTAAAG	TCATGTAAGT	1860
TGAAATTTTC	TAAGCAAGCG	CTCACATTTG	TACCCATTAT	TGTAACCATA	TTGTTTATAT	1920
TATTTATAAA	TTGGTATTTA	AACGTAAATT	TATGGAATGG	TCGACAAATm	AGTTTGTTTA	1980
CAGCGAGTTT	TAATGCAATT	ACATCGCTAT	TAATTTCTAT	AAACGTCTAT	CAAGTTATCA	2040
ATTTTGAAGA	AAATATTGGT	CACTTTAATC	ATATTTTAGG	AAAAGCTAAT	AGGCTAAATT	2100
GGTTAAATGC	ATCAATGATT	TTTACTTATA	CTATTACAGC	CATATGTATT	CTATTAGCAT	2160
CAATTAATTT	ATTGTGGCAT	TCACATGATA	TGAAAATAAC	ACTTATGTTT	ATAGGCGTaT	2220
CATTGTTTTT	CAATGTaATT	ATATTACTGC	TACTTTTTAT	TTTTAGTATT	TTCATTAAAG	2280
ATGTAATGGC	TATTGTTGTC	GGAGTTTTAA	TGTTTATTTT	TAACGTTTAT	TTTGGATTAG	2340
AAGTGCTTGG	AGATCATTCG	TGGTTCTATT	TACCAATCAC	ATATGCTACA	CGTTACGTTT	2400
ATATGTTTAn	CGAAGGGGAG	TATACCAGTT	ACATTAACAT	TGGGCAATCT	ATAThATTAT	2460
CACGnTGCCG	AT					247

(2) INFORMATION FOR SEQ ID NO: 643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

ATAATATAGG AATTATTTCG ATMACAGATT TTACGAATCG TGCTACGATG CAAAATGAAM 60

ATAAAGATCC ATATGGCGAA AAGTTAGCTT ATGGAATTGC TTTTAATGGC AGTGTGGATA 120

TGCAAGGGGA TAAACAAGTC ACAATTCCAA AATATAGTGT AGTTACAATT ACTGGCGAAA 180

ATAGTAAAAA TTATCGTGTT ACCGCCGATA ATAAGACTTA CTATGTTAGT AAAGATAAAT 240

TAGAATATTT TAACCCGGCA GGTTTATATC AAACGCATAG TTTTAAAAAA TTAGCACCAT 300

ATATGAAATC AAATTATAGT AATTACTATG CATACTTTAA TAGTCAATTA CATAAAAAGC 360

	CACAACAACC GATACAATTA CTTTTCAATG ATAATAATCA GTTATACGGT TTTGTTTATC	480
_	CAATTGTAGA TAAAAAAGAA TTAAAAGATA AGTTTAATAT TAACAATAAC ATTTGGATTA	540
5	CTAAAGTTGG GAATGGATAT TGTATTGCCA ATTTGAAAGA AGACAAATGG ATTTATATTG	600
	AATTGTAGGT GTAAAGATGC TAGATAATAT TATTTTATAT TTTAAA	646
10	(2) INFORMATION FOR SEQ ID NO: 644:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 426 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:	
20	TAATATCGGA ATTTGATAAT GAAGATATCT AATTTTTTAA TATTCGTAGC TTTTATTTTT	60
	CTACTTATTT TATGTTTATT TTTAATCTTA CAAATGACAA ACCATTAAAA GTAGCATCCC	120
25	AACATCAAAC AAAAAAACAA TTCATCAAAT AAAAATCGCT ACAAAACCAA GTCATTAAAC	180
25	ACGCAATAAT TAAAATTTTC CACTCATTAT AATTCTGAAT TCCAAATGTC GAATTCCGAA	240
	AACCAAACTC CAAATTCCAA AAACGCAACT CCAAAATTAA AAGCATTTCC CTACCATTCG	300
30	GGAAATGCTT TTTACATACT GGATTACTCT GTCATTAATG ATTTTACAAC GGGAAACCAT	360
	GTCGtCATGT ATGACCaAAG TAGCGTCGCT AtCaTaAgGt GGTTCGGATC TTTATTGGAT	420
	AATnAT	426
35	(2) INFORMATION FOR SEQ ID NO: 645:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 3241 base pairs	
40	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(b) TOPOLOGI: Tinear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645:	
45	nTTATTTACC CACAACATGT TGCGACATTA GGTAAATGGG TACCTTATTT ACTTGGTATT	
	GTTATGTTAG GTATGGGATT AACAATTACA CCTAATGATT TCAAAATGGT CTTTAAAGCA	60
	CCTAGAGCAG TAATTATTGG TGTCTGTCTA CAATTCAGTA TTATGCCCAC ATTAGCATTT	120
50	ATAATTGCAA AGTCTTTTCA TTTACCACCT GATATTGCTG TTGGCGTAAT ATTAGTTGGA	180
	TGTTGTCCGG GTGGGACATC AAGTAATGTA ATGAGTTATT TAGCCAAAGC TAACGTAGCA	240
	TARCETAGCA	300

	ATATATCTAT	TTGCAAATGA	ATGGTTGGAA	GTATCTTTCG	TGAGTATGTT	GTGGTCAGTT	420
	GTTCAAGTTG	TATTAATTCC	AATTGCTTTA	GGTATTGTTT	TGCAAATTAT	TAATCGTAAA	480
5	ATTGCTGAAA	AAGCTTCTAC	AGCTTTGCCA	ATTATATCAG	TTGTTGCTAT	TTCATTAATT	540
	TTAGCAATAG	TTGTAGGTGG	CAGTAAGCAC	CAAATCTTAA	CTACAGGATT	ATTAATATTT	600
	TTAGTAGTTA	TTTTACATAA	CGTATTAGGG	TATACGATTG	GATATTGGTT	AGCTCGTCTT	660
0	TTAAAATTAG	ATCGACAAGA	TCAAAAAGCA	GTCAGTATTG	AAGTTGGAAT	GCAGAACTCT	720
	GGTTTAGCTG	TGTCATTAGC	aGCATTGCAT	TTTAATCCAA	TTGCAGCAGT	ACCAGGCGCA	780
5	GTGTTTAGTT	TCATTCATAA	TATAACAGGG	CCTATTTTAG	CAAAGTATTG	GTCAAAAAAG	840
	TTATAATTGC	ACTAATAGAA	TGAAGTGGTC	ATCGGACTAT	GTTAAGCTTT	GATAAAGAGA	900
	AAAAATAGAG	GAGTAAATAT	ATGTATAGAG	CAGTTATATT	TGATTTCGAT	GGAACAATAA	960
0	TAGATACGGA	ACAACATTTA	TTTAATGTTA	TTAATAAACA	TTTAGAGATG	CATAATGCCG	1020
	ATCCTATAAG	CATTGATTTT	TATCGTTCTT	CTATTGGAĞĞ	AGCAGCTACA	GATTTGCATG	1080
	ACCATTTAAT	TAAAGCGATT	GGTTCGGAAA	ATAAAGATAA	ACTTTATGAA	GAACATCATC	1140
25	TTACTAGTAC	AACATTACCG	ATGATTGATA	CGATTANATC	ATTGATGGCA	TTTTTAAAGC	1200
	AACGTCACAT	TCCTATGGCA	ATTGCCACAA	GTAGTGTGAA	AGCGGAAATA	ATGCCCACCT	1260
	TTAAAGCATT	AGGTCTAGAC	GATTATATAG	AGGTAGTTGT	TGGTAGAGAm	GATGTTGAAC	1320
30	AAGTTAAACC	TGACCCTGAA	TTATATTTAT	CTGCAGTACA	ACAATTAAAT	TATATGCCGA	1380
	CACAATGTTT	GGCTATTGAA	GATTCTGTAA	ATGGTGCAAC	AGCCGCGATT	GCAGCTGGAT	1440
35	TAGATGTTAT	TGTTAATACG	AATAAAATGA	CAAGCGCACA	GGACTTTTCT	AATGTAGATT	1500
	ATGTAGCAAA	AGATATTGAT	TACGATCAAA	TTGTAGCGCG	TTTCTTTACG	AAATAGGAGG	1560
	CGTATCATGA	TGGGTTACAT	TATATTGTTI	TTTCTAGCTG	GTCCAGTAAT	TTTAGGCGTT	1620
40	GGAAATTTGG	TGATTGGTCC	TATATTTAAC	AAACAGACAC	CATTTCGCGT	GCAAGTAAGA	1680
	TCTTTTGTTG	kTGGkTCmAT	GrTTTACTTA	ATACTCGCA	CAATTGGCTA	TTTTTTACTA	1740
	TTACAAGGTA	AACTTTAACG	AGAAAACCAC	CTTACCTCAT	TAAATGGACG	ACCATATGTA	180
45	TGTGAAATGG	TAGAACGTTC	ATGTTTATGT	ATGAGATAG	GTGGTTTAAA	TAGTTACATA	186
	TATTTTAATA	ATAACGTCAC	GATGATAAGT	r acaattaag	A TAATATCTAT	GCCTACCATA	192
	ATTGTAGCTC	TTGTTGCAIT	ACTTCCTTG	TCTTTTGCT	ATTTCATAGO	ACGGTAGTTT	198
50	GGCACAAAGC	TAATAATTAC	TAAGATTAA	ACAATTACA	CAATTAATGO	TGTTGTCATG	204
	ATGAACGACC	. 4.0.0444	י יייייייייייייייייייייייייייייייייייי	מ ממיירר מממ	т ааасстассі	ATCACACCA	210

	CAATAATTAA	TGCAATCGGT	AAAGTCGTAC	CGAGTTTAAT	CTTGCGCTCT	GGAGAATTAA	2220
	TAATAGTAAA	TACTGTAAGA	CAAATGAGTA	TGAAAGCAAG	TGTTGCAATA	ATAGTTCTTC	2280
5	CAACTAAATA	TAGGATGTCA	GGTTTTTCCA	TACCGATATA	ATTTATGATG	AAAAATGCTA	2340
	CAGCAAAGAG	TACCGATATT	TTTGTAGCAC	GTAGCAGTAT	TTGTTTTAAC	ATTGATATAC	2400
	TCCTTTTTAA	TATTATTAAA	ATTATATCAT	AATTACCAAG	AATAGCTGAA	GTTGTATGTG	2460
10	ACTCAACGGT	ACTTGAGCAA	CTTTTTTAAT	TTTTTAGAAA	AATCACAAAA	TAATTGTTTG	2520
	CAAAGTTGCA	AAAGCCTGCT	ATAGTAGTTC	TGTAAACGAT	TGCATGGTAT	GCAAATATTA	2580
15	ATGTACCAAA	ATCGATAATT	TATAGTATAA	TTACGGCAAT	AAGTTTTTTT	ATGGATTTAT	2640
,,	TTAGTATCAA	TCAGAGATGG	GGTAAGAAGT	TATGGAGAAC	AATGAACTAC	AAAGGGGATT	2700
	GAGTGCCCGT	CAAATTCAAA	TGATTGCACT	TGGTGGTACG	ATTGGCGTGG	GGCTTTTCAT	2760
20	GGGTGCGACA	AGTACAATTA	AATGGACAGG	CCCATCAGTT	ATCCTTGCAT	ATTTAATTGC	2820
	GGGTATCTTT	TTATTTTTAA	TCATGAGAGC	AATGGGGGAA	ATGATTTATT	TAAACCCTAC	2880
	AACAGGATCA	TTTGCAACAT	TTGCAAGTGA	TTATATACAT	CCTGCAGCAG	GTTATATGAC	2940
25	AGCATGGAGT	AATATATTCC	AATGGATTGT	AGTTGGTATG	AGTGAGGTCA	TCGCAGTAGG	3000
	AGAATATATG	AAGTTTTGGT	TCCCGGAATT	GCCAACTTGG	ATTCCTGGTG	TTATTGCTAT	3060
	TTTATTATTA	ATGGCAGCGA	ATTTATTCTC	GGTAAAAGCG	TTTGGAGAAT	TTGAATTTTG	3120
30	GTTTGCTTTA	ATTAAAGTTG	TAACAATTAT	TTTAATGATT	ATTGCTGGTT	TTGGTCTTAT	3180
	nnTCTnTGGT	TTTGGAAATG	GTGGCCATGC	GGTAGGTATT	TCTAATCTAT	GGACAAATGG	3240
	С						3241
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(2) INFORMATION FOR SEQ ID NO: 646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1311 base pairs
- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646:

AGGCGTCAAC	TCAGATGGTT	TAATAATTGC	CGTATTACCT	GCTGCAATAG	CACCGATTAA	60
AGGTtCGAaC	ACTAGTTGAA	AAGGATAGTT	AAATGGTGCA	ATGATCAAAA	CIGTTCCATA	120
AGGTTCTTTT	TTGATATAGC	TTTTTGTTGG	TATAAATAA	AAAGGTGTGT	CTACATTATT	180
TGTTTTAGTC	CAGTTTTTAA	GTTCcTTACG	GGCAATTTTG	ATACTTYTCA	AAGTTATGCC	240

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AAIAICGCIC	ICGIAIGAIT	TAATAGCTTT	GCTTAACTTC	TTTAATTGCT	CITICIAAA	360
ACTAATATCT	TTAGTTTGTT	GTGTATTGAA	AAAAGCTTTA	CTGTCATAAA	ATTTTTGCTC	420
AATGATATTC	ATAATGAAAA	GAACCTCCTT	ATATGATTAT	TTTGGAAAAA	GCGATTAATT	480
GATTTGAATG	TTGTGGCCGT	TAATTTTAAA	TGGTCTTTCG	TATATATAA	GTTGAAAGTT	540
GAAAATAGAG	CGATGAATCG	TGTACATAAT	AATATTTATA	ACTITAATCA	TAACGAAAA	600
GGTAGGAAGA	AAACAAAAAT	TTATACTCAA	CATCGCAAAT	ATTITAAGAA	AATGTAAAGA	660
CAAAAGGGGA	ATTGTATAGA	AATCACTAAT	CTGTGGGTTA	GGGTAGCTAA	AGGAATAAAA	720
ACTACTATTG	AAAAAGGGTT	GTAAATTAGT	CAAACGTAAA	TAAAAAACAG	TTCATTGAAA	780
GTGAAATAAA	TTCTACTTTA	ATGAACTGTT	AGTTAAATAC	AACATGTCTA	TAATTAGACA	840
GTAATATAGT	ATTATTTTGT	TAATGCTTCA	GTGATTTGAG	GTACGATTTG	TTTTTTTCGA	900
GAAACGACAC	CAGATAAGAA	GGCCATGTCA	TCTTCTAATT	GAACATTGAA	TGtTCGCCAA	960
CTTTATCTTT	TTCAGCACCT	ACAACTAAAA	TTTTAGAATC	ACTATTAATG	ATGTCAGTAA	1020
CAACAAGTAC	AAATAAGTCA	TATTTTTCTT	GTGCACTTAC	AGCTAACATT	TCTTTTTCTA	1080
PATCTTC TTT	ACGATTTAAC	ACTTCGTCAA	GGTCAACAGC	ATTAACTTGT	GCAATACGAG	1140
TCACATAGTC	ACCCATAGTA	AATGATTTAG	CATCCATGTT	TAATAAGAAT	TCAACTGATT	1200
TATCAGTTGT	TGAAGCACCT	GCTTTtAACA	TATCTAAGCC	GTACTTTTGA	ATATCAACTT	126
TAGCAATATC	TTTnAATTCT	tCAGCTGCTT	TAACATCTTG	TTGTGTACAT	G	131

(2) INFORMATION FOR SEQ ID NO: 647:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1498 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647:

CATATACTIT TTCATTTCTT TACGAGATAC TTTACCAGAG GATTTAGACT TCATACGCTG 60

ATCCATATGT GCTTGCGTTT CAGAATGTCC ACAAACACAA CGATATACCG CTTCTTTCCC 120

TTTACCAAAC AACGTTAATT TCTTTTTACA GTTTGGACAT CTTGCATTTG TTTTGCGCTG 180

TACATTCTTT TTCGTCTTAC AAGATGGATC TTGGCACACA AGCATCTGAC CATTTTTAGT 240

TTTAACTTTA ATCATGAATT TACCACACGT TGGGCATTCT GTGGTTGTTA AATTATCGTG 300

TTTATATTTA CGATCACTAT TTTTAATCCC ATTTACAACA TCTTTCGTAA AATCTTTCAT 360

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	CCATTGTGCA	GTTAAAAGTG	GCGACGTTAA	TTCTTCTGGT	GCTAATTCTA	ATATTTGTTT	480
	ACCTTTTGAC	GTTACTTTAA	TTTTACCGTC	TCTTGATTCA	ATGGCATTCA	AATAAATTAT	540
	TTTATCGATA	ATGTCGGCCC	TTGTTGCAAC	TGTGCCGATA	CCACCTGTTT	GTTTTAAAGT	600
	TTGCGCATAT	TTTTTATCCT	TCAATTGAAT	AAAGTTCTGA	GGGTTCTCCA	TCGCTTTTAA	660
n	TAACGAACCT	TCATTAAAAT	ATTCTGGAGG	TGTTGTTTCA	TGTTCTCTAA	TATTTGTTTT	720
,	TGAAATCTTC	ACTTCATCGC	CTTCTGAAAA	AGGCTGTTGC	ATCTCTGTAA	TAGATTCACC	780
	TTGTCTAATA	GATTTAAAAC	CTAAAACAGT	TGTTACATTC	TCTTTCAAAA	CAAATGTGTG	840
5	CCCTGCAACC	TCTAAAGTTA	CAGTTATCGC	GTCATACTCG	TGCGGAGGCA	TTAAAGCTTC	900
	TAAAAAACGC	TCGACAATCA	TATCGTATAA	CTTTAATTCT	CTATTACTTA	AGTCTGACAT	960
	GACAGGTCTC	ACTTCTGTAG	GAATAATTGC	ATGGTGATCA	GATACTTTTT	GATTATTAAA	1020
)	TATCGACATT	TTTGATGAAA	ATGTTTTAGA	CATTAATGGG	CGTGCTTGGT	CTTTATATGT	1080
5	TGTTGCCATC	GTCACCTGAA	TACGTTCTTT	CATAGTATCT	ACCATATCAG	TTGTTAAATA	1140
-	GTTTGAATCT	GTTCTTGGAT	AGGTTACGAC	TTTATGTCTC	TCATATAAGC	TTTGAAGTGT	1200
•	ATTCAATGTT	TCTTTAGGTC	CAATTTTATA	ACGTCTATAC	ATATCTTGTT	GTAAATCTGT	1260
	TAAATTGTAC	AGTGATTGCG	GATACGACTT	CTTATGTTTA	GTAGCAACAG	ATTTAATCTT	1320
9	ACCATCGACA	TTTTTCAAAT	TATTAACCAT	CTGTTCTAAA	GTTTCTTTAW	TGGtATATCG	1380
	CTGATTTGaw	TCTAGCTGAA	AATCAAACCC	TTTTACCGTT	AATGATAATG	TAAAGTATTG	1440
	TTGTGGnTTG	AACTGATTAA	TCTCTTGTTG	GTCGTGTAAT	TTACTAAATT	GAAACGGn	1498

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO: 648:

- - (A) LENGTH: 1044 base pairs
 - (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648:

TAAAACAATT CGTTTTATTA ATACAGTTTG TAAAAGTATT CTCTTAGTAC TAATAGCTAA 60 TGTAATGATA GAAAATACTA GTGTTATTAA AGATTTGAAT AAAATAAAAG AAACTGAGAA 120 ATATTGGAAT GTATTAGATG ATTATTACAC GATTGAATTT GCACCTTATC ACGAAACAAA 180 ACAAAGTTTG ATTGATAATA TGGTGCGATC AGAACAATTA GTAAAGGCTA GTGAAGCAGA 240 AAATAATGCG ATTTTATTCA AACCAAAGGG TGACTCCGTT GACAATGACA ACTTTTCGCC 300

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TCAACCTGAT	ATTCCGATAA	AAAATCAAAA	AAATAATGTC	GAAGTAATTA	TTCCACAAAA	420
GTTTCATGCA	ATGCGTAATG	AAATCAATCA	AGCATATCAT	TCATGGTTTG	AATTTGTACA	480
AAATAAAAAT	AATAAAGAGA	ATAAGTTATC	TATACAGTTT	ATCAACAAAA	ATGATTGTCG	540
AATTTTTTCA	TTTGATGCAC	GAGATAGTCG	CCATTTGTCA	TTTATAGAGG	CGCCAATCAT	600
TGTGAATGTT	CAGGCATCAG	ATTTATCGaA	TGATTTttAT	TATGCCATGa	TCaGTCaAGG	660
CGGGTATTTa	TTCaAAAATT	ATGaCGCGCT	AGTAAAAAAT	ATTGGAAAAG	TATCCATCTT	720
GATGGGGAAA	TCCAGTGGAA	TAACCAATTA	TAAAGATAGC	GTGATGGAAA	TGTATCATGA	780
AAACAATTTG	AAATTAACAG	TACTCAACTT	TTCACAAATC	ATTATCGCAA	TCATTTTAAT	840
TTATTATTAA	TTATTTGATG	TGAAATATTA	TTTTGAACAG	CATCGAAAAT	TACTCGTAAT	900
CAAAAAGCTA	TATGGTTATT	CAACATTAAG	AGCCAATTAC	CAATACTTAT	TAATAAATAA	960
TATAGTTGTT	ATTTTTATTG	GAATATTGAC	GAATGTAATT	TTACATTCTC	ACTATATAAT	1020
GATGTTATTT	GCAACGATTC	TTGT				1044

(2) INFORMATION FOR SEQ ID NO: 649:..

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649:

GAACATATTG GGTTATGCAA GGnGGTCACT CTTCACACTT ATAAACAACA TTTTAATAAT 60 GTAAAGTTTA ACCAGCTAAC ACTTTTGTTA GCTGGTTTTT ATTTTCCTTC AATTTTTAAA 120 TGGTTAAGTC CCCTTCTATA TCTTATAAGA CAATCATTAT AATCAATTCA ATTAATACAT 180 TAACAACCAC AACTAATAAA TATAGTAACT TCAAAATCCA TATTTATGTC TAAAGATAAT 240 CTCAATGTTG TTCACGTCAA TAAAATTATC CCTAGGTTTT TAAAAATTGT ACATGTTTAA 300 ACAATCAAAA GTGTACATTA TTAAATTATC ATTTCCAGTT AGATTTAGAA ÄACATTCACA 360 399 CCACGCATGG ACCAACGTAT TCGTCTTCAT TCATTTTAG

(2) INFORMATION FOR SEQ ID NO: 650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650:	
	GTACTAGGTT CTANGATTCC CTACTGTAGT CATAGATATT TTCCAAACAG AGCCTGACAA	60
5	CTTTTCATTT TTAATAGTGA TCACTATATT AATCGCTATT GCAATTTATG CATGTCGATT	120
	TGTTTGGGTT TATTTCTGGT ACAAAGATTT TTATTTCCCG AAAAATATAC AATCTTATCT	180
	AGACGAGGAA CATGATTCAC ATGAAACACC ACCTTCTCGA GTGCGTTACG CATTTATTAT	240
10	GACCATGTGT GGTATTCACG GTACAATTTC ACTTTCAATG GCACTTACAT TACCATTTAT	300
	CATTACAAAA GGACAAGCAT TCGAATACCG TAATGATTTA TTGTTTATTG CATCTTTCAT	360
15	GGTATTAATT AGTTTAATCT TAGCGCAAAT TGTTTTACCT TTAATTACAC CATCTGCCGA	420
15	AGATACTACT TTTAAAGGTA TGACTTATCA ATCTGCCAAA ATTTTCATTG TTCAAAAAGT	480
	GATCCAGCAT TTTAAAAACG AAAGTAAAAA AGACAAAAAC GATACAAATT ATCGCCCAGT	540
20	ATTAAACCAA TACTATGGAG AATTGTTATT TTTATTAAAT TCAGAACCTG ATAATCAAAA	600
	TACYAAAGAa CTCAAACGTT TAGAAGATAT TGCAAAAGTA ATCGAAACAT CTACACTTGA	660
	GCGTTTAATT GATAAAGGTA AGGCAACATA TCAGGATATT AATAATTACC GCAATATTGT	720
25	CGAATTAACA GAGACACCC GTACTGC	747
	(2) INFORMATION FOR SEQ ID NO: 651:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1373 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651:	
	ATACAATACT CTTTTATTAT TCAATAAGCC ACTTCCTATA GCAAATGTTT AACTTTAAAT	60
40	ATTTTCGAT GCTAACAAAA AATCACACTA TCATCTTTTA AAATGAAAGT GTGATTACAA	120
	GCAAATCTGT AAAATTTATA AAGCAGAAAC AATTCAACTT TATCATTATG ACATTTCAAT	180
	TARACCTTCT ACATTATAGT TCCAAGCATC TTACACATGA ATGCAAGTAT TTAACGATTT	240
45	AATTGTGACA TAGCCTGTTG ATATTGTGTT TCATTGATAT AATTTTGTTG CTTCATTTTT	300
	TCTAAGTTCG TGCTTACACG TTGCGTAAAA TTCTCTGACA TATTATTGAT ATTATATACG	360
50	CTAGGTGCAT TGACTTTACT AGCTAAAATA GCGCTTTGTA AAACTGTTAT GTGAGACATT	420
	GTTGTACTAT TTTTATTCAC GGTTGTTCCA AAGTAATGGT TTGCTGCGCC CTCAAGCGTA	480
	TATTGATTAT CCCCAAAGTA AATATTATTT AAATAAAAGC TTAAAATTTC GTTCTTATTA	540

TCATTATCAT	TTAATAAAA	TTTGACAACT	TGTTGTGTAA	TGGTACTACC	ACCTTGCACA	660
TCTCTGTCGC	TAATCGTTGA	AAATAAAGCT	CTAGTTGTAC	CTTTCAAATC .	GAATCCATGA	720
TGATTGTAGA	ATCGTTCATC	TTCCATTGAA	ATAAAGGCAC	CTTTAACATA	CTCTGGCATG	780
TTATCAGCTG	ACACAAAACT	ACTTTTATTT	TCAATTTTTC	TTAGTTCATC	CACATTATCG	840
CGTGTAGATA	AAAAATACAT	GATACCAATA	AACAATGCGA	TAATGATTAG	AATGGTTAAT	900
AATATTTTTA	ATAGTATTCG	TTTACTTTTT	TTCTTTTTCG	GCGGTTTGCC	AACTGGTTGA	960
TAATACGTAT	TATAGTGAGG	TTCGTGTTTC	ATATGCTCAA	AATGTTCATT	TGAGTTTGAG	1020
TACCTATCGC	TTCTTTTCAT	GCGTTTGCTC	CTTCTTTTAA	AACTCACTTA	GtATATACCT	1080
TGaGTTTACC	AGTACTATCA	CAAATAGGCT	ACACTTTTTG	GGAAAATCAG	TCCAAGGGCT	1140
TACAATCGTA	TACGCCATCA	TACTTACTTT	TTTGTTTTTT	GAAAAAATTA	TAGATAAATC	1200
ATTGCAATTT	TAAATATTAA	TCATGTCAAA	TATTGTTATA	TTTTATAAAA	ATAAAAGACC	1260
ATCCCTATTA	AATGCCAATA	GAGACGACCT	TTTATTTGTT	ATTCATTTAT	TAAAACTAAA	1320
ATCCATATTT	CATTTCAAAC	GAAAATATAT	AAATTTTAAC	AATCGTTAAC	CAC	1373

(2) INFORMATION FOR SEQ ID NO: 652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 859 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652:

60 GGCAGATAAT TTAGTCATTG TTGAATCGCC TGCAAAAGCA ANAACCATTG AAAAGTATTT AGGTAAGAAA TATAAAGTTA TAGCTTCAAT GGGACACGTC AGAGACTTAC CAAGAAGTCA 120 AATGGGTGTC GACACTGAAG ATAATTACGA ACCAAAATAT ATAACAATAC GCGGAAAAGG 180 TCCTGTTGTA AAAGAATTGA AAAAACATGC AAAAAAAGCG AAAAAACGTCT TTCTCGCAAG 240 TGACCCCGAC CGTGAAGGTG AAGCAATTGC TTGGCATTTA TCAAAAATTT TAGAGCTTGA 300 AGATTCTAAA GAAAATCGCG TTGTTTTCAA CGAAATAACT AAAGACGCTG TTAAAGAAAG 360 TTTTAAAAAT CCTAGAGAAA TTGAAATGAA CTTAGTCGAT GCACAACAAG CGCGTCGAAT 420 ATTAGATAGA TTAGTTGGCT ATAACATCTC GCCAGTTCTT TGGAAAAAAG TAAAAAAAGG 480 GTTGTCAGCG GGTCGAGTTC AATCTGTTAG CmTTCGTTTA GTCATTGACC GTGAAAATGA 540 NATTCGAAAC TITAAACCAG ANGAATATTG GACTATTGAA GGAGAATTTA GATACAAAAA 600

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	AAAAGATGTT GAGAAAATTA CAGCTGCATT AGATGGAGAT CAATTCGAAA TTACAAACGT	720
	GACTAAAAAA GAAAAAACGC GTAATCCAGC AAACCCATTT ACAACTTCTA CATTACAACA	780
5	AGAGGCGGCA CGTAAATTAA ACTTTMAAGC AAGAAAAACA ATGATGGTCG CACAACAATT	840
	ATATGAAGGT ATAGATTTG	859
	(2) INFORMATION FOR SEQ ID NO: 653:	
10 15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 747 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653:	
20	TTCAACTTCG TTTGGAAATC ATGTTCCTCA ATTGTTGGAC TTAAACGAAT TTCTTTAACA	60
	TTGATAATTT TTTGTTTCTT TTTCATTTCT TTTTCTTTTT TCTGTTGTTC GAATTTGAAT	120
	TTACCGTAAT CCATAATTCT TGCAACTGGT GGTTTCGCAT TCGGTGCAAC GACCACTAAG	180
25	TCTAAATCTA CACGTTCAGC CATTTCTAAA GCTTCACGCT TTGATTTAAC ACCAATTTGT	240
	TCACCATCTT GACCGATTAA ACGTAATTCT TTTGCACGAA TTTTGTCATT GATTTGAGTT	300
30	TGATCTTTTG CTATGGTTGA CACCTCCAAA ATTTTTACGA AATTTGCACC AAGCAAAAAG	360
	GAAGAGCAGG TATAAAATAC CCGCTCTTCC TTATACACAG TTATGTGTAA TGTGATTAAC	420
	CTGCCAACTG CTTTATGCGT CGCTACAGGT GAGAAGCGGG TGCTTCTACT TGGTTCGTTT	480
35	CGTATTCAAC GTTATTAATC ATATCAACAA TTCACATTTA AGTCAACACT ATAACTGTAA	540
	TTATTTTAT TTTAACCTTT TATTTCATCC ATTGACACGT CTTGACGTAA ATCTACTTGT	600
	TCTAATGGAA TTTTTTCGT TTTATATCGA AGCTTATGAT AAATAAAGAA TGCTAAAAAT	660
40	ACTGGAATTC CCATATACGT AATTAAGAAG CGACTAAAAT TAAAATCTCC TGTnTTAATA	720
	AAGTCAACAT CTTGCCCAAn AAnTACT	747
45	(2) INFORMATION FOR SEQ ID NO: 654:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 501 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654:

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TIGIGCTICT	TTTTTAGCTT	CTTGAACCTC	TIGIGCCTCT	TGTGATGTAT	CACTYAAATT	120
ATTTGCACTT	GCTTCTTCTT	TTATCGCTGC	TTGTTGTGCT	TTCAATGCCA	CTGCTTTTGr	180
TTCTTYATTT	GATACAGCCA	CACTTTTATC	CGCTTCTGCT	TGTGCTTCTC	TTTTAGCTTC	240
TTGAATCTCT	TGTGCTTCTT	GTGATGTATC	ACTTAAATTA	TTTGCACTTG	CTTCTTCTTT	300
TATCGCTGCT	TGTTGTGCCT	TTAATGCCGC	TTGCTCATTT	TTAGATTTGT	TTAAAAATCC	360
TTCAACACGT	TCTTTTGTAT	AGGCAACCGT	TTCTTCAAGT	TGCGTTTTTC	TTTCTTCAAA	420
CTTTTGCGAC	AGTTCTTGTn	CTTTGACTTT	nAAATCATCT	GCTTTTTGAT	AAACTTTATT	480
TTAAAATACC	AACCTAAAGC	С				501

(2) INFORMATION FOR SEQ ID NO: 655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655:

CACCTTGTCA	TAATTAATTT	TTTGATTTTT	CATTTTACTG	ATAATAGGTT	CAGCATTAAT	60
CATGATTTAA	CCTCCCACAT	TTAATCATTA	ACTTCTATTA	TATATGATTC	ATATTAAATG	120
TCAGTCAAAA	AAGTTAGAAA	TTCATTTTAA	TGCATTTATA	TTTCGAAAAT	CCCTTATGTA	180
TCTAAAAGCA	TTTTTTAAAC	TTGAATTTTA	AAACACTAAA	CAACACATAC	GTCTCTGTGT	240
CATTTTCATT	TTTTGTATGT	CATATATATG	TTTACTTCAT	TTAAATCAAT	TTCATCTTAT	300
AATTTATCGT	GTATTTTACA	AAAGATTGAC	TTCAATTCAT	CGTAAAAGTT	ATACTTTTGC	360
CATTTTTTAA	TGTAACATGG	TGTTAGTAAT	АААААТААТА	CATTGAGGTG	TTTTACATGA	420
CAGCATTATT	CCCTTATATC	GCTTTTGAAA	ATTCAAAAGA	AGCCCTTGCA	TATTACGAAG	480
AAGTATTTGG	TGCAACTGAC	GTTAAACGTT	TAGAAGTTGG	CGAAGAACAA	GCGTCACATT	540
TTGGTATGAC	TAAGGAAGAA	GCGCAAGAAG	CAACTATGCA	TGCTGAATTT	GAAGTGCTTG	600
GCGTAAAAGT	GTTATGTTCT	GATTCTTTTG	GTCGCGCTGA	CAAAATTaAT	AATGGCATAT	660
CATTATTAAT	TGATTATGAT	GTTAACAATA	AGGAAGATGC	TGATAAAGTT	GAAGCATTCT	720
ATGAGCAAAT	TAAAGATCAT	TCTTCAATTG	AAATAGAATT	ACCGTTTGCT	GACCAATTCT	780
GGGGTGGCAA	AATGGGCGTC	TTTACCGATA	AATACGGTGT	TCGTTGGATG		830
(6)			F.C.			

(2) INFORMATION FOR SEQ ID NO: 656:

5	(A) LENGTH: 539 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656:	
10	GTATCCATGG GCCCGTTnCG CACAACATTT GGnACAATTA GGTACACGnG TTGTCaTCGG	60
	TCGTTTCGGT ATAATTTTAT CGAATGAAGG CGGTGCGTTA CAAACAATGA AACTACCATA	120
	CGAATATTAC ATTGGTGGTA AATTAGGTTC TGGTCAACAA TGGTATTCAT GGATTCATAT	180
15	CAATGATTTA ATTCAAGCTA TTTTATTTTT AATAAATAAC GAGTCAGCTA GTGGTCCGTT	240
	TAATTTAACT GCACCTATAC CTGAACGTCA AAATTTATTT GGCTACACTT TAGCAAGAGC	300
	TATGCATAAG CCTCATGAAA CTTGGGCACC AAGTCTTGCA ATGCGTCTCA TACTTGGTCA	360
20	AATGTCAACA GTAGTATTGG ATACTCAAAA AGTATTACCT aATAAAATTC AAGCATTGGG	420
	attccaatit aaatatagta atttaaaaat ggnacttgaa gatttaatta aagaataatc	480
25	AATACCATTA ATGAGCATTA GAAACAACAT ATGTACTAAA TGTAATGTCT AGAGCGACT	539
	(2) INFORMATION FOR SEQ ID NO: 657:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1106 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657:	
	ATCAAGTTGA ATATCATCCA TATTTAACCC AACATAAATT GArATTATAT TTGGCAGCAC	60
	AACGTATCGT GATGGAATCT TGGTCACCAT TGATGAATGC ACAAATTTTA AATGATGAGA	120
40	CAATTAAAGA CATTGCTCAA GAATTAGGAA AGTCACCTGC CCAAGTTGTT TTAAGATGGA	180
	ATGTGCAGCA TGCTGTGGTT ACAATCCCTA AATCGGTGAC ACCAAACAGA ATCTCTGAAA	240
45	ATTTCCAAAT ATTTGATTTC GAATTATCAG ATGAACAAAT GACGCGAATT GATGGTTTAA	300
45	ATCAAGATAA GAGAATTGGA CCTGATCCAA AAAAATTTGA AGGCTAGATT AAAATCGCTC	360
	AACTGATGAA AAGGTTAGAT GAATTGTCAG GGCTTGGGAC ATTAAGTTCT TAGGCAATGT	420
50	AAAAAAGCTG ATTTCTATTA ATTATTTGAT AGAAATCAGC TTTTTTGATA TGTATTTTAT	48
	AATGTACAGC TCGTTGAGCT GCTATTTTCC TTATATTAAG TGCCATTAAT ACAAAACCTA	54
	GCTCTCGTTT AACTTTATTT ACTCCTCGAA CTGACGTTCG AGTTAAACCC AAAATAGCCT	60
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	CTGGTTCAGA AAGCTTTTGA TTAATTTGGA CTTTAAAGTA TTCCCAATTA TAATTCTTCA	720
	TGATTETCTT ATTGGATTTT GAATTTGGTT TCATGCATTG TTGCCTCAAA GAACATGCTG	780
5	AACAGTCATC GCATTCATAT AGTTTGAAGT CTCGTTTAAA ACCATATCTA TCATTACGGT	840
	ATGCATATCT TITAAAACCT ATTCTTTTGT TATTAGGACA TATAAATTCA TCATTAAGTT	900
10	CGTCATATTT CCAATTTTGA GTGTCGAAAA TGTCACTTTT AAACTTTCTA GTTTTATCLT	960
,,,	TAATAAACAT GCCATACGTA ATAAGTGGCG TTTTATTAAA ATCATCTATA ATGGCCATAT	1020
	AGTTTTGGCT CACTACCCAT AACCTGGCAT CAGCTACCAA ATGAACCGAA GGGATTTTTG	1080
15	GAATCCATTG GTTGAAAAAA TGGGAA	1106
	(2) INFORMATION FOR SEQ ID NO: 658:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658:	
	TTTTAACTTT ACTCTTTGAT TTAAAGAGTG ATAAATGTTT ACAGTTTAAT TAAAACTGCA	60
30	TAAGAACTTC TAGCTTTTCT CTTTCGTTCA AAGAGAAGCA GCTGTTCGCA GTTTAATCAA	120
00	AACCACATAA AGCTTTTAAC TTTACTCTTT GATTTAAAGA GTGATAAATG TTTACAGTTT	180
	AATTAAAACT GCATAAGAAC TTCTAGCTTT TCTCTTTCGT TCAAAGAGAA GCAGCTGTTC	240
3 5	GCAGTTTAAT CAAAACCACA TAAAGCTTTT AACTTTACTC TTTGATTTAA AGAGTGACAA	300
	ATGTTTACAG TTTAATTAAA ACTGCATAAG AACTTCTAGC TTTTCTCTTT CGTTCAAAGA	360
	GAAGTTCTAA TACCACCATA TCGTGCGATC GGGAACGGTA	400
40	(2) INFORMATION FOR SEQ ID NO: 659:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1899 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659:	
	ATAATTACAA TGGCTACTGC AATTATTGTT GGAATTATAT ATTTCAGTTT AGTCATCATT	60
	TATGCTCCCT TGATTTCAAA TTCATATCAT TAGTTTACCA TATTGAAGAT GATATAATAA	120

	AACTTTAACT	GAGCTTCATG	GGGCACCAGG	TTTTGAAGAA	GAAGTAAAA	ATTATATGAC	240
	TCAGCAAATG	GCGCCGTACG	TAGATGAATT	TATTGAAAAT	CGTATGGGTG	GATTTTTTGG	300
5	TGTGAAAAAA	TCTAAAAATC	CAAATGCAAA	ACGTGTAATG	ATTGCAGCAC	ATATGGaTGA	360
	AATCGGATTT	ATGATTACAA	ATATCACTAA	AAATGGAATG	ATTCAATTCA	CAAATTTAGG	420
	TGGTGTTGCA	AATGATATTT	GGCAAGGACA	ACGCTTAGTA	ATAAAAATA	GAAATGGCGA	480
0	TAAAATTATC	GGTGTTGTTT	СТААТАТАСС	TAAACATTTT	CGTACTGGTA	GTGAAGGTGC	540
	ACCGGAAATT	AAAGATTTAA	CATTAGATAT	AGGTGCTCAA	AATGAAGATG	AGGTGCGTGA	600
5	gCGCGGAATA	GATATAGGAG	ATACAATTGT	ACCTCACACG	CCATTCACAC	AGTTATCTGA	660
	ACATCGATAT	AGTGCTAAAG	CATGGGATAA	TCGTTATGGT	TGTGTCTTGG	CAATTGAAAT	720
	ACTAGAATTA	TTAAAAGATA	TAGAATTAGA	TGTAGACTTG	TATGTTGGCG	CAAATGTTCA	780
20	AGAAGAGGTT	GGATTACGAG	GTGCGAAAGC	ATCTGCAGAG	ATGATAGACC	CAGACGTTGC	840
	ATTTGTAGTT	GATTGTTCAC	CTGCCAATGA	CGTTAAAGGA	AACCAACCAT	TATCTGGTGA	900
	ACTTGGTAAA	GGGACGTTAA	TTCGCATAAA	AGACGGTACA	ATGATTTTAA	AGCCTGTATT	960
?5	TAGAGACTAT	TTATTAAAGT	TAGTAGAAGC	ACATGACATT	GAACATCAAT	ACTATATGTC	1020
	ACCAGGTGGA	ACAGATGGTG	GAGAAATTCA	TAAAGCTAAT	ATTGGTATTC	CGACTGCAGT	1080
	TATTGGTGTA	TGTGCACGAT	ATATTCATAG	TACAGACTCA	GTATTTGATA	TAAGAGACTA	1140
30	TTTTGCAGCT	AGATCTTTAC	TTTCAGAAGC	CATTTGTAAT	TTAGATAATA	ATCAAATAGA	1200
	AACATTACAA	TATAAATAAT	CGGGTAATAA	CAACTATTAT	CTCTAAATAG	TTATATATAA	1260
35	TCATTAATTA	AGGAGACATA	AAAATGAAAC	AACTTGAATC	AGAACAACAA	TTTGAATCTT	1320
	TAAAACAAGG	TGCTACAGTA	TTTGAATTCA	CTGCAGGCTG	GTGTCCAGAT	TGTAGAGTGA	1380
	TAGAACCAGA	TTTACCGGAA	TTAGAAGCGA	GATATCCTAT	GTTTGACTTC	GTATCAGTAG	1440
40	ACCGTGATAA	ATTTATGGAT	ATTTGTATTG	AAAATGGTAT	TATGGGTATT	CCAAGTTTTC	1500
	TAGTATATAA	AAATGGAGAA	CTGCTTGGAA	GTTATATTGG	AAAAGAACGA	AAATCAATTG	1560
	AACAGATAGA	TGCATTTTTA	GCTCAATACG	TGTAATTTAG	ACTAGAGAAA	AACGGGGTAA	1620
45	TACTCGTTTT	TCTCTGTTAC	TATGTGTTGA	TTTATTGTAA	ACTATTATAA	GGTGCGAAAT	1680
	TAGGAGTGTT	ACATATGAAT	ACCTTTCAAA	TGAGAGATAA	ATTAAAGGAA	CGTTTAAGCC	174
5 <i>0</i>	ATTTAGACGT	TGATTTTAAA	TTTAATCGTG	AAGAAGAAAC	TTTGCGTATT	TATCGAACAG	180
50	ATAATAACAA	AGGTATCACG	ATTAAACTTA	ACGCTATAGT	CGCAAAATAT	GAAGATAAAA	186
	AAGAAAAAAT	TGTAGATGAA	ATTGTTTATT	ACGTTGATG			189

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3774 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660:

10	GTATAATATC	CTTTCAATCT	GTTTTCATAT	TTATATATTT	TTTTAAATAT	AAGTGCTAAA	60
	TGTTTTAACT	AAAGCATAGA	TTGACAAGAT	GTTATACAGA	ATTTCAAATT	CTATCCAATA	120
15	TTGTTCGAAG	TGTAGTATCA	CTGGATTGGT	ATTAAACAAT	GTAAAGGAGA	GATTGCAAAT	180
	GCCGTATAAT	TACAAGAAAC	AAAATGGAGA	GTTAATGTCT	GTAATGAGCC	AAGGTGAAAA	240
	GTTTATTCAT	CAATCACCCG	TTAATGATGA	ACTTAGTGCA	TTGATTAAGT	TATTAATTTC	300
20	TAAAATTAAC	GGTTGTCATT	ATTGTGTTGA	TATCCATAAA	AAAGAATTAA	AGGAATTGGG	360
	TGTAaCACAA	ATGAAAATTG	ATGAAGTCTT	GAGTTTTAGA	CATTTAGATT	TATTTACTGA	420
	TCAAGAAAAA	GTGACGCTTG	AATTTGCAGA	AATGTTAAAT	TCAATCAAAG	ACTTTAAGAA	480
25	GTTTGAAATT	ATTGACCGGC	TAAAATCATT	TTATGATGAA	GAACAAATTA	TTGATCTTGT	540
	CTTTGTTGTA	AACCAAATTA	ACGGTTGGAA	CAGATTAAAT	ATTATTAGTG	ATAGACTATA	600
30	ATTGTTCATA	TAAATGCAGA	GTTTCATCTC	GAACGCTATA	TCATAACAAA	TCATGCCACT	660
	ATACAGGTCA	AATCTTGTAT	AGTGGCATTT	TAATTTATCC	CTTTGAATAC	TGTTATTTAA	720
	CGAATATCGG	TCCACCTGGT	CCAACAGGGA	TACCTAATAG	GAACCAAATG	ATGACAAATA	780
35	CTGTCCATAC	AATACTTAGC	GCGATTGAAT	ACGGCATTAA	ACTAGAAAGT	AAGGCTCCGA	840
	GTTTCATGCG	TTTATCGTAT	TTTTGTGCAT	AAGTTAATAA	TAAAGGTAAG	TACGGCATCA	900
	TCGGTGTAAT	TGGATTGGTA	ATTGAATCGC	CTACACGGTA	AATGACTTGT	GTGAATGCGG	960
40	GATGAAAGCC	GATAAGGATT	AACATTGGTA	CGAATATCGG	TCCTAAAATA	CCCCATTTAG	1020
	CCGATGCGCT	TCCGATTAAC	ATGTTGACCA	TTGCACTCAG	TACAATAATA	CCTAGTATCA	1080
	ATACAATACC	GTTTTGATGT	TCTAATAATT	TGGCACCTTT	AACAGCAGCG	ATAATTCCTA	1140
45	AATTACTCCA	CTTTAAATAC	GCAAGTAGCT	GTGCTGCAAA	AAACACAATA	ACGATAAATG	1200
	TTCCCATTGA	TCCTACAGCA	TCGCCGAACA	TTTTACCTAA	GTCTTTTGTA	TTTTTAATTT	1260
50	CTTTGCTTAA	AATCCCATAA	ACTAATCCAG	GTACTAAAAA	TACGACAAGA	ATAATTAATC	1320
	CGACACCGTT	AATTAATGGC	GCATCGTCTA	GTAAGCTGCC	TGTTTTAGCA	TTTCTTAAAA	1380
	AGCTATGTTC	AGGAATGGCT	מדיים מדים מדים	ТААТАААТА	TGTGACTATG	АААСТСАТАТ	144

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	CATCATGCAT	TAAACTGTCA	TCATATTTTC	CTAATCTAGG	AATAATGAGC	TTAGTTGTAA	1560
	CTAGCAATAT	CGTAGGAAGT	AATACAACGA	CACTCGCTGC	GATAAAGTAC	CAGTTCATAG	1620
5	CAACGTTTGT	TTTAATAGAA	TCTGAAACGA	TACGTGTTGC	CGGTTCTGTA	AATGAATAGA	1680
	CCAAAGCATC	TTGCATACCA	ACAACTATAT	TTGCTGCAAA	TCCTCCAACA	GCGGAAGCAT	1740
	ATGCCATCGT	TAGTCCAGCG	ATAGGGTGAT	AGCCAATTTT	AATAAAAAGC	ATTGCTGCAA	1800
10	GCGGCGGCAA	GATAATTGTC	GCAGCATCGC	CGGCTGTACT	ACCTAAAATA	CCAATTAATA	1860
	TAATAGTCGG	TAAAATTAAG	AAACGTGGTG	CGCGATTCAC	AACAGAAATC	ATTAACTTAT	1920
15	CGAAGTATCC	TGTTTTCTCT	GCAACACCAA	TACCAATCAT	CACTGCTAGT	ACTAAGCCTA	1980
	ATGCTGGGAA	CTCTGAGAAA	TTTTTAATCG	TATCATTCAT	TATCATCGTA	AATCCATCAT	2040
	GGCTAATTAT	ATTTTTAATA	TAAATGGTTT	GATGCGTACC	TGGATGCTTA	ACAGATACAT	2100
20	TAAATAATGA	GATAACCCAT	GTCATAATGG	CTAAGCCCAC	ACACATTAAA	AAGAATAAGA	2160
	CGCTAGGATC	TGGCAATTTA	TTTCCGATTT	TTTCAACACT	ATTCAAGAAA	CGATTGACGA	2220
	TAGACCCCTT	TTGTTGATGT	TTTGATGTCA	TCAATTATTC	CCCCCTTTGT	ATTTATAAAT	2280
25	AAGTGTAACA	AAAAATACTC	TCAAAAGTAA	CAATTTTCAG	GAAATAAAAA	AACTAATATT	2340
	GTTAAATATT	TTGAGTTATT	CAATAGAAAG	TGTATAGCAG	AGTAGTTAAG	ACTGCCTGAA	2400
	GACTTATCTA	TTAGGTTTAT	GAAGCATCGA	ACAGTGGAAA	ATAAGGACTG	TAAGTTTAAG	2460
30	ATATGTTGTA	TAGGAGTGAC	TGAATGAAAC	GTTTGGAAAA	TAAAGTAGCA	GTCGTAACAG	2520
	GAGCAAGTAC	AGGTATCGGT	CAAGCTTCTG	CAATCGCTTT	AGCTCAATAA	GGTGCGTATG	2580
35	TATTGGCGGT	AGACATAGCT	GAAGCGGTAT	CGGAGACTGT	CGATAAAATT	AAAAGTAATG	2640
	GTGACAATGC	GAAGGCGTAT	AATGTGGATA	ATGCAAGCGA	ACAACAAGTG	GTAGACTTTG	2700
	TGTCTGACAT	AAAGGAACAG	TTTGGAAGAA	TCGATGTGTT	GTTTAATAAT	GCCGGTGTGG	2760
40	ATAATGCGGC	TGATAGAATT	CATGAGTATC	CAATAGATGT	GTATGACAAG	ATTATGAATG	2820
	TAGATATGCG	TGGGACATTT	TTAATGACGA	AAATGATGTT	ACCTTTAATG	ATGAATCAAG	2880
	GTGGCTCTAT	TGTTAATACG	TCTTCATTTT	CCGGACAAGC	AGCAGACTTG	TATCGCTCTG	2940
45	GATATAATGC	TGCGAAAGGT	GCAGTGATTA	ATTTTACAAA	ATCAATCGCA	ATTGAGTATG	3000
	GCCGTGATAG	CATTCGAGCC	AATGCGATTG	CACCAGGTAC	AATTGAAACC	CCGTTAGTAG	3060
50	ATAAACTGAC	AGGTACGAGT	GAGGATGATG	CAGGTAAAAC	ATTTAGAGAA	AATCAAAAAT	3120
50	GGATGACTCC	GCTGGGACGT	TTAGGTAAAC	CAGAAGAAGT	TGCTAAATTA	GTAGTCTTCT	3180
	TAGCATCTGA	CGACAGTTCA	TTCATAACTG	GAGAGACGAT	TCGAATTGAT	GGTGGTGTGA	3240

AATTATTAA	AATCGATATC	CAGTGGAAAA	GAATTTGGCA	TGAAGTAGGC	AATGTATGCA	3360
TATTGTCGCA	ATGAAAGACA	TTTAAAGCGG	AGATTAATTA	ATCTTTGAAA	ATCACATATT	3420
GTTCATTTGA	AGTGTATTGC	TTAAAGCTTG	TTTTAACGTA	TTGTAGGTCG	TGCATCTAAT	3480
TTATCAGAAT	CTCGAGTTCA	AACTTTTGGA	GTATCTTTAA	AATAAGCTGT	ATTTTGTCTA	3540
TTCTAATAAA	TTAAGGAGAA	TTTTATGTTA	AAAGAAAAAG	AAAGTTTTAG	ATTGCTATAT	3600
CAAGCTATAA	GAGAGATTGC	AGATAAAATT	GGAGATAATC	AGTTAGAAAC	TAATTCCGTT	3660
AGTTTATLAT	tATTGGACTT	TGATTTTGAA	CATGAAGTAT	TTGATGAATT	GTATCTTGTG	3720
ATTTLAAAAI	ATTTAAATAC	AGTAAGTATA	GAGAACATAA	GTCATAGTGA	GCTT	3774

(2) INFORMATION FOR SEQ ID NO: 661:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1078 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661:

TACTGGTTTT	GGATTTTGGA	GGTAATACAG	TACCTAATAG	TAATHATGGT	GICGICANAA	60
TTATATCTTT	CCGTGATGTT	CTTACTCATT	AGAACATCnG	CCTTCAGAGG	AATCATGATA	120
CGAGGAATAA	GAAATTTAAA	TGTGAGCGAA	GTCAATATAG	TATTTGCGAT	TATTTTTATT	180
AACTCCATTA	TTATTGTTAG	TTTGATTTTT	CGAGGATAAC	TTCAATTTTT	GCATTTTGAG	240
GTTTTTTAAC	ATATCTATTT	GCATCAGTTG	ATGGCAACCT	TTTACTTAAA	TCTATTGTGT	300
AGTTATTGTC	TGCACCTGTT	ATTTTAATTT	GTCCTTTATT	ATAAGAATTA	TTATATATT	360
TTTTACTTTT	AATTAATGTT	TGACGAATAC	GAAAATCTAA	TTCTTTTAAA	GTTAAAACAG	420
GCTTATTGCC	TTCATAAACT	GGAAATCCGC	CAGTAAACGT	TTCTGCTTTA	TCTTTATATG	480
TTACATTCAG	TTTATAGTGT	TTATCGTTAG	ATGTTGCTGC	AGGAGTAACA	CCACCAGTAA	540
ACGTTTCTTC	AGATAATGCA	AAAGaATCAA	TGGTTTCTTG	GTCTTTTATG	Суалалатат	600
CAACGCTTTT	ATTTCTTAAT	TGGTTGATAT	TGCCCCAACT	TTCAGGTCCA	TAAACTTGAA	660
TATGACTATA	CCAAGAAAAC	TGTAACAACG	TTGCATGAAT	CGTACCGTTA	TCTTTTTGCC	720
ATAACGTACT	GTTAGAGAAG	GTTAAATATT	TTTGCGAGTA	ATATTTAGTT	AACTCATTAA	780
CGTTAGTTTC	GTTTTGATTT	ATATAAtAAG	cTTTCGCTTC	AGATGAAGAA	TTGATAKGTG	840
TATTAGGAAZ	TTGTGTAGAT	GCTGTACCTA	ATAGTAACAA	TGTTGTTGAT	TTTAATAAAA	900

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ATAAAAAGGG GTTAATTAGA TAATTGAAAT TATCCGCATT TACAAAAGGT AATAGGTTAG

1020
TTAGATTTTT CGAGTATGAC TCAATTTCTG CATTACGAGG ATTTTTAACA TAACGGTT

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(2) INFORMATION FOR SEQ ID NO: 662:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1398 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662:

ATTAA 60	TATTAATT.	ATTTCACTTG	AATAGCTTTA	CGTTAATATT	TTAGTATCTA	AACTTGCTTT
AAGTA 120	TTTTAAAG	TTTGTTCCAT	GATAACTTTC	CTTTCAAATC	TAAATACCTG	ATCAGCTGTG
TCTGA 180	CTCTGTCT	TCACTAATAC	TAAATCTATA	TCGATAGTCT	TTCGCTTGCT	AACAGTATAT
TTATT 240	GATTCTTA	CTAATATTT	ATCTTTATAA	TATCCTCTAA	GATTTAACTC	TTTTAAAACT
GGAAC 300	CATATGGA	ACAGTGaTTG	TGTACCGTTC	TATTTTGGCT	CTTGATAAAA	aaatgttaag
GCTGC 360	GCTTAGCT	TTATCTAATG	ACTTGATGAT	GGTGTAACGA	GAATATCCAT	ATGGACTTTA
GCTAA 420	CTAATGCT	GCTAAAACAC	ACCTGTTGAT	TAAAGTTTGC	TCATTATTAT	GGCAGACGCT
TTCGT 480	TGTAATTC	TCCTTTTTTG	AAATTATCTC	TAAATTTCAT	ATCAATGACT	AGTTGTTGTA
'AATAA 540	TAATTATA	AATTAACTGA	CTATTTTTTG	CAGACTTTCT	TAATTATAGC	ATTTGCAACT
TTAAC 600	TTTGATTA	TTCTTTTAAT	CTGTTAAAAG	TTTTTTAACA	TTAACAATAA	TAAATTATCT
ACTTA 660	TTCAAACT	TATACCAAGC	TGGTTTTGTT	AAATGTTGTT	ACAATACCTA	TAATTAATTT
CAGCA 720	ATTTACAG	TGTCGATTAT	CTATTAGATT	TTCTTAATTC	CAACATTCAT	AATGTCATAA
TTAAA 780	TTAATTTA	GATTTAATAA	ATATAAATTC	TTACTTAAAA	CAAAAAACAT	TCTTTATACT
ATGAT 840	TGATAATG	ATAAAAGGAG	TGTAAGCTAT	TCTATTTTGT	CAATTTTGCA	TTTAGTTAAT
AAATTT 900	TAGCAAAT	ACACTTGCAT	AAAAGTTGCA	ATTCACTAAA	ACAAAATCCA	GGTGAAAAA
TGATAC 960	AAGATGAT	GAATCTAAGA	TGCCAAAGCC	CTGaCAATAG	GGTGCACTTA	ATTATTAGTT
AAACTG 1020	ATCCAAAC	ACCGTTTTGT	TATGTTATCG	ATAACGTTTA	TTAGTTAGTC	TGATTTGAAG
rgatgt 1080	ATAATGAT	TATATTAAAA	ACAATCTTCT	ATTTAATCGG	AAACGCGCTG	GGGGCAATAT
rgtgaa 1140	GTAATGTO	AAATTATTAA	TGCATCAGAC	TTGATAATGG	AATGAAGCAT	CGTAATATTC
CAAAAC 1200	GGGACAA	CAATCAGGGT	CGGCCGTTCT	CACCTGTACT	CCTTATCAAA	AAAAGAATAT
T	TAAGTAAZ	GTAGCGATTG	AGATGGTGGC	CTGTTGCAGA	TACTCATCAA	TGAAGGTAGC

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CAACAAAGGC TTTGTTTATA CAAAAATAGA GAAAAATGGT AAGAACGTTC ACGTTAT	rccc 1380
TACACATACA CAATCTGA	1398
(2) INFORMATION FOR SEQ ID NO: 663:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1200 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663:

TTGTAATTGG AACGTACGAA CTTTTCTAGG TAAGAAACGT CGAATCTCGT CCTCATTATA 60 ACCAACTTGT AGTCGTTTAT TATCTAAAAT AATTGGACGA CGTAATAAGC CAGGATTATC TTGAATGATT GAATATAAGT CTTGTAATGG TAGTGAATCA ATATCAACAT TTAATTTTTG 180 GTATGTTTTA GAAGGTGTAG AAATGATTTC ATCAGTACCG TCTTCAGTCA TTTTTAATAT TTGCTTAATT TCATCAATTG TTAAATGTTC AGAAAAAATA TTACGCTCCG TATACGGAAT .300 GTCcATGTTC tTGkTAACCA TGCTTTCGCT TTTACGGCAA GATGTGCAAC TTGGtGaAGT 360 AAATAATGET ACCATACATC TCACTCTCCT ATTTGAATGA ATAAAATTCA TTGCTTAAAA 420 TTTAGTTATA GATCAAGAAA AAACATTTTT TTCTAAAATT CTTAATCGTT ACTATTTATT 480 540 ATAACTATCT AACATTAAAA TTAAATGAGA AAAACCTAAT TTTTCAGATA AGTTTCTACA CTTATAAAAA AGATTATTAA TCCCTTTGTT AGTAGTAAGT TATACGTATA TTCTAACACA 600 TCTTACATTT TTAAGAAATA CTGTTATAAT GATAATTATT AAAATATTAC TAAGAAAGTA 660 GGCATTTAAA TGGAGACATT ATTTTCAGGC ATCCAACCTA GTGGAATTCC TACTATTGGA 720 AATTATATTG GCGCACTAAA ACAATTTGTT GATGTGCAAA ATGACTATGA TTGTTATTTC 780 TGTATCGTAG ATCAACATGC AATTACAATG CCACAAGATC GTTTAAAATT ACGTAAACAG 840 900 ACCAGACAAT TAGCAGCGAT TTATTTAGCT TCTGGTATAG ATCCAGACAA AGCAACATTG TTCATACAAT CTGAAGTCcC TGCACACGTA CAAGCAGGAT GGATGTTAAC TACGATTGCT 960 1020 TCTGTTGGAG AATTAGAGCG TATGACGCAA TACAAAGATA AAGCTCAGAA AGCAGTTGAA GGTATACCTG CTGGTCTATT AACATATCCA CCTTTAATGG CAGCTGATAT TGTTCTTTAC 1080 1140 AATACTAATA TCGTTCCAGT TGGAGATGAC CAAAAGCAGC ATATCGAATT GACTCGTAAC CTTGTAGATA GATTTAATAG TCGCTATAAT GATGTGCTTG TGAACCTGAA ATTCGTATGC 1200

(2) INFORMATION FOR SEQ ID NO: 664:

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5	(A) LENGTH: 787 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 664:	
10	TGTACCTTTT GCTTTAATAA ATACTGTTTC TTTATCATAA TTAGGTTCAG TTAAGAAATT	60
	AAATTGTAAG CTTTGAGTAA TATTTTTTTG ACTATCACTT GTTGTAGCTG TACGTGTATA	120
	CATTTAGTA TCACCATCAA GATTCTTCTC AGAAACTTGT TTGATTTCAG AATTAATCTT	180
15	TGCAAATGAA GTAGCTGGTA ATACAGTGAA AGTAGTCGAT AGTGCTAAsG WACAAATTGT	240
	GATATTTTTA CATAGTTGTT TAATCATTAG TAATCCGCCC TTTCAATATT ATCCTTCTTT	300
20	ATAAGGTTTA TTGTCATCAG AATATTTATC AACGACTTTA ACTGTTTTAT TTTTCCAATC	360
20	AACTTCATAA GTGACAATTA ATCTTTGACC ATCTTTATTT TtcTCTAAAA TTGGAGGTGC	420
	ATAATGTATY CCAGGTCTGT TTTTCAAAAT ATCTTGATTT CGTGTGTATG TTACTTCAAA	480
25	TTGCGTTTTC TCATTTGACT TTTCATTAGA TAAATAAGTT AAAAATTCTG GATTAAAGCC	540
	ACTTCTTACT AATGCTGGGT ATCTATATTT TGAAGCAAAG CTTAGTTCAG GGTTTTCTAC	600
	AGTAGCAATT CTCGTATTTC TATAGAATAA TAATTCATCA TTTCTATTTT TCACTTCTCC	660
30	ACCATACTTC AAGTCATTCG CAATAACTGA CCAGTGTACA TGGCCAGTTn ATTTATTTTT	720
	ACCGCTGGCA ATTGTGTCAT AATTTGCTGC ATCATCAACT AATCGTTTTG GAAGTAGCTA	780
	TTTGCTG	787
35	(2) INFORMATION FOR SEQ ID NO: 665:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 533 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 665:	
	TTATCTGTCA TTAACCACTG GTACATGTGA ACCCGGCnTn AATCAATATA TATATTTAAA	60
	AGCAAAGGCG CGCCATGTGC CTTTtTTnTA tTTTGTATAT CTGTATCAAA ATCGATTTGA	120
50	TTAAAATCCG CTTTATTTTA TCATCTATTC AAATGATTTT AGTGCGCTTA TTTTACTATG	180
	GCATTATTGC CTAACCTGTT TGAGATATAT TAATATTTGA TGATTCGTAT TCAAAGTTTT	240
EE	CATTTAACAT GTATTTAGTA TCATGATAGC TGCTTCATTG ATGATATACT ACCTACTTTT	300
<i>5</i> 5	•	

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CAGAGGCAAT ATTGAACAAT TCTTCATCAT GACTATTTTC CATCACATAA CTATGCTTAG	420
CGAACGCTAA CATATCTTTA TCATTATTCG CATCTCCGAA GGCCATGAGC TCTGAAGGAG	480
ACATTTCCCA TTTATCTAAC AATCGTTTTA ATGCCTGnCC TTTAGTCATG TTT	533
(2) INFORMATION FOR SEQ ID NO: 666:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 666:	-
GACTTCTCTT GCACTAAAAA TTGCTCAAAT TGCTCGCTGT CATAACCAGG CGGTGTTTCC	60
AACCATACAT ATATGCCACC TTTAGCATGA ACAAATGGCA AATCAGCTTT TGCAAGCATG	120
GCTTCGAATC GGTCACGACG TGTTTTAAAT ACATTGCTTT GTTCTTCTAA AAAATCATCA	180
TAATGGATTC AAAGCATATA TTGCGGTCAT CTTGTAAATG CACCAAACAT CCCAGCATTT	240
GTGTGCGTTT GGTACTTTTT CAAAGCTTGA AATCATATCT TTATTACCAA CTGCCAAAAC	300
	360
CGACTCTGAA AACCTGGACA TGTTGATGAA CCTTTnAGAC AAGGGAAGAA ATTTGCAATC	
GCAACATCTT TGCCCATTTT nCCGAAGCAA GTGnGACTAG	400
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 412 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667:	
TCTCCAATGC TACTCAAATT AAAAAGGTTT TAAATATTGT TAATTCTGAT CCAGAGCGAA	60
AGATTGTTAT CGTTTCTGCT CCAGGTAAAA GACATGATAA TGATATTAAA ACAACTGATT	120
TGTTAATCAG ATTATATGAA AAGGTCATTA ATCATCTTGA TTATCATGAT AAAAAAAGAG	180
AAATTATTCA GCGTTATGAT GATATTGTAA AAGAATTGCA AATGGATGAA AGTATTTTAC	240
GGACGATAGA TGTGACTTTG GAACATTATA TAAATCAATT AAAAAATGAA CCAAAGAGAC	300
TATTAGATGC ATTACTTTCT TGTGGTGAAG ATTTTAATGC GCAAYTGALA GCYTTATATA	360
ATAALAGTCA GGTLACCAAC AAMATWTATA TCCcCGAAGG AAGCGGGTAT TT	412

(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668:	
	TTACTCGTTA AAGATATTGT AAAAGATGAA GTGACAGAAT ATGACATTCA TCAAATGTTA	60
	CCGCATCCGA TTAATATGGT AAGGGTTAGA CTTTTTGGTG TGAAATTAAA AGAGATTATA	120
15	GCTAAAAGTA ATAAACAAGA nTATATGTAT GAACATGCAC AAGGTTTGGG TTTCAGAGGG	180
	AATATATTG GAGGATATAT TCTTTATAAT TTAGGGTACA TTCATTCTAC AGGGCGTTAC	240
	TATCTGAATG GAGAAGAAAT CGAGGACGAC AAGGAATATG TACTAGGTAC GATAGATATG	300
20	TATACGTTCG GTCnTATTnC CCAACATTGA AGGATTACCA AAGAGTATTT AATGCCAGAG	360
	TTTTTCAGAG GTATATTAA nGAAAATTAT TGGCTATTTA	400
25	(2) INFORMATION FOR SEQ ID NO: 669: (i) SEQUENCE CHARACTERISTICS:	
3 <i>0</i>	(A) LENGTH: 1236 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669:	
35	TGTTCGATAT TTTTAAATTT ATCTTTTAAA TACAACAACT GTTTCCGTAA TGATTTAACT	60
	GTTTTATGAC TAATGCCATT GAATATTTCT AGCGTTTTAT TTAACTTATC GATAATCGCA	120
	TGTAAATCCT TCAAAATGTC TTTTGTTTCA AAAGTAAATA CATTATGGAA GCGATGAATA	180
40	TCATCATCAT AAACATCAGA ATCATTGATA ATCGTAAATA TCGTTGAGAA CAATTGCTCA	240
	TTTAACTCAT GAATCTCATT CATACTAGCC TTCAAGCCAA AAATATCAAT TGGTGCAATA	300
45	TCTAATTTT CCAAAATTCG CTGCTTTTCC AGTTGATCAA TTGCCTTTAA CAATTTTCA	360
	TTTTCGTTTT TACCAATCAA ACCAAGCTGA TATTTAATAT CAGCATAACT CAACTCATTT	420
	GTCACTTGAT TTAAGGCATA GTCTGGTAAG CGATGTGCTT CATCCACTAT ACAATCATCA	480
50	AACAATTGAT ATATTGAATT TTCAACATCA GAATGAATTA AATGTGCATG ATTTGTAATA	540
	CCAATTTGAA TGTTCTGTGC ATTTCGCTTA ATAAAATTAT AATAATGAAC ATCGTGACGT	60
	GCCGGTACAT ATGTTTCAAT TTTCTGGTCA AAATACATCT TTTGACCACC TTTTAAATTT	66
C C		

ATATTCACLT	CGTAATTACT	TGTGTCATCT	TTTAAAATTT	GACTAATAAG	CCCCAATGAA	780
ATGTAATCaC	TTLTACTTTT	AATCAATAGT	GCATTAATTT	TAAAATTCAA	CGCTTCATTC	840
ATTGCTGGAA	TATCTTTTTC	TAACAATTGA	CTTTGCAGTA	ATTTAGTATT	GGTAGAAATC	900
ATGACATGCT	TCCCAGTTTC	AATATTATAC	ATCAAGGCCG	CAAGTAAATA	TGCTAATGAT	960
TTACCACTGC	CTAGTGATGC	TTCAATCATT	GCTTTTTCAC	TATGCATGAG	CTGATCTAAT	1020
ATAGTTTCCG	СТАААТАТАА	TTGTTGCGGT	CGATATGTTA	AGCCAAGTTG	ATCTACAGCT	1080
TTGCTATATA	AAGACTTCAA	GCTGCCATTA	TAATTTGTTG	TCGGCTTTTT	AAAATCAACT	1140
TGCTTACGAT	AGATAATCTG	TTCGAACTTT	TCGTACGATT	TATCCAATGG	CTTTGCATCA	1200
TATTGCCTAA	CCATCTCAAA	GAAAATATCA	TACAAA			1236

(2) INFORMATION FOR SEQ ID NO: 670:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1819 base pairs

 - (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670:

ı	ACASAATTAT	TGACCAATAT	GACTCGTGGA	CTGATATGTT	TAAAGCACTA	CTGCATGAAA	60
	CATTTAAAGC	ATATGGCGTT	CTATTTATAG	ATGCGCAGTT	TGAGCCGTTA	AGAAAAATGG	120
	AAGCGCCTAT	GTTTAAAAAG	ATTTTGAAAA	AACATCAGTT	GCTTGATGAT	GCTTTTAGAG	180
i	CAACACAACA	ACGTACTCAA	AATCAAGGCT	TGAATGCGAT	GATACAAACA	GATACAAATG	240
	TTCATTTATT	CTTACATGAT	GAAAATATGC	GTCAATTAGT	tTCGTATGAT	GGTAAGCAYT	300
	TTAMATTAAA	TAAAACAGAT	AAGACATATA	TAAAGGAAGA	AATTATAAAT	ATTGCGGAAA	360
)	ATCAACCKGA	ATTATTTTCT	aATAATGTAG	TGACAAGACC	ATTAATGGnA	GAATGGTTAT	420
	TTGAACACGG	TGGCATTTGT	TGGAGGACCG	AGTGAAATTA	AGTaCTGGGC	TGAACTAAAA	480
5	GATGTATTTG	AACTATTTGA	TGTTGAAATG	CCLATCGTGA	TGCCAAGGCT	TAGAATTACT	540
Ci Ai T T A T T T	TATTTAAATG	ACCGTATAGA	AAAATTACTT	TCGAAATACA	ATATTCCATT	AGAAAAGTG	600
	TTAGTCGATG	GTGTTGAAGG	AGAAAGAAGT	AAGTTTATTA	GAGAACAAGC	ATCACATCAA	660
0	TTTATTGAAA	AGGTAGAAGG	TATGATTGAA	CAACAGCGTC	GTCTAAACAA	AGACTTATTA	720
	GATGAAGTGG	CGGGGAATCA	AAATAATATT	AACCTTGTGA	. АТААААТА	TGAAATTCAT	780
	ATACAACAGT	ATGATTATTT	GTTAAAACGT	TATCTTTAA	ACATTGAAAG	AGTAAACGAC	840

	GAAAGAATAT	GGAATCCACT	TCAAATTTTG	AATGATTTTG	GGACAGATGT	GTTCAAGCCC	960
5	TCCACCTATC	CACCACTTTC	TTACACTTTT	GATCATATTA	TTATAAAACC	TTAATATACC	1020
5	AAGGGTTTAG	CCCGATTTAT	CTTAATGATA	AATCGGGCAT	TTTTTTGTTT	TTTAAAATAA	1080
	ATTTCACAAA	TTTTGTATAA	ATAGTGGTGG	ATAGTGGGGA	GATGTGGTAA	ATTATATATA	1140
10	AGGTGAGGTG	ATAAAAAATG	TTCATGGGAG	aATACGATCA	TCAATTAGAT	ACAAAAGGAC	1200
	GTATGATTAT	ACCGTCCAAG	TTTCGTTATG	ACTTAAATGA	GCGTTTTATT	ATCACAAGAG	1260
	GCCTTGATAA	ATGTTTATTC	GGTTACACTC	TAGACGAATG	GCAACAGATT	GAAGAGAAAA	1320
15	TGAAAACCTT	ACCTATGACA	AAAAAAGACG	CACGTAAGTT	TATGCGTATG	TTCTTCTCTG	1380
	GTGCTGTTGA	AGTAGAACTT	GATAAGCAAG	GGCGTATTAA	CATCCCTCAA	AACTTGAGGA	1440
00	AATACGCTAA	TTTAACTAAA	GAATGTACAG	TAATCGGTGT	TTCAAATCGT	ATTGAGATTT	1500
20	GGGATAGAGA	AACTTGGAAT	GATTTCTATG	AAGAATCTGA	AGAAAGTTTC	GAAGATATTG	1560
	CTGAAGATTT	AATAGATTTT	GATTTTTAAA	ATGGAGGAAT	TGAAGLGTTT	CATCATATCA	1620
25	GCGTTATGTT	AAACGAAACC	ATTGATTATT	TAAATGTAAA	AGAAAATGGT	GTGTACATTG	1680
	ACTGTACGCT	AGGTGGAGCG	GGACAnGCCC	TTTATTTACT	AAATCAATTA	AATGACGACG	1740
	GAAGATTAAT	AGCAATCGAT	CAAGACCAAA	CTGCAATTGA	TAATGCTAAA	nGGGTATTAA	1800
30	AGGATCATTT	GCATAAAnG					1819

(2) INFORMATION FOR SEQ ID NO: 671:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 609 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671:

ACCAATTATT GGACAGGAAT TAGCAAAAAA TGCAATGCTT GCATTAATCT ATGCATCGAT 60 AGGTATCATC ATCTATGTAT CATTACGATT TGAATGGCGC ATGGGTCTTT CATCTGTATT 120 GGCATTATTA CATGATGTAT TCATTATAGT AGCGATTTTC AGTTTATTTA GAATTGAAGT 180 AGATTTAACA TTTATCGCCG CTGTATTAAC AATTGTCGGT TATTCAATTA ATGATACAAT 240 CGTAACGTTT GACCGTGTAC GTGAAAACTT ACAAAAGGTT AAAGTGATTA CGACAACAGA 300 ACAAATTGAT GATATCGTTA ATAGATCAAT tAGACAGACA ATGACACGTT CAATTAATAC 360 AGTATTAACA GITATTGTAG TAGTAGTTGC TATACTATTC TTCGGTGCTC CTACGATATT 420

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TGCCGTTCCG	CTATGGGGAA	TAATGAAAAA	ACGTCAGTTG	AAAAAATCGC	CGAAACACAA	540
ATTAGTTGTA	TATAAAGAAA	AGAAATCGAA	CGATGAAAAG	ATTTTAGTTT	AAAAtGaATT	600
AAGCGGTAT			٠			609

(2) INFORMATION FOR SEQ ID NO: 672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672:

CTTAAAACAG CAATTTGAAC GTTTACAAAA TGAACAAATC TTTGTTTATG TTTGTCATGG	60
TAATCACGAT CCTTTATCAT CAAAGATTTC ATCAAACTGG CCAGATAATG TENTTGTATT	120
TTCAAATAAA GTTGAGACGT ATGAAGCAAT TACTAAATCT GGTGAAACAA TTTATATTCA	180
CGGATTTAGT TATGAAAATA GAGCAAGTTA TGAGAACAAG ATTGATGAAT ATCCATCAAG	240
TCAAGGCCAA AAAGGCATAC ATATTGGTGT CTTGCATGGT ACGTATAGTA AATCTTCAGT	300
TAACGAAAGA TATACCGAGT TCATTTTAGA AGATTTAAAC AGTAAATTGT ATCATTATTG	360
GGCTTTAGGT CATATACATG AACGTCAACA ATTAAGTGAT ATGCCTGTAA TTAACTATTC	420
AGGTAATATT CAAGGTAGAC ATTTTAATGA GCAAGGTGAA AAAGGTTGCT TATTAATCGm	480
GGGTGACCAC TTAAAATTAA AGACTAAATT TTATCCTACA CAGTATATTA GATTTGAAGA	540
AGCAACTATT GAAACGGATA AGACATCTAA GCAAGGTTTA TACGAGGTCA TTCAAAACTT	600
TAAAGAACAA GTGAGAGAAG AAGGAAAAGC CTTTTATCGT TTAACGCTTG TTATTAATAG	660
TGAGACATTA ATTTCACCTC AAGATTTATT ACAAGTTGAA GAAATGATTA CAGATTATGA	720
AGAAAACGAA AATCAATTTG TATATATTGA TGAGTTAAAA ATACAATATG CACAAAATGA	780
TGAGTCACCT TTAGTTAATG AATTTTCAGC GGAATTATTA GTCGATCAAA CTGTTTTTGA	840
TAAAGCGATG TCAGATTTAT ATTTAAATCC AAGGGCATCT AAGTTCCTAG ACGATTATGG	900
AACATTCGAC CATACAGCAT TAGTTAATCG TGCTGAAGAA ATATTAAAAG CTGAAATGAG	960
AGGTGAACAA AATGATAATT AAATCACTTG AAATTTATGG TTACGGTCAA TTTGTTCAaC	1020
GTAAAATTGA ATTTAATAAA AACYTCACTG AAA1TTTTGG TGAAAATGAA GCGGGTAAAT	1080
CGACGATTCA AGCATECATC CATTCGATAT TATTTGGATT TCCAACTAAA AAGTCTAAAG	1140
AGCCAAGACT AGAACCACGT CTAGGTAACC AATACGGTGG TAAATTAGTA CTTATTCTTG	1200

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	TATATTTACC	TAATGGTGCT	GTGCGTGATG	ATGCTTGGTT	ACAAAAGAAA	CTTAATTATA	1320
	TTTCTAAAAA	GACATATCAA	GGTATCTTTT	CATTTGATGT	ACTAGGGCTT	CAAGACATTC	1380
5	ATAGAAATCT	AAATGAAAAA	CAATTGCAAG	ATTATTTATT	ACAAGCmGGG	GCTTTAGGAT	1440
	CAACTGAaTT	CACGTCAATG	CGCGAAGTGA	TTAATCGTAA	AAaAGATGAA	ТТАТАТАААА	1500
10	aATCAGGTAA	AAATCCGATC	ATTAATCAAC	AAATTGAGCA	ATTAAAACAA	CTAGAAAGTC	1560
	AAATTCGTGA	AGAAGAAGCA	AAGCTAGAAA	CATATCATCG	CTTAGTAGAT	GATCGAGATA	1620
	AATCATCACG	TCGATTAGAG	AATTTAAAGC	AAATTTAAA	TCAATTATCA	AAAATGCATG	1680
15	AAGAAAAACA	AAAAGAGGTT	GCTTTACATG	ATCATTCACA	AGAATGGAAG	TCTCTAGAAC	1740
	AACAGTTAAA	TATTGAGCCA	ATCACATTCC	CAGAAAAAGG	TGTGGATCGT	TACGAAAAAG	1800
	CACGAGCGCA	TAAGCAATCG	TTAGWAAGAG	ATATTGGTTT	AAGAAATGAG	CGTTTAGCTC	1860
20	AACTTAAAGA	AGAAGCGACT	CAATTAGAGC	CAGTTAAACA	ATCTGATATT	GACGCCTTCA	1920
	TTAGTTTGAA	TCAACAAGAA	AATGAAATTA	AAAATAAAGA	ATTTGAACTT	ACTGCAATCG	1980
05	AAAAGGATAT	TGCGAATAAA	CAACGTGATA	AAGATGAATT	GCAATCAAAT	ATTGGTTGGT	2040
25	CTGAAACGCA	TCATGACGTA	GATAGTTCAG	AGGCAATGAA	AAGTTATGTC	AGTGAGCAAA	2100
	TCAAGAATAA	ACAAGAACAA	GCTGCATACA	TTAAACAATT	AGAACGTAGT	TTAGAAGAAA	2160
30	ATAAAATCGA	AGATAATGCG	GTTCATAGCG	AACTAGATTC	TGTTGAAGAA	AAATAGTTCC	2220
	TG			٠			2222
	(2) INFORMA	ATION FOR SE	EQ ID NO: 6	73:	·		
35		EQUENCE CHAP (A) LENGTH: (B) TYPE: n (C) STRANDEI (D) TOPOLOGY	406 base pa cleic acid DNESS: doub	airs			

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673:

TTGCAGGTAT CATTTTTTA ATGCCATATG GATTATGTT TCTACCGTTT TATAAGCAAA 60

AAAAGAAAAA ACAGACATTT AAAAAATACA TGGTTTACAC TACGATTGGT TTGTCAATTT 120

GTCTAGGCTT ATCTCTAGTT TTGGTTCACA CTACGAAAAT TTATATGGAC GAAGGTGGCG 180

TAAGATACTA TTACGGTAGT TTTGTAATGA AACAAGCGGG CGGTTATGCT TATTTAGCTT 240

TAGCGGTACT TTCAACGTTG TTAATTGTTG CGAAAAAAGC TACAAATAAA AATAAAGAAA 300

TCGAAACCGT CGACAATACA AATATAACGG AAAGATAATT AAGGGAGTGC TCATTCAGGA 360

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(2) INFORMATION FOR SEQ ID NO: 674:

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 927 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
0	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674:	
	CCACTTTGTG GATTTTCTTT ATATTCTCCA CGCTTGtACT ACAACTTCTT TCGTTTCTGT	60
15	TTCATCACCG ACTGCCGCAT TCGTTAGCAC ATGTAATAAC TCTTTTGCGG TTAATACATT	120
	CTCATCTATA ATCTTATCTT TTTGTTCTTG TATATATTGC TTGATGTGCG GCTTTTTCAA	180
	TAACCTACAC GCTGTCACAT GTGCGCTATT TGCGTTATAT CCTGYTTTTA TGGCACTTTG	240
20	TGTTACATTC AGTGTTCTAA TATACTCATT CACAAAACGT GCTTGCTTTG CAGTTAACTC	300
	ACTCATTTTA TCACCCCCAC AATTTTATCT AATATGGTTT CATACCATAA TATTACAGAT	360
	TGTTCTGAAC AATCTAAGGC ACTACTAATA TCTTGATAAC TAAGTCCTTG TATAAGGGAG	420
25	TCAAAAATAT AAAACTCTTT ATCGGTCGCT AATCTGTCAA CAATCATTTC TATGTGATTC	480
	TTTATAATAT GATCATTGAC ATTATCGTCT GTCATCAATT CGTCAGAATC TTCATCACCT	540
30	ATTAAAAAGA AATCATCAGT ATTTATTTCA TCATCGCCCC GTTAACTAGC TTTGAAGTCT	600
00	TTAGCACACT TGCATATACC GGCTGTCGTG CTGGCKAGAT ACTAGCATTG AAGTGGTCTG	660
	ATATTGATTT TGAAAACAAC ACGATTAGTA TTACTAAAAC ATATTACAAT CCAAATAATA	720
35	ACAAGAAGAA ATATCAGATA CTTCCCCCTA AAACTGAAAG TTCTATCGGT AAGATTTCCG	780
	TTGACCCAAA TGTAATAAAG GEGETGCGEG ATTATAAGAT AAACGTTCAA AATAATTGGA	840
	AAAACGAATT ATATAATGAT AACCATTGTA ATGAAAAAAC TATCAATGTG GATACAAACC	900
40	ATTATGTCAC GTACCAGCAT ACTCAAA	927
	(2) INFORMATION FOR SEQ ID NO: 675:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1100 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675:	
	GATGTTAANA TAAGTACATC ATTTTGACTC CCAAATATTG GCTTTAGACC TTGAAATGCT	6

CTCATAATGG	CATCAGGTAC	cAGGGGTTGG	GaccAGGTGT	TAATAACAAC	GGTTGATGAT	180
AATACATTTA	TATGCCTCCT	ATAAATAAGA	TTTCACTATT	TTAGCAAATT	TTCTGAAAAT	240
TTAAAAGCCT	AAAAAgtGAT	AACGCTATAT	TGTCGAACAA	ACGTTATCAC	TTAACGATTT	300
TATTTGGCCT	GAATGATGGG	ATAGATTTTT	ATGTCCACAT	TATTTCTTAC	AGCATTTGAA	360
ATCATGCAAT	TATTATCTGC	AATTGTTATC	AATTTTGGTA	ATCGCTTTTC	TAATTGTGCT	420
ATTTGATCAC	TTGGAATTTG	AATTTGAGGA	TGGTGCACAA	TTTTTGACAT	ACTGAATTTT	480
CCGTTATTTA	AACAAGCTGT	TCCAATCGAT	TGTTGTkCAA	TTGAAATATC	TGTGAACTTT	540
GCACGTTCAA	GAGTAGCTGC	TAATGAGATG	ATATAACATG	ATGAAGCGGC	TGATACTAAC	600
ATTTCATCGG	GATTTGTTCC	TATACCAACA	CCACCTAAAG	AAGCAGGTAT	AGAAATATTC	660
TCTGAAAGTA	TGTCGCCTTG	AACGTTTCCG	ACATTGTTAC	GACCACCTTG	CCAAGAAGTT	720
TGGACTTTAA	AGTCATGTTG	ATGCAATTGC	TTTAACCTCC	AATATAATTG	TGATAGTTTA	780
ATTTTAGAAT	AGTTTATCAA	AGTTTAACAG	AAAGGTGACT	TATCAATGAC	TCTGAATAAA	840
CTGAAAGATG	AATTACAAAT	TGTTTCGCAC	CGTGGATTGC	CGAGTGATTT	TCCTGAAAAT	900
ACAATGGTCG	GTTATCGAGA	GGTAATGGGG	CTCAATGTTG	CTATGTTAGA	AATAGATGTT	960
CATTTGACCA	AAGACCAACA	TTTTGTTGTG	ATACATGATG	AAACAATTGa	TAGAACATCG	1020
GaTGGtArGG	GGCGTAwTGc	TGaTTACACA	TTATCGCAAT	TAAAATCATT	TGATTTTGGT	1080
AGTTATAAAG	ATGTTGCTTT					1100

(2) INFORMATION FOR SEQ ID NO: 676:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676:

ATTAATTCA TATGGAAATA GTTGAACTAA CTGCGCTGTA TAAGCTTCAA CAGTTTGATG 60

AATTAACGAT TGATCTTCAA TATATCCGTA GAACAAATCT TCAGTACAAA CTACTTTACC 120

TTTATCAGGT TTAATTGCAC CTGCCAACAA TTGACCTACC AACGCTTTGG AAGATTCAGG 180

TTCACCAATT ATACCTAATG CTTCTCCTTG ATAAATATGT AAACTAATAT TGTTTAAATC 240

GATATCTTCA GCATCATATC CAAAAGGTAA ATACCATTTC TTATTCTGTT TATTCCTATA 300

GTAGTGTGTT ACTTTTAGTA ACTTTAAAAC AATTGAACTT CCCATCTATT TTCATCCTTC 360

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	EP 0 786 519 A2	
	CCCCACGCAA AAATACCTTT TAATCTTDCT ACTTTAAAAT (2) INFORMATION FOR SEQ ID NO: 677:	460
o	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1451 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677:	
5	GTCAAGTTTT CGGCTAGATT TTAAACGCTC ATCACTATGT AGAATGAAAC TTTCGAAAAA	60
	CTGTAAATCA TCATAACCTT TTACATAAAC ATAACCTTCG CCACCAATTG CTTGAATTAA	120
	ACATTGGGCG GCCATTTGAA TTTCTAAAGA TTGTTTTTCT AGCCTATTAA AGATACCTAT	180
20	TAGTTGTGTG TTTAAGATTT TTGACATCTT TATCCTCCAA TCTACTTATA AAATATTGTA	240
	ATTAATGACT ACATATTATG CAACGGCTTA AATTGTATAA AAATGTATAC GTTTGCATTT	300
	AGTATAACTA TCGCATTTTT CAAAAAATAC ACATTTAATC TGCAGTATTT CAATGCATTG	360
25	ACGCTATTTT TTTGATATAA TTACTTTGAA AAATACGTGC GTAAGCACTC AAGGAGGAAC	420
	TTTCATGCCT TTAGTTTCAA TGAAAGAAAT GTTAATTGAT GCAAAAGAAA ATGGTTATGC	480

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GGTAGGTCAA TACAATATTA ATAACCTAGA ATTCACTCAA GCAATTTTAG AAGCGTCACA 540 AGAAGAAAAT GCACCTGTAA TTTTAGGTGT TTCTGAAGGT GCTGCTCGTT ACATGAGCGG 600 TTTCTACACA ATTGTTAAAA TGGTTGAAGG GTTAATGCAT GACTTAAACA TCACTATTCC 660 720 TGTAGCAATC CATTTAGACC ATGGTTCAAG CTTTGAAAAA TGTAAAGAAG CTATCGATGC 780 TGGTTTCACA TCAGTAATGA TCGATGCTTC ACACAGCCCA TTCGAAGAAA ACGTAGCAAC AACTAAAAA GTTGTTGAAT ACGCTCATGA AAAAGGTGTT TCTGTAGAAG CTGAATTAGG 840 TACTGTTGGT GGACAAGAAG ATGATGTTGT AGCAGACGGC ATCATTTATG CTGATCCTAA 900 AGAATGTCAA GAACTAGTTG AAAAAACTGG TATTGATGCA TTAGCGCCAC ATLAGGTTCA 960 GTTCATGGTC CATACAAGG TGAACCAAAA TTAGGATTTA AAGAAATGGA AGAAATCGGT 1020 TTATCTACAG GTTTACCATT AGTATTACAC GGTGGTACTG GTATCCCGAC TAAAGATATC 1080 CAAAAAGCAA TTCCATTTGG TACAGCTAAA ATTAACGTAA ACACTGAAAA CCAAATCGCT 1140 TCAGCAAAAG CAGTTCGTGA CGTTTTAAAT AACGACAAAG AAGTTTACGA TCCTCGTAAA 1200 TACTTAGGAC CTGCACGTGa AGCCATCAAA GAAACMGTTA AAGGLAAAAT TAAAGAGTTC 1260 GGTACTTCTA ACCGCGCTAA ATAATTAATA TTTAGTCTTT AAGTTATTAA TAACGTAGGG 1320

	AATAAATAAA ACAGTTTGAT TTTAAAATGA AAGCGTAAAA ATGGTAAAAT ATATCAAAAT	1440
	TGATTGTGAT A	1451
5	(2) INFORMATION FOR SEQ ID NO: 678:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 668 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678:	
	nGTATTGAAG CGGTTAAACA AACACCTAAT GCAACTGACG AAGAAAAGCA GGCTGCTGTT	60
	AATCAAATCA ATCAACTTAA AGATCAAGCA ATTAATCAAA TTAATCAAAA CCAAACAAAT	120
20	GATCAGGTAG ACACAACTAC AAATCAAGCG GTAAATGCTA TAGATAATGT TGAAGCTGAA	180
	GTAGTAATTA AAACAAAGGC AATTGCAGAT ATTGAAAAAG CTGTTAAAGA AAAGCAACAG	240
	CAAATTGATA ATAGTCTTGA TTCAACAGAT AATGAGAAAG AAGTTGCTTC ACAAGCATTA	300
25	GCTAAAGAAA AAGAAAAAGC ACTTGCAGCT ATTGACCAAG CTCAAACGAA TAGTCAGGTG	360
	AATCAAGCAG CAACAAATGG TGTATCAGCG ATTAAAATTA TTCAACCTGA AACAAAAGTT	420
20	AAACCAGCTG CACGTGAAAA AATCAATCAA AAAGCGAATG AATTACGTGC TAAGATTAAT	480
30	CAGGATAAAG AAGCAACAGC AGAAGAAAGA CAAGTAGCAC TAGATAAAAT CAATGAATTT	540
	GTAAATCAAG CCATGACAGA TATTACGAAT AATAGAACAA ATCAACAAGT TGATGATACA	600
35	ACAGTCAGCG CTGATAGCtT GCTTTAGTGA CGCCTGACCA TATTGTTAGA GCGCTGCTAG	660
	AGATGCGT	668
	(2) INFORMATION FOR SEQ ID NO: 679:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1906 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679:	
50	GATCCAAATT TAAAAGGAAA AATAGCCTTT AACGAATTTA CGAAACAAAT TGAATGTTTA	60
	GGGAAAGTGC CATGGAATAC TAATTTTAAG ACACGTCAAT GGCAAGACGG TGATGATAGC	120
	AGTTTAAGAA GTTATATCGA AAAGATTTAT GACATACACC ATTCAGGTAA AACAAAAGAT	180

	ATCGTGGGAT	GGACATAAAC	GCCTTGAAAA	GTTATTTATC	AAATACTTAG	GTGTTGAAGA	300
	CcTGaAGTGA	ATAGAACAAC	TACCAAAAAA	GCATTGACTG	CTGGAATCGC	TAGAGTAATG	360
5	GAGCCTGGAT	GTAAATTTGA	CTATATGCTT	ACACTTTATG	GTCCTCAAGG	TGTAGGTAAA	420
	TCTGCTTTGC	TAAAAAATT	AGGTGGTGCA	TGGTTTTCTG	ACAGTTTAGT	TTCTGTTACA	480
	GGTAAAGAAG	CTTATGAGGC	CTTACAAGGC	GTTTGGCTAA	TGGAAATGGC	AGAACTTGCA	540
10	GCTACAAGAA	AAGCTGAAGT	TGAAGCTATT	AAGCATTTCA	TATCTAAACA	AGTTGACCGA	600
	TTTCGTGTTG	CTTATGGGCA	TTATATTGAA	GATTTTCCAA	GGCAATGTAT	TTTCATTGGT	660
15	ACAACTAATA	AAGTTGATTT	CTTAAGAGAT	GAAACTGGTG	GAAGACGTTT	TTGGCCAATG	720
.0	ACTGTAAATC	CAGAGAGAGT	TGAAGTGAAC	TGGTCTAAAC	TAACCAAAGA	TGAGATTGAC	780
	CAAATTTGGG	CAGAAGCTAA	ACACTATTAT	GAACAAGGAG	AAGATTTATT	CCTTAACCCT	840
20	GAACTAGAAG	AAGAAATGCG	TTCAATACAA	AGCAAACATA	CTGAGGAATC	TCCATATACA	900
	GGCATTATTG	ATGAATATCT	TAACACACCm	ATTCCtAGCa	ATTGGGATGA	CTTAACTATC	960
	TTTGAACGAA	GACGATTTTA	TCaAGGTGAT	GTTGATATGT	TACCAACAGG	AAATGTaGAT	1020
25	TACGTTAAAA	GAAATAAAGT	CTGTGCGCTT	GAAGTGTTTG	TTGAATGTTT	TGGTAAAGAT	1080
	AAGGGAGATA	GTAGAGGATC	TATGGAAATT	AGAAAGATTT	CAAACATCTT	AAGACAATTA	1140
	GACAATTGGT	CTGTATATGA	TGGTAATAAA	AGTGGGAAAA	TTCGATTTGG	AAAAGATTAT	1200
30	GGTGTACAGA	TAGCTTATGT	AAGAGATGAA	AGTTTAGAGG	ATTTAATATA	AGAAATATTG	1260
	AATAAATATG	CATTTTAGAG	TGTTGTATCA	GATGTTGCAT	CATTTTTTGA	GTGATGCAAC	1320
35	ACGGGAGTGT	AAAAAGTAAT	CGTAGGTGTT	GTATCATTTT	TGGTGATGCA	ACATTGATGC	1380
00	AACAAATGAT	ACAACACCTC	TTTCCTTTCT	AGCTGTAGGG	TTCAACCCTG	TTTGTTTCCA	1440
	ATGTTGCATC	AAATTCACTA	TAAAGTTTAA	AAAGTAGTGT	TAGGGAGTAA	AGGGGTATAG	1500
40	GGGTAACCCT	CTAACAGCTA	TTTTTAAAAG	TTTGGCAAGA	ATTGATACAA	CATCGGAACA	1560
	CAAATATAAA	TTTTGTATAC	AAGGTGAATA	AATGAAAGAA	TCGACATTAG	TTTATAAAAA	1620
	AGTGAAAGAG	ATAACAAAGC	TAAACGGTTI	ATGTTTAAAA	TGGGTCGCAC	CTGGAACAAG	1680
45 .	AGGTGTGCCA	GATAGAATTA	TTATTATGCC	AGAAGGAAAA	ACATATTTT	TAGAAATGAA	1740
	GCAAGAAAAA	GGAAAGTTGC	ATCCTTTACA	AFAATATGTG	CATAGACAAT	TTGAAAATAG	1800
	AGATCATAAA	GTATATGTGT	TATGGAATAA	AGAACAAGTA	AATACTTIT	TCAGAWTGGT	1860
50	AGTGAACATI	TGGCGATTGA	CTTTCAAACC	ACATAGCTn1	CCAAAG		1900
	(2) INFORM	MATION FOR S	EQ ID NO: 6	80:			

5	(A) LENGTH: 948 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680:	
10	AATTATTTGA ATAAATTAGC AATTAAAGAG TTGATTTGTC AGTTTAAGYA TTTGAGTGCA	60
	TTTGAAAAAG ATGTCATGTA TTTAATGTGT GAACAATATA AGCCGAGAGA AATTGCTCAA	120
	TTGATGCATG TAAAAGAGAA AGTGATTTAT AATGCCATAC AACGATGTYA AAATAAAATA	180
15	AAACGTTATT TCAAAATGAT TTGAAAAGCG CCTTAGGACG TGAATTGAAT	240
	TACTTACTGA TGGTTTGACA TTTGTTATAA ATTTTATGTA TAGTATACTG GTATTATAAT	300
	GAATAAAGGT GAATTATTGT GAGAAAAATA CCTTTAAATT GTGAAGCTTG TGGCAATAGA	360
20	AATTATAATG TTCCTAAGCA AGAAGGCTCG GCAACAAGAT TAACCTTAAA GAAATATTGT	420
	CCAAAATGTA ACGCGCACAC AATTCATAAA GAATCGAAAT AAATACATTC GAAATAATAC	480
25	TTTGATAATA TGTTCAAAGG ATTTGGAGGT TGAGCAGATG GCTAAAAAAG AAAGTTTCTT	540
	TAAAGGCGTT AAGTCTGAAA TGGAAAAAAC AAGTTGGCCG ACGAAAGAAG AGCTATTTAA	600
	ATATACTGTA ATTGTAGTTT CTACTGTTAT ATTCTTCTTA GTCTTTTTCT ATGCCTTAGA	660
30	TTTAGGAATT ACAGCATTGA AAAATTTATT ATTTGGTTAG AGGAGTGAAG ACATGTCTGA	720
	AGAAGTTGGC GCAAAGCtTG GTATGCAGTG CATACATATT CTGGATATGA AAATAAAGTT	780
	AAAAAGAATT TAGAAAAAAG AGTAGAATCT ATGAATATGA CTGAACAAAT CTTTAGAGTA	840
35	GTCATACCGG AAGGAAGAAG GAAACCTCCA GTAANAAGNT GGCCAAGCCT AAAACCGCCT	900
	GTTAAAAAA ACCATTCCCC TGGGnTANGG TTTTAAGTGG GAATTTAA	948
40 4 5	(2) INFORMATION FOR SEQ ID NO: 681: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 863 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681:	
50	ACANATAATA ACAAAGCGCT IGCTAGTACC TCTTAAAAAG ATGATGCTAG CAAGCGCTTk	60
	TCTATACTAT ATATTATTT TCTAAAATTT TAACACCCTC TTGAGTGCCT ACAATAACTT	120
	GATCTGCCAT ATCTAAGAAG TATCCTGTCT CAAACACACC TGTCAGATGA ATTAAATACT	180
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•	TATCAGTTAT	AAATGCGACA	TCTTCGTTTA	CACGACGTTC	TACTTTTATA	TCAGCGTATG	300
1	ATTCAATTTT	ACGTAATATG	TGATACCAGT	TAAATTTATC	CACCTCTACT	GGTAACTTAA	360
į	ACGTCTCACC	TAAGTATTGA	ACTATTTTCG	TTTCATCGAC	AACCACAACA	AAACGCGATG	420
,	CCATTTCATC	TATAACTTTC	TCTCTGAACA	GCGCACCACC	GCCACCTTTA	ATTATATTA	480
	AAGATGGATC	TACTTCATCA	GCACCATCAA	TTGCTAAGTC	GATATGATCA	ACATCATTGA	540
	TTTCACATAT	TTTAATACCT	AATTCTTTTG	CTAAAAATGC	ATTTTTATTA	GAAGTGCATA	600
	CACCTGTAAT	ATTGTAACCA	CGTTCTTTAA	TTAGTTGCGC	CATTTGAGGT	AAGAGTAATT	660
	CCATTGTACT	TCCTGTACCA	ATTCCCAGCG	TCATGTCACC	ATTGATTKGA	CTTAAAACAT	720
	CATTTAATGT	CATTAACTTG	AGTGCTTTGA	CATCTTTCAT	GAAGGTAGCC	TCCCATATTT	780
	ALGTAATCTA	TTCAATTCAT	ATTTTACATG	ACTCGTATAA	ATTAACATAC	CCTTATnGCT	840
	AACCATTTGT	GTTAAACATA	TCG				863

(2) INFORMATION FOR SEQ ID NO: 682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682:

TTCATTTTTG TTGTTCAGCA ATTTTGGTCC GAATTTCAAT TCATCAGATG ATAGCTCTAT 60 TAATTCTGTA GAATATTCTG CLACAACAAT TTCATAAATA TGGCCTTTTT CTTCCATTAT 120 TATTTCATCA ATTATTTCAT AATTCAATTG TTGTAATGTT TGTCTTAAAT TTTCAGTTTG 180 GATATTACTT TGTAAAATCA ACCTTGGATG TTGACTTAAC TTATCTTGCC CATCTTTTAA 240 AATTTTAGCA ATAAGTGGTC CGCCCATACC ACAAATTGTG ATATTATCGA TTACGTCCTC 300 AGGTTGAATA ACACTTAAGC CATCCCCTAA ACGTACATCA ATTCTATCTA CTAATTGGTT 360 TGCAGCTACA TTTTTCACAG CAGCTTGAAA AGGGCCTTGA ATAACTTCTC CAGCAATACC 420 GATTCGCATA AATGGTTTTG AATTGCATAG ATTGGCAAAT AAGCATGATC TGAGCCAATA 480

(2) INFORMATION FOR SEQ ID NO: 683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683:	
	CTGCAAAAAA TATTGGTATA ATAAGAGGGA ACAGTGTGAA CAAGTTAATA ACTTGTGGAT	60
5	AACTGGAAAG TTGATAACAA TTTGGAGGAC CAAACGACAT GAAAATCACC ATTTTAGCTG	120
	TAGGGAAACT AAAAGAGAAA TATTGGAAGC AAGCCATAGC AGAATATGAA AAACGTTTAG	180
	GCCCATACAC CAAGATAGAC ATCATAGAAG TTCCAGACGA AAAAGCACCA GAAAATATGA	240
10	GTGACAAAGA AATTGAGCAA GTAAAAGAAA AAGAAGGCCA ACGAATACTA GCCAAAATCa	300
	AACCACAATC CACAGTCATT ACATTAGAAA TACAAGGAAA GATGCTATCT TCCGAAGTTT	360
15	ggcccaagaa ttgaaccaac gcatgaccca agggcaaagc gactttgttt tcgtcattgg	420
	CGGATCAAAC GGCCTGCACA AGGACGTCTT ACAACGCATA ACTACGCACT ATCATTCAGC	480
	AAAATGACAT TCCCACATCA AATGATGCGG GTTGTGTTAA TTGAACAAGT GTACAGAGCA	540
20	TTTAAGATTA TGCGAGGAGA GGCGTATCAT AAGTAAAACT AAAAAATTCT GTATGAGGAG	600
	ATAATAATTT GGAGGGTGTT AAATGGKGGA CATTAAATCC mCGTTCATTC mATATATAAG	660
	ATATATCACG GTAATTGCGC ATATAACTT	689
?5	(2) INFORMATION FOR SEQ ID NO: 684:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 858 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684:	
	TTATTAAATT GGTATGTGTT CATTATACAT ATGACAAATA TGAATGTAAA CCGATAATTT	60
	AGATTTTTTG GAATAACCTG AAAATTCAAG TTATAGCGTT GCTTATATTT TAAAAGGTGG	120
10	TGATAATGAG ACTTTTTGAA AAATAAAATT CAAAATACTT ATAGCATAAT CAATATGCAC	180
	ATTAAATAAA TGTACTCTTT TAATGCGTTG ATAACTGTAT TTGTAATTTA GAGAAGGGGT	240
15	GTTCACTATG CTGATGTGTT AAAAAATAAA ATAAAAAGGA CACCTCGATG CTATAAATAT	300
45	TAGCATCGAG ACGCCCAGTT AATGTCTATT AAATTGAATA TAGTCTCGGA CATGAATCAA	360
	TGCCCTAGGC CCTGCAATGT TATATTGACA GTAGTTGACT GAATGAAAAT GACTTTGTAG	420
50	CTAGCTTTTT TCAATCCTTG TCGGTGCAAC ACATAGAGAA ATTGGATTCC TAATTTCTAC	480
	AAACAATACA AGTTGCGGAA TAAGTCCCAA TATAGAAGGT GACAGTAAGC CAACTTACAA	540
	TAATGTGCAA GTTGGTCGGG CCTCAATACA GAGATTTTCG AAAAGAAATT CTACATATTA	600

GCCACCTTGT	TTATTTAAAT	CGATAACACG	GTTTGCGATT	GTATTGATAA	ATTCAAAGTC	720
atatgaagta	AAGATAATAG	AACCTTTGAA	TGATTTAAGT	CCATCATTAA	CAGCAGTAAT	780
ACTTTCTAAG	TCTAAGGGTT	GTGGGTCATC	AAGTAAAAGA	CGTTGCCCTG	ATAACATCAT	840
TTACTAGCAn	CACGACTT					856

(2) INFORMATION FOR SEQ ID NO: 685:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685:

TTAGTATTTT CAGGNTGGAA ATTGATGTTT GAAATTCACT GAAATGGGCC AGAACCTGAA 60 ATGAAACTTT ACCAACAATT TGGtCTTCAT CAATGAGGCC AAACGCACGG CTATCTTTAC 120 TTACTTCACG ATTATCTCCA AGCACTAAAT ATTTACCTTT TGGAATGACA TTTGATTTAG 180 GATTCGCATT CGGTAAATCT TTAACTTGGA AAGTCCCAGT AATGTAATCA CCTTGTTTAT 240 GTTTTAAATT GTAGTTTAAA TATGGTTCAT CTTGTTTTTT ACCATTGACA TATAATGTAT 300 CATTTTGTA TTCTACTTTA TCACCAGGAA CACCGATGAC ACGTTTAACA TAGTCATCAT 360 TTTTGTTTGC ATGGAAGACA ACTACATTAC CTTTTTCCAA ACCACCTGTT TTATATCCAA 420 CAATGTTTAC AGCTACTCGC TCGCCATCTT TCAAAGTTGG ATCCATTGAT TCACCTTTAA 480 TTGTATATGG CGTAACAATA AATTTACCTA CTATAAATAA AATGACAAAA GCGACTGCAA 540 TTGAAATAAT CCATTCCAAT ATTTCTTTTT TCAATTTTGA CACCTCTTTT TAAGATTTGA 600 ACTGAACAGT CCATTTTGAA AAAGGATAGT ATCGTAAACL AACATTACCA ATAATALCCT 660 TTTTATCGAT TAAACCAAAT TGTCTTGAAT CGTGCTTGTK ATTATCTTGA TCATTTAGCA 720 CAACAAATT GTTTGGCGGA ATAATATCAC CATCTAATTC TTTAAAATTG CGCAAACTAA 780 AATCTTTAAT TTTTCTGTTC TTGGCATAAG ATGCGTCAAC CGGTCGGTCA TCACGGTATA 840 ATTGTCCCTG ACGAAACGCC ATTGATTGAC CAGGTTTGGC AATAATTCGA CTAGTATATA 900 TCTCGTTACC ACGCCTATAT GTAATGATAT CACCATTATT CAATTGATTA AATGTAACTT 960 TAATTTIATT TACAATAACA CGATCCCCTT TGTTAAGGGT TGGTGACATA TCATTATTCG 1020 GAATGACATG ACCAACTATT ACAAAAGTTT GTACGAACAG TACAATGATA ATAGCAAGTA 1080 TCAATGAAAT CAAATATTTT ACAACTTTTT TCACGATGTC ACTCCTTTTT CGATCCCATA 1140

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	ATCCCTCTTA	AAGGATGCGT	TAAAATTGTA	GTAATTTCCT	TACCTAAATA	ACCTAAAATA	1260
-	ATTGTTGAAA	CTAACTTTGA	TGATGCCAAA	ACAATGAAAT	AATATTTAGG	TCTAATATGA	1320
5	GATAGACTCG	CTACAAAATT	TATTAATGTA	TTTGGCGTAA	AAGGAAAACA	AAGTAAAATA	1380
	AACAATGGGA	TTAATCCTTG	GCGATCAATA	AAACTAATCA	AGCGTTGAAC	AGCAGTACGT	1440
	TGTTTAATTC	GCTGCATCCT	CTCAGTGTTC	ACCAATCGTT	TACAGATCAA	ATAGACTGTA	1500
10	AATGTTCCAG	AAATTAATCC	AAGCCAACTA	ATCAATATAC	CTAAAATAGG	TCCATAAGCT	1560
	TGAATGTTAA	TTAAAATATA	GAGTGCTAAA	GGAAATACTG	GAATTATAGC	TCTAATATAT	1620
15	AACAATATAA	ATCCAGGTAA	ATAACCAAAC	TGTCGAAATA	TCTCAAACCA	TTCTTCTACT	1680
	TGATGAAACG	ACAAATCATC	AATCCCTTTC	TTTGGTTGAA	GATAATTATT	CTTACATTAT	1740
	AAAGTTA						1747

(2) INFORMATION FOR SEQ ID NO: 686:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 645 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686:

•	CGTAAAGATT	ACTATTTAGG	AGGGTGACTA	TGAAAAAGAA	ATTAGGTATG	TTACTTCTTG	60
•	TACCAGCCGT	AACTTTATCA	TTAGCCGCAT	GTGGGAATGA	TGATGGAAAA	GATAAAGATG	120
•	GCAAGGTAAC	AATTWAAcGa	CaGTTaTCCm	TTGCAATCAT	TTgCAGAGCA	AATTGGTGGA	180
	AAACACGTGA	AGGTATCATC	AATCTATCCA	GCAGGGACAG	ATTTACATAG	CTATGAACCA	240
	ACACAAAAAG	ATATATTAAG	TGCAAGCAAG	TCAGACTTGT	TTATGTATAC	AGGGGATAAT	300
•	TTAGATCCGG	TTGCTAAGAA	AGTTGCATCT	ACTATCAAAG	ATAAAGATAA	AAAACTGTCT	360
	TTAGAGGATA	AATTAGATAA	AGCAAAGCTT	TTAACTGATC	AACACGAGCA	TGGTGAAGAG	420
	CATGAACATG	AGGGACATGA	TCATGAGAAA	GAAGAACATC	ATCATCATCA	TGGTGGATAT	480
	GATCCACACG	TATGGTTAGA	TCCTAAAATT	AACCAAACTT	TCGCTAAAGA	AATTAAAGAT	540
	GAATTAGTGA	AAAAAGATCC	АаААСАТААА	GATGACTATG	AGAAAACTA	CnaAAATTAA	600
	ACGACGATCT	TAAGAAAATT	GATAACGATA	TGAAGCAAGT	TACAA		645

- (2) INFORMATION FOR SEQ ID NO: 687:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 956 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687:	
	TTTGTTACTG CTTCTAAAAT AATATCCTTT AATTGTTTAA CATGTTGGAT TGTCATATGA	60
10	GGTGATGGTA CATTAAAAGG ATTTAATTCA TCTATTTGTG CATATTGATT TATGACATCT	120
	TGATGCATTG AAATAGGGTT GATATCATTT GTTACTACTT TATTAGATTG GTCTTGTGAC	180
	ATACTAATGG TGCCACCAGT ATGAATAACA AGTAGATGTT TCATATATTT CCTCCTATAT	240
15	TTAATTTACC TAATTATGAT AAAATATTAT TCATAAAACG ACAAGGAAGG GAAATGACGC	300
	ATGAAAGCCA TTAATATTGC ATTAGATGGT CCAGCTGCTG CCGGAAAAAG TACAATTGCG	360
	AAACGTGTAG CCAGCGAACT ATCAATGATT TATGTCGATA CAGGAGCAAT GTATCGTGCA	420
20	TTAACATACA AATATTLAAA ATTAAACAAA ACTGAGGACT TTGCAAAACT AGTTGACCAA	480
	ACAACATTAG ATTTAACTTA TAAAGCAGAT AAAGGTCAAT GTGTCATTTT AGATAACGAA	540
05	GATGTAACAG ACTTTTTAAG AAATAATGAT GTGACGCAAC ATGTTTCATA CGTTGCATCT	600
25	AAAGAGCCAG TACGTTCATT CGCCGTTAAA AAACAAAAAG AGTTAGCTGC AGAAAAAGGT	660
	ATCGTAATGG ATGGTCGCGA TATCGGAACT GTAGTGCTAC CAGATGCAGA TTTAAAAGTA	720
30	TATATGATTG CATCAGTTGA AGAGCGAGCA GAAAGAAGAT ATAAAGATAA TCAATTAAGA	780
	GGTATCGAAT CAAATTTTGA AGATTTAAAA CGTGATATTG AAGCTCGTGA TCAATATGAC	840
	ATGAACCGTG AAATATCACC ATTAAGAAAA GCAGATGATG CAGTGACATT AGATACGACm	900
35	GGCMAGTCGA TTGAAGAAGT TACTGACGAN ATTTTAGCGA TGGTGAGTNC AATTNA	956
	(2) INFORMATION FOR SEQ ID NO: 688:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1166 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	4 ') Greenwar Bregninger (BD 10 10 10 10 10 10 10 10 10 10 10 10 10	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688:	60
	AAAAGGGAGG AAAGAGAACA GTTAAATATG AATACAAAAT AATTTTGTTT TCGGACAGCA	60
50	GGGGTATTAG ACGCGATTGA CAATGTCIGT TIAATTAAAC GTAATGTTTA TTTAAGCGAT	120
	GAATATTAGG TGAAAAGTTT TTGAATTTGA ATGTAATTGA GGTTTATTGA TTAGACATTT	180
	TATTGAATTG CGTGTTATTA TATAAATGTA AAAATAAGAC GACATGCGCG AACATGTCGT	240

	TAATGCGGAA	TGGTTTTTTT	ATTTTCCGCT	AATTGAAATA	AAAATGACGT	TATATATAT	360
	TATGGGCTAG	GTGGTTTGTA	AGAAAGGGTT	AGTTATTAAT	GTTTTATGAA-	TTAAGGAAAT	420
5	TTGAGTTTAA	GGTTTAATCA	ATTGTGATTT	TGTTGATGAA	GCGTTTAGTT	AGAGTATTTT	480
	CGCCACCACT	AGTTACTCCT	TCTCCCACTT	TACCCGAGAC	TGGAGAAGAg	CTATCTGAAG	540
10	AATAAATAGA	TACTTTTTGG	CCATTTTGTA	GTAAACCAAG	ACCTTTTAAC	TKCTCGGTTA	600
	GAGAATTCCA	TGTATTTTTA	GCATCTAGCT	TTTTGTTAAA	GTCAYCGTAG	ACATTTTCCT	660
	TAGTTAAATC	AATTTGTTTT	AATCCTTTAA	AGTCTATAGA	TTGTGTTAGA	TGGCCTCCAT	720
15	CATCATTTCc	AGGAGCAGAA	ACGCTGCTAG	AATATCCATT	GCTTAATAAA	TAAGTAACGT	780
	TGATTGTTTC	GTACTCGTTA	СТТААААТАА	TATCAGAATC	ATGTAAgAAT	CTTTAACTTT	840
	TTTCCATAAT	TGACCATCTG	TCATTTTTC	TTCTGCTTTA	GCCGTTTTAA	CAACTTTATT	900
20	TGTATCTAAT	CCTAAGTATG	AAGAATGTAA	GCCTGTTCCT	AATGTTGTTA	ATACTAAAGC	960
	ACTTGCTACT	aATGTTTTAC	CTAAAAAttT	TGTATTCATT	TTTATTGCTC	CTTtTTTTAT	1020
	ATTGTAAACG	TTTACAATGA	ATATATAATA	ATAATTTTTT	AAAAGAACAA	TTAACTAAAT	1080
25	ATCAAAAATG	TATTAACTAT	CTATTAACTA	AAAAATAGAA	TAATTTTTTA	ACATAGTTTT	1140
	GTTGTTTTGA	ATTATAAAAA	CTAAAG				1166
	121 THEODNE		10 TB NO 6				

(2) INFORMATION FOR SEQ ID NO: 689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689:

AGCACTGAAG	GATGGCTAGT	TGTCATAGCA	TATGCGGTCA	TTGGTATAGT	TATAACGAGC	60
GTTTCTTATA	TGTTGTCTAT	TAAAATTTTT	AACAAACAAG	AACTAKAATT	GTCGATTTTG	120
GTGATGATAG	TATTTGAAAT	AATATTTAGA	GCAGGTGATA	AATCTTTACG	ATTGTCATCT	180
GTTCTTTTkG	GTGTGGAATG	AAATGTGGGG	GATAAGTATA	GGTGACATAT	CTATATTGAT	240
TTATTTGTTT	TGAGGTGGTT	ATGTTGTGTG	GGAATTATTT	CCTTTTAGAT	AGCGGGGATT	300
AGAGGATATA	TGTTATTTAT	AAGTATCATT	TGATGATTGT	ATAGGCTAAC	GATTTCCTCG	360
GAAATATTTA	AAAACCTCGA	TCATGTAGCA	TAACTGAAGT	TTGTCACAAA	AGTATAATGT	420
GAAGTTCGAC	ACTITIGGAT	TCAGTTCAAA	TACTTTGACC	GAGGTAAATA	CTATTTATTC	480

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TGATACTGAG	ATAATCATTA	CATGGTCGTG	ACCTTTAAAT	AAAAGGCTGA	CAATATAAGA	600
CATAACGAGT	ATACCTAGTG	AATATGAAAT	ATACTTCGCG	TTTGTCAGTT	CATTATGGAA	660
ATAAGGCGTG	ATTAACCATA	ATCCAATATA	GAATATTAAA	ACACTGATAT	ACATCATATT	720
AATTTCAAAC	AAGTCATTTA	GTTTATTGTT	ATTACTAAAA	ACAATTGCAG	CATTAATCAC	780
ACCTAAAGCG	ATATTGATTA	ATAGATGCGT	ATACGATAAA	CGGAAACCGA	TAGATGTTAA	840
TTTATGATTA	TTTTAATATA	CAGTAATGAT	CCAATATACA	CCGAAAAGAC	TAAATTAAT	900
CATAAATTGG	AAATATATAA	TGTAACTAAA	ATGATCAATG	CTAAATGATG	ACGAAGCTAA	960
ACCAACCAGT	ACCTCGCCAr	AGWTALAATT	GTTAGTAACG	AAAAACGTCT	ACTAAATGCA	1020
TCATATTAAC	AGGTnTAATA	CAAGTATTTC	TGAAATGGAA	TAAGnCTGTC	GCTGCATGAT	1080
ACG						1083

(2) INFORMATION FOR SEQ ID NO: 690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690:

TTAATCATCT GGATGTATTT AGTATTNAGA ATAATAANAA AACGATCATG TTGTATLTGA 60 GTAGCGATTG GTTTGCGGAA TTAGGCTTTA CTTTCTTTAA TTACCACTAT ACAGCAAAGT 120 TGATTAAATC ATCCTATAAT TTGAAATGTC TACTATTAAA ATTGACATAT CGATACCTTG 180 ATAATCAGCC TCTTAATGAC GCTGATAYTA GAAAATTACA GGATATTATT AAAATCATTG 240 CAAAAGAAGC AAGTATGGAT AAAAAGATTG CACAAAATCA ATATCGATAT GCGTATTATG 300 GTGATTTGCG TGATGAGCTC GAATATATTT ATCAAAATGT AAATCAACGA TTGACATTAA 360 AAAGTGTCGC TGATAAATTA TTTGTCTCAA AGTCAAATTT GTCATCACAA TTCCACTTAC 420 TTATGGGCAT GGGTTTTAAA AAATATATTG ATACTTTGAA AATNGGTAAA TCGATTGAAA 480 TTCTACTTAC TACTGATAGT ACTATTAGCA ACATAAGTGA nCATTTAGGT TTTAGTAGTA 540 GCTCCACTTA CTCTAAAATG TTTAAAAGTT ATATGGATAT CACACCGAAT GAATATCGTA 600 ATTTATCAAA ATATAATAAn TGTTTAC 627

(2) INFORMATION FOR SEQ ID NO: 691:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 641 base pairs

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	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691:	
	TTGAACGTAA TGCTAGCAAA TGACTTTGTG CCATAAAATA TTCTTCCCAT TTGATTCTTT	60
10	CCAAGATGTT CACCTTCCAT ACTTAAAATT TAGTAACATT TTCTAATAAT ATAAGATTAA	120
10	TCACAAAAA TAAAATTTGC AATTAAAATA ATCCATTATG TCGTGAAATA AGATTTCAGT	180
	TTATCAAAAG TTTTACTTCC AAAACCTTTT ACTTTTTTCA AATCGTCAAT TTCTTGAAAT	240
15	GCACCTTGTT GGTTGCGATÁ TTCAACAATT GCATTAGCTT TAGCTTGCCC AACTCCAGGA	300
	ACAGACATCA ATTCTGATAC AGATGCCGTA TTTAAATTTA CTTTAGTATT ATTTGTGTTC	360
	CCaTTTTTT CGTGCACACT GTTTACTTCA ATTTGTGGTT CAACATTCTT TTGTCCTTTA	420
20	TGAGGTATGA AAATCATTTT TTGATCTGTT AATTTTTCAG ACAAATTAAT TTGACTTACA	480
	TCTGCATCCT CCAATAATTG TGCTTTATCA AGTAAATCAA CTACTCTATC CTTAGATGTC	540
	ATTTTATAAA CATTAGGATG TTTAACAGCA CCTTTTACAT CGACATATAC AGGACCCTTA	600
25	TTTTTGGAAT TATCTCCATC TTTGACCTGG ACATCTTCTA C	641
	(2) INFORMATION FOR SEQ ID NO: 692:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 631 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692:	
	TATTAAAGNA CTTGATGAAC CAAATCATAA AAAGCNATAT ATGTTATTTG CAGCTGGCAT	60
40	TGTGTTnGCA ACTATTTTAC TTATTTCGGC ACATTTATAC AGCAGAAAGA GAGGTAACCA	120
	AGTTTGAGAA TCATAAAGTA TTTAACCATT TTAGTGATAA GCGTCGTTAT CTTAACCAGC	180
45	TGTCAATCTT CCAGTTCTCA AGAATCAACT AAATCCGGCG AATTCAGAAT CGTACCAACA	240
45	ACTGTTGCAT TGACAATGAC ATTGGACAAA TTGGATTTAC CAATTGTCGG CAAACCCACG	300
	TCATATAAGA CATTGCCTAA TCGTTATAAA GATGTACCGG AAATTGGTCA ACCAATGGAG	360
50	CCGAATGTTG AAGCTGTTAA AAAGTTAAAA CCAACACATG TTTTGAGTGT GTCAACGATT	420
	AAAGATGAAA TGCAACCATT TTACAAACAA TTAAATATGA AAGGCTACTT TTATGATTTT	480
	GATAGTTTAA AAGGGATGCA AAAGTCGATT ACACAATTAG GTGATCAATT TAATCGTAAA	540

	GCAGCTAAAC AAAAGAAACA TCCCAAAGTA T	631
	(2) INFORMATION FOR SEQ ID NO: 693:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1111 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
•	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693:	
15	AATTTAACTA TGTTTTCCAC ATTGTTTCAT GTCACGAAAA GGACAACGCG CGACTATAAG	60
	TATCAACTAT TTCCACAAGT TTTATTGGTG TTTTTATTAT TCATCGATAC GCTTCATTTT	120
	CATCTCTCCA ACACAAAAA GAAGCTAAGC AACTTATGTT GCCTAACTCC TCTATACTAT	180
20	CCATATTTTA CTATTATCCA TATTTCATTG AATTATCTAA TGTTGGCTTC TATTTTTTCA	240
	ATATTTCTAC CGTCAATGAC GTCACTCATG CGATTTGTTT GTAATTTTTT ATTAAGTTCA	300
	AACGTATAAT AGCCGCCATC TTTCATTATC ACTTTTATCT TACTATCTTT AGGAAACTTT	360
25	TTATACAGAT CAAAATTTTG AATTAAATAC TGTCTCAATT TAAAGTCGAG TTCTTTAAGT	420
	GAAATCTCTT CTTTATAAAT GTAGTGTACT CTACCGTACG TAGCAATACC GTCACCTTCA	480
	TCTCTCTTGA TTTGAAATCT TGGTGCGTTT ATATAATCAT AATAAGCGTC TTGATTTTTC	540
30	TTAGTGACAC CACCATATGA AAACACTGTG CCATTACGGT TTTCCGCTTC TTTAACAACA	600
	AATATGTCTA ATCCCGGATT TTTACGTGCT TTAAATCTTT CAATATCTTT ACCAAATATC	660
	TGTACTCTTG TGAATTTTCT ATTTTTATCA AAGATAAGGT AATGCTTGCC ACCTTTGCTA	720
35	TAACGATAAC CAGTAACATT TTTAAGTTCC TTACTTGCGC CACTATAGTA ATCTCTTAAG	780
	TCAAAGATAT CTTTTGTCAC ATTTTCATAT TTTGCTTTAT GTTCACTCGC ATTTACAGTT	
	•	840
40	TGATGCAATG ACGTTATTGT TCCTGTTGCT AAAATACCTA ATGCTAAACT TGCTTTCGCA	900
	ATTGCTGTCA TTTTCATAGT TGTATGCTCC ATTCGTAATT ATTAGATTTG TTCGCTTACG	960
	TCTATTGAAT CATACAGCTT TATTATAGTT AGCGTATTTG ACCTTTCACA TTAAACCATG	1020
45	TTTAATAATC ATTGAATCAT TATTAAGTAA ATTAAGGALC TATAATGTTC GTTAAATAAA	1080
	CTGAnCCCGT TGTGCTTCAC ACCCGnTnGA T	1111
50	(2) INFORMATION FOR SEQ ID NO: 694:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 426 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694:	
5	TTATGGATGG ATTAAGAGGT CGTGTTGAAA AAATCAACGA TAACTCTGTT ATTGTTGACT	60
	TAACAATTAT GGAAAATTTT AATGACCTTG ATTTACCGGA AAAAACTGTT ATCAATCATA	120
	AACGATATAA GATTGTTGAA TAAGAAGGTA AGTTATAATG AATAAAATCT CGAAGGCTTT	180
10	AACTTGGTTT ATTATAAGTT TCATTATATT TCATCTCATA TTATTTATTA TGTGGGGCGA	240
	ACACCAAGAA TACTGGTATT TATATACAGG TATAATGCTA ATTGCTGGTA TCAGTTATGT	300
15	ATTTATCAA AGAGATATTG AATCTAAGCG GTTGCTTACA TCAATTGGTG TTGGTATTAT	360
	TACGGCAATT ATTTTAATTA TGCtTCAACT TTTATKCTCA CTTATAACTT CTAATTTAAG	420
	TTATAG	426
20	(2) INFORMATION FOR SEQ ID NO: 695:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 737 base pairs (B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695:	
30	AAAAGGGGnG TAAGGTTTAG CTCAAGTACG AGAAGTCTTT GGTGATGAAG CAATTGATGA	60
	AAATGGTGAG ATGAATCGTC GTTATATGGG TGATCTAGTG TTTAATCATC CAGAAAAACG	120
35	CTTAGAATTA AATGCTATCA TACATCCTAT CGTGCGAGAT ATTATGGAAG AAGAAAAGCA	180
	AGAATATTTA AAACAAGGAT ATAATGTAAT CATGGATATT CCATTATTAT TTGAAAATGA	240
	ATTGGAAAAT GCAGTAGACG AaGTGTGGGT TGTATACACT TCTGAAAGTA TACAAATGGA	300
40	TCGTTTAÄTG CAACGTAATA ATTTGTCATT AGAAGATGCG AAAGCACGTG TCTATAGCCA	360
	AATTTCTATT GATAAAAAA GCCGAATGGC CGATCATGTT ATCGATAATT TAGGGGATAA	420
	ACTTGAATTA AAACAAAACC TTGAGAGATT GTTAGAAGAA GAAGGTTATA TTGAAAAGCC	480
45	GAATTACGGA GAAGAAGATT AATATTACAC TATAAATAAG TCATTACTTT ACGTACGCGT	540
	TGATGTATGT AAGTAATGAC TATTTTTAT AAAAAAGATA AATAAATCAA CGGAAAACGC	600
	TTTCAAATTT CATATAATAT GCTATACTAA TTCCATAAAG TATAACACAT AAAGATCAAG	660
50	GGGTGCTTTT AATGTCAACG AATATTGCAA TTAATGGTAT GGGTAGAATT GGAAGAATGG	720
	TATTACGTAT TGCATTA	737

(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 432 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696:	
10	AACGATAAGA ACAAAAGATA TATTACAAAG CGTTTATTTA AAACGTTATT TATTACGCGC	60
	GATGATGGCA GGATTTATTA TCGGGATTAT TACGGTCTTC GTATTATCAG TTAAAGCAAC	120
15	ACACGAACCA GATTTACCGC CAGGCATTGT GAATATGGCC AGTGCCATTA CATTCAGCTT	180
	TGCGTTAGTA CTCATTTTAT TTACAAACTC CGAACTACTA ACCAGTAACT TCATGTACTT	240
	TACTGTAGGC CTGTATTMTA AAGTAATTAA ACCAACTAGA GTATTGAAAA TATTTTTATT	300
20	ATGCTTTGCA GGAAATATTT TAGGTGCTGC TATTTYATTT AGTTTCATGC GTTTTTCAAA	360
	TGTAATGACG CCAGATAWGt TAAAYCAGTT ATCAGCAGTT ATAGAGCATA AAACGTTGTC	420
	TACTGGTTTT GT	432
25	(2) INFORMATION FOR SEQ ID NO: 697:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 782 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697:	
	CTTTTATACG AAAGTTAANA TCAAATATAA CATTAATGTT TGATGGGGAT TTTGCGGGTA	60
	GTGAMGCAAC ACTTAAAACA GGTCAAAATT TGTTACAGCA AGGGCTAAAT GTATTTGTTA	120
40	TACAATTGCC ATCAGGCATG GATCCGGATG AATACATTGG TAAGTATGGC AACGATGCAT	180
	TTACTGCTTT TGTAAAAAT GACAAAAGT ÇATTTGCACA TTATAAAGTG AGTATATTAA	240
	AAGATGAAAT TGCACATAAT GACCTTTCAT ATGAACGTTA TTTGAAAGAA CTAAGTCATG	300
45	ATATTTCGCT TATGAAATCA TCGATTTTGC AACAAAAGGC TTTAAATGAT GTTGCACCAT	360
	TTTTCAATGT TAGTCCTGAG CAATTAGCTA ACGAAATACA ATTCAATCAA GCACCAGCCA	420
50	ATTATTATCC AGAAGATGAG TATGGCGGTT ACATTGAACC TGAGCCAATT GGTATGGCAC	480
	AATTTGACAA TTTGAGCCGT CAAGAAAAAG CGGACNAGCA TTTTTAAAAC ATTTAATGAG	54
	AGATAAAGAT ACATTTTTAA ATTATTATGA AAGTGTTGAT AAGGATAACT TCACAAATCA	60

	TATCAGTGAT GCTGTGCAGT ATGTTAATTC AAATGAGTTG AGAGAAACAC TAATTAGCTT	720
	AGAACAATAT AATTTGAATG ACGAACCATA TGAAAATGAA ATTGATGATT ATGTCAATGT	780
5	TA	782
	(2) INFORMATION FOR SEQ ID NO: 698:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 714 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698:	
	AAATCATTGG CAAAATATAC GAATTGCATT TAAATCGTCA ATTTACATAT ATTTTTGCGT	60
20	AGTAATCAAT CGTTATCATT GTTATTTATC GTTACATTAT TTCGAGTATC AGTATGTATT	120
	TCGGGCTTCG TTTGATAACG ACATTTCTTT GTGACATCGC TTCATCAGTG TAACAACAAA	180
	TACAATGATT TCGTGATGTT AGTTACCCAT TTTATGTGTT GCATAAAATA TGTTGTTATA	240
25	AAACATTTTA AATCATTTTA TATAAACAAT CTATATATTT TTGGCATTTC CAAAATATCA	300
	CTTGTTATAT TAAAAACCGA CAAGACATTT TATCTTATCG GTTGAAATTT GTTATTGTTA	360
	TTTGTAATGT TTTTAGGTTT CTTTTTAATA TAATATATTT CAGTGAAAAT ACATGATTGA	420
30	TTGTGATTTC ACTGAAACAT GGTTAATTGC GTTGTTGATG AATAACTTTA GCATAAATAT	480
	AGGAAGTTAT TTTGTACATC GCCATATATA GAAACGAAAT TATAATGACA GCTAGTACGT	540
35	AACTTGTTAA AAATATATGA TGGTTATTAA TACCTATCAT ATTTAGTAAC GTATATACAA	600
33	TGTTACTAGA AATTAATGTG TGAATCAGTG CTACTGTTAT TGGTATLGCG AACAAGAAAG	660
	TCATTTGATT TCGTGTTATC TTTGCTATTC TTCCATTATC TAAACCAAGT TTTT	714
40	(2) INFORMATION FOR SEQ ID NO: 699:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 361 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699:	
50	ACTGAGAGCA ATAATTTAGT AACTTCTACT CAAGGAATTA TTAAAGAAGC ATTGCATAAA	60
	TTGGGATTTG nnTTTAATTA AAGAACCTTT AAGAATGTTA CAAGTGCGTA TCCCTGTACG	120

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	TGGACCAACA AAAGGGGGCG TGCGTTTCCA CCCAGATGTT GATGAAGAAG AAGTAAAAGC	240
	ATTATCAATG TGGATGACTT TGAAATGTGG CATTGTGAAA CTTACCATAC GGTGGTGGTT	300
5	AAGGGTGGTG ATCGTTTGTG GATCCACGTC AAANGAGCAT TCCATGAAGT TGGAACGTTT	360
	A	361
	(2) INFORMATION FOR SEQ ID NO: 700:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 943 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700:	
20	GTCCTTAATT GGTATCCACC TTTAGCACCG CGTACACTTC GAATTAACCC CGCATTTCTT	60
	AAAGGACCTA CAAGCTGTTC TAAATATAAA TCACTCAAAT TATTTTCTTC AGCAATTGAC	120
	TITAATGATA TACATCCTTG CCCCTCTTTT TTAGCAAGAG AAATCATCAA TGTAAGTCCA	180
25	TATCTCCCTT TAGTAGAAAT TTTCATTGTA TAACCTCACT TAATTCGAAT ATTGATATTC	240
	CCATTTTAGC ATTTTTTGAG TTAAGATAGT ATAAGAAAGG TGTGACAAAT GTGAGTACAG	300
	AACCATTAGC ATCGAGAATG CGCCCAAAAA ATATAGATGA AATCATTTCC CAACAACATT	360
30	TAGTTGGACC AAGAGGCATT ATCAGAAGAA TGGTTGATAC AAAAAAATTA ACTTCAATGA	420
	TTTTTTATGG TCCACCTGGT ATAGGCAAAA CAAGTATTGC CAAAGCAATT TCGGGCAGTA	480
	CGCAATATAA ATTCAGACAA TTGAATGCTG TAACTAACAC TAAAAAAGAT ATGCAACTTG	540
3 5	TTGTTGAAGA AGCTAAAATG TCTGGTCAAG TTATCTTGTT ATTAGATGAA ATACATCGAC	600
	TAGATAAAGC TAAACAAGAC TTTTTATTAC CTCATTTAGA AAATGGCAAA ATCGTCTTGA	660
40	TCGGTGCTAC AACTTCAAAT CCTTATCATG CTATCAATCC AGCGATTCGT TCAAGAGCGC	720
	AAATTTYCGA GTTATATCCT TTAAATGACG AAGATGTGCG CCAAGCGTTA ACTCGTGCAA	780
	TAGAAGATGA TGAGAATGGT TTGAAAMCAT ATCAACCCAA AATTGATGAA GATGCCATGA	840
45	CCTACTTTC TACACAAAGC CAAGGTGATG TTCGTAGTGC GTTAAATGCA TTGGAATTAG	900
	CTGTATTAAG CGCAGATAAT GACAAAGACG GTTATCGACA TGT	943
	(2) INFORMATION FOR SEQ ID NO: 701:	

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 445 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701:	
5	CATTAAGTGA AGTTGTTGAT ACACCCATGC ATCAAGTCAA TTGTTCTGTT GATTTAGATA	60
	CAGAAAGCTT ATTAGGCTTT AAAACAATTA AAACAAATGC GGAAGGTCAA CAAGAAATTG	120
	TCTTTGTAGA TGGTCCAGTT ATTAAAGCTA TGAAAGAGGG GCATATTTTA TATATTGATG	180
10	AAATAAATAT GGCTAAACCT GAAACATTGC CTGTATTAAA TGGGGTCTTA GATTATCGTC	240
	GTCAAATTAC GAATCCATAC ACTGGTGAAG TAATCAAAGC TGTACCAGGA TTTAACGTTA	300
	TAGCAGCGAT AAATGAAGGT TATGTTGGtA CTTTGCCAAT GAATGAAGCA CTAAAAAAAT	360
15	CGCyTTGTTG TTaTTCACGT kGATTATATT GATGGGGACA TTTAAAAAAT GTGANTAAGG	420
	AGCAAGGTTT ATTACAAGAT GTTAA	445
	(2) INFORMATION FOR SEQ ID NO: 702:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 752 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(b) TOPOLOGI: Timear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702:	
	TGCAAGATAA ACAAATTTGT CATTGTTTTG GTTGTAAAAA AGGTGGCAAT GTTTTTCAAT	60
30	TTACTCAAGA AATTAAAGAC ATATCATTIG TTGAAGCGGT TAAAGAATTA GGTGATAGAS	120
	TTAATGTTGC TGTAGATATT GAGGCAACAC AATCTAACTC AAATGTTCAA ATTGCTTCKG	
		180
35	AYGATTTACA AATGATTGAA ATGCATGAGT TAATACAAGA ATTTTATTAT TACGCTTTAA	240
	CAAAGACAGT CGAAGGCGAA CAAGCATTAA CGTACTTACA AGAACGTGGT TTTACAGATG	300
	CGCTTATTAA AGAGCGAGGC ATTGGCTTTG CACCCGATAG CTCACATTTT TGTCATGATT	360
40	TTCTTCAAAA AAAGGGTTAC GATATTGAAT TAGCATATGA AGCCGGATTA TTATCACGTA	420
	ACGAAGAAAA TTTCAGTTAT TACGATAGAT TTCGAAAATCG TATTATGTTT CCTTTGAAAA	480
45	ATGCGCAAGG AAGAATTGTT GGATATTCAG GTCGAACATA TACCGGTCAA GAACCAAAAT	540
	ACTTAAATAG TCCTGAAACA CCTATCTTTC AAAAAAGAAA GTTGTTATAC AACTTAGATA	600
	AAGCGCGTAA ATCAATTAGA AAATTAGATG AAATCGTATT ACTAGAAGGT TTTATGGATG	660
50	TTATAAAATC TGATACTGCT GGCTTGAAAA ACGTTGTTGC AACAATGGGT ACACAGTTGT	720
	ሮስርስጥርስስሮስ ጥስጥጥስርጥጥጥጥ አጥክርርላአክርጥ ጥክ	200

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 830 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 703:	
10	nCGTTTTGT nAAACnGCTT ATATGTATAA CTTTTCCCAA TTTATCATAA GTTTTGATAG	60
	AAGGAGTTGG ATCGCTAAAG AAAATATCTC TAAAGATATC ATCTTCAATG ATAGGAATAT	120
	TATGTCTTC GCTATAAGTA ATTATATTTT TCTTTTGCTC ATTCGTTAAA GAACGACCTG	180
15	TCGGGTTATT AAACCTAGGT TCTATATAAA TCGCTTTATT TTTAAAATTA ATAAATCTAT	240
	CAATGATGGT ATCAATTTCA TTAATTTGAT TATAAGGAAC ATCAATATGT CTAAAATTCA	300
20	ATTGCTCAAA AACATTTGTA GAGTGAATAT ATGATGGTGT ATTCGAAATT ATTATGGCAT	360
	CTTGACCTAA AAACCCAATA GATAAAAGTT GAATGGCATG TAAAGCGCCT GAAGTGATCA	420
	TTACATTTTC TCTACCTACA TTTATACCTT GCTTTGACAT TCGTTCAACG ATAATATCTC	480
25	TTAACTTGAT ATAACCATAG CCATTATTAT AACCAAAAGA TAAGTCTTCA ATATGACTGG	540
	CTGTATTAGA CATGGCTTTT TTCAATTGAA TATGTGGCAT TAACGATATA CCCAATTCAC	600
	CTTTACTTAT ATGTATATAC GAATCATCTG TCTCAATTTT ATTAATTAAT TGCACCGTAT	660
30	ACTGACTTCT TTGTTGAGAG GACCATAACA TCATTTCAGA CCACTTATTT GTAATATGTG	720
	CTTCATTCAA ATAGTCATTA ACATATGKTC CACTACCTAC TTTAGTATAG ATAAATCCTT	780
	CAGCTTCTAA TAACTCAATA CTTTTAATAA TCGTTACTCT ATTTACGTTG	830
35	(2) INFORMATION FOR SEQ ID NO: 704:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 659 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704:	
45	AGTGGTGTTG GAAAAGCTAT TATGAAATTA TTACGTGAAC AACAAGTTTA ATAAAAAAAG	60
	AGGGGTCAAA TATGAAAGGA TTAATTATTA TTGGCAGTGC ACAAGTGAAT TCACATACAA	120
50	GTGCACTAGC AAGATACTTA ACTGAGCATT TTAAAACACA TGATATTGAA GCGGAAATAT	180
	TCGATTTAGC AGAAAAACCG TTAAATCAAT TAGATTTTTC AGGAACAACA CCGTCTATTG	240

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	TATTAGGAAC GCCAAACTAT CATGGTTCAT ATTCTGGAAT ATTGAAAAAT GCATTAGATC	360
	ATCTAAATAT GGATTATTTT AAAATGAAAC CTGTAGGCTT AATAGGAAAT AGTGGTGGTA	420
5	TTGTTAGTTC AGAGCCATTG TCACATTTAA GAGTAATCGT CAGAAGTTTA CTAGGCATTG	480
	CTGTACCAAC TCAAATAGCA ACACATGATT CTGATTTTGC TAAAAATGAA GATGGTTCAT	540
	ATTACTTAAA TGATAGTGAA TTCCAATTAC GAGCAAGATT ATTTGTCGAT CAAATTGTAT	600
10	CTTTTGTGAA TAATAGTCCA TATGAACATT TAAAATAATA TTAANAAATA TGTAAATNT	659
	(2) INFORMATION FOR SEQ ID NO: 705:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705:	
	nCACCATATA GTAACTGGCA CCAACTACAT TACCGTCTTT TAAAAAGATT TTTTTATAGT	60
25	TATTATCAAC ACTATTAAAT ATTTCAATAC CTTTAATTTC TGCATTTTCT ACAATTTGAC	120
	CAGCACTATA CAAGTCACAC CCAGAAACTT TTAATGACGT AAATGTTGTT GATCCCTTGT	180
	ATCCGTTCGT TTCTTTATTT GTTAAATGAT CAGCTAATAC TTTACCTTGT TCATATAGTG	240
30	GTGCAACGAG TCCATAAACT TTGCCGTTAT GTCTGCACAT TCACCAACTG CATATACATT	300
	GCTATCACTT GTTTGCATCA CATCATTGAC AACAATACCA CGATTACATC TAGACCTGAT	360
	CTTGGCACTC CTGGGAAGGC GGAACCACTG CATACAACTA	400
35	(2) INFORMATION FOR SEQ ID NO: 706:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 380 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706:	
	TTAAAAATAC AGCTACAGGT AATTTTAATG ATTTTTCATC AATATCAAAT TTGGGATTAT	60
	GGTGTGGCGC TGTAATACCT TTAACCAGTC AGAAAGAATG CACCTGGTCG TACTTTCAAA	120
50	TAATGTGAAA AATCTTCTCC AATCATCATT AAATCTGATT CATTAAAGCG TACATGTAAG	180
	TCATTTGTTG CTTCTTTAAT AACTTGGATA TGCTTTCTCG TTTATTATGG ACAGGCAAAT	240

	GCTTAATCCA TTTTGTCCAT ACATGATTCT GTATATCTGA AATCGAAAGT TCTNACTGTA	360
	CCTTTACAAA ATGCCTTGnn	380
5	(2) INFORMATION FOR SEQ ID NO: 707:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707:	
	CADAAAGGAT CAAAGTGATC GGTATAGTGA TAATTAGCTC CAAAGAAAGA ATATTCTAAA	60
	TCAAATCCAT ACCAAGCAGA AAGTATTAGC GAATATCAAT TTAAATGGTA CCGATTCAAA	120
20	TAAAGAAACA CGACATATAG AATTTTTACT TGATGATTTT AGTGAATCAT ATGAACCAGG	180
	AGATTGTATA GTAGGATTAC CGCAAAACGA CCCTGAATTG GTTGAAAAAC TAATATCCAT	240
	GTTAGGTTGG GATCCGCAAT CTCCGGTGCC AATTAATGAT CATGGTGATA CAGTTCCTAT	300
25	TGTTGAAGCA CTAACATCAC ATTTTGAATT TACTAAATTA ACATTGCCAT TATTGAAAAA	360
	TGCAGATATC TATTTTGACA ATGAAGAATT ATCTGAnCGT	400
<i>30</i>	(2) INFORMATION FOR SEQ ID NO: 708: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 447 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708:	
40	TAATGCTGGT ACGGGTCATG CAGCATTATG TGAGTTGAAC TACACAGTTT TACAACCTGA	60
	TGGTTCTATC GACATCGAAA AAGCGAAAGT GATTAACGAA GAGTTTGAGA TTTCAAAACA	120
	ATTCTGGGGT CACTTAGTGA AAAGCGGTAG CATCGAGAAC CCAAGAGAAT TTATCAATCC	180
45	ATTACCACAC ATCAGTTATG TTAGAGGTAA AAACAATGTT AAATTCTTAA AAGATCGTTA	240
	CGAAGCGATG AAAGCTTTCC CTATGTTCGA TAATATCGAA TATACTGAAG ACATCGAAGT	300
50	AATGAAAAA TGGATTCCAT TGATGATGAA AGGCCGTGAA GATAACCCTG GTATCATGGC	360
	GGCAAGTAAA ATTGACGAYG GTMCAGATGE AAMCTYCGGT GAATTAACAC GTAAAATGGC	420
	TAAAAGCATT GAAGCACATC CAAATGC	447

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709:

10	GTGTCTACCT	GTTTTTGTTG	TTCAATTGTT	AACTTTTCTT	TTTGAATAGT	AGTATTCGAT	60
	AATTCTTTAT	CGCTTATAAA	ATCATCTAGT	GGATGGCTTT	CTTTGAAACT	TTTATTTTCA	120
15	GTCATCAATC	ATCTCTCCAA	TAGTTGCTAT	TTTACATCAA	TCTTGATGAT	GTTTTTGATG	180
	TAACTTATTT	AATTCCATTT	СААТАТСТАА	ACGTTCATAA	TCATCTTCGT	TGAGACGCTT	240
	TAAATCAGCG	ATTAATGTTC	GTTTGACCTC	ATCCAAAGTA	ATTCGTGTTT	GTTCTAACTT	300
20	TTGCTGTTCA	TTAATTGATT	TTTTGGGCAT	TTTTGCTAGA	CGTGTATATG	CATCAACCAA	360
	ATTTAAAGCA	TTATCAATAT	GAGAATAAAA	AAAGCCTTCA	ACTTTATAAA	ATGATGCAGG	420
	TCTCTGTCTA	ACTGTCGTAT	AAATAGAACG	TGAAATTTGG	TATATATCAT	TAATCTGCCT	480
25	AAAATCTTTA	ATTGATCTTA	TATTGACATA	CGTTTTTAAA	ATACCTCTAA	GTTTTTGGTG	540
	TGTATGATTT	AACTGATTTC	GAATATAGCG	ATAGTCTTTT	CTAGTCAAAC	CAATTTCGTT	600
	TAAATATTTG	CGTGAAGTGA	GTTTTTGTAT	CGGTAGGTAT	GTCATTAAAA	AGCCAACAAT	660
30	ACCAATAGAC	ATATCAATTA	AAAAAGATAC	ATCAAGTGCA	ATCATCCCAA	ATATGCTTGT	720
	TAAAAACGCT	ACAGGAATTC	CCACTAACAC	CCCAAATATA	TGÀGAAATAT	TATATCTCAC	780
35	TGTCATCTTC	CTTTATTTAG	CATTTTATAT	TGATCGAAAA	TCCGATAATT	TTTGATTTAG	840
	TTCTAACTCT	TCAAGTTGAT	GGCTTGTTAC	ATTTGATGCT	GGTGAGGCAC	CTTCAATTAC	900
	ACCTTGAATA	AATCTCTCTA	TATCTGCGTC	ATCCCCTTGT	GCATATATCT	CTACATAGTC	960
40	ATCTACATTT	TGAACAGTAC	CGACAATGTT	ATAGTTCATT	GCAATGCGTT	GTGTAAAATA	1020
	TCTAAATCCG	ACGCCTTGAA	CGCGTCCGAA	TACTTGTAAA	TGTATATGtC	TCaTTTTTAC	1080
	CACCTCATAA	TGTTATTATA	CGTAGTTTTA	СТТАААААА	CTAATAATTA	CTATAGTTAC	1140
45	TACTTTGTTT	GTTTCAAGTC	GTCAAACTTG	ATTTTCAGAG	GATAAAGGTA	TAAAAATAAG	1200
	TATAGAGTTT	TTGAAGTATG	GAAGGGGTCT	TTAATAATGT	GGACAGTTAC	CAAAATTAGA	1260
	GCCGATTATG	AGGGATGGTG	GTTATTCAGT	GACTGGCCAG	AAAACATTGT	TGAAAAATAT	1320
50	CAATATCAAG	ATTTTGATGA	CATGTTTAAG	CACTATCAAC	AATTGATTAA	TCAATGTAAA	1380
	GTTCAGTTCG	ATAACTATGT	CACAGGCAAA	TATAATATTT	ATGCATTTTA	TAATAATTGT	1440

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(2) INFORMATION FOR SEQ ID NO: 710:

5	(A) LENGTH: 519 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710:	
	GCTGNAAAAT ATGTTAGAAG CAGATGCATG GGCAAAGCTG GGGTCCTTAT TTATTGTCAG	60
	GTAAAGATGT CTTCAATTCA ACTATTGGAA TATATGGTAT GGGAGATATT GGTAAAGCTT	120
15	TTGCAAGAAG GTTGCAAGGG TTTAATACTA ATATTCTTTA TCATAATCGA TCAAGACATA	180
	AAGATGCAGA GGCGGACTTT AATGCAACAT ATGTTTCTTT TGAAACGTTG TTAGCAGAAA	240
20	GTGATTTTAT CATCTGTACA GCGCCACTTA CAAAAGAAAC ACATCATAAA TTTAATGCTG	300
	AAGCATTTGA ACAAATGAAA AATGATGCAA TTTTTATTAA TATCGGTAGA GGACAAATTG	360
	TAGATGAAAC AGCATTAATC GATGCACTAG ACAATAAAGA AATTTTAGCA TGTGGTTTAG	420
25	ATGTATTAGC AAATGAACCG ATTGATCATA CACATCCATT AATGGGACGT GATAATGETC	480
	TGaTTaCACC aCACATTGGG TAGGCGCATT CAGTTAACn	519
	(2) INFORMATION FOR SEQ ID NO: 711:	
<i>30 35</i>	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1349 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711:	
40	CTATTACAGG TGGCGAACCA ATGTTTTCTA AAAAGTCTAT TAGAAATGTT GTTAAACCTC	60
	TATTAAAGTA TGCACATCAT CGAGGTATAT ATACACAAAT GAATTCAAAC CTAACATTGC	120
	CTCAAGATCG TTATTTAGAT ATTGCTGAAT ATATCGATGT TATGCATATC TCACACAACT	180
45	GGGGAACAAC TGATGAATTC GCAAATGTTG GCTTTGGCGC AATGAAGAAG CAACCACCGT	240
	TAAAAGCTAA GTTAAAATTA TATGAACAAA TGATTTCGAA TGCACGTACA TTATCAGAAC	300
	AAGGAATGTT TGTATCTGCG GAAACAATGC TCAATCAAAG TACGCTACCA CATTTACGAA	360
50	AAATACATCA AGAAGTCGTT CATGATATGA AATGTAGCAG ACACGAGATT CACCCTATGT	420
	ATCCAGCTGA CTTTGCAAGT CAATTAAATG TGTTAACTCT AGCGGAAATG AAAAAGACAA	480

	TGTTTCCATG CTTAAAGGAT GATGAAGATC AAAAGTTACT ATCACGTTTA AGAAATGCTA	600
	AAAATGTAAC GACTAGAAAT GACCCGGATG GCCGTAGTCG TTTAAATGTC AATGTATTTA	660
5	CAGGTAATGT AATCGTAACT GATTTCGGAG ATGAAACAGG TACAATTTCG AATATACAAA	720
	AAGATAAATT AACAGATGTA TITGATAAAT GGTTATCCTC TGATCTTGCT AAATCATTAA	780
	ATTGTCATTG TTCCGAGTTT AGTTGTTTAG GGCCAAATGT TCTTGTTAAA AATATGTACT	840
10	ATCCGAATAT GGATTTTAAA GATAATGAGC GTCATATGCA CAAACAACCA CAAATTATAC	900
	AATTTTAAAA ACTCTTAATT ATGCGGAGAA GCACTTTATC GATAAGTAGT CTCCGCATAT	960
15	TTTAATGCTA TTATAAAATA AAAAACAATT AATTGCTGGC AGTACTCTAC TTAAATAATA	1020
	AAGGGCATTT AATAGGACTA ATAGTCTATA ATAAAAGGGG TAAATTTTAA CTAAAAGCAT	1080
	AAACGTGCAT AATCAAAAAG ACAGATTGTA GGTGGAATAT TCGAACATAA CAGTTCAATT	1140
20	CATCCTTÄAC AATCTGTCTT TATATTTTTA GTCTCTAATA TGTTGCACTT GAGCTAAATA	1200
	TTCAATTGTT gTTTACTTtC AaTGCGaCGt GCTTttCTtC GTtCAaCaCG TgwGGTGCTG	1260
•	TATCATAAAA CCATTTTTCA ACATCATCTT CTGGATATAC ACCAGGTACA TGTTTAGGTT	1320
25	GCCTTCATCA TCTAACGCAA CAAATGTAA	1349
	(2) INFORMATION FOR SEQ ID NO: 712:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 377 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712:	
	GAAATTAAAA AAGCAATTGG ACAAGATGCA ACAGTGTCAT TGTTTGATGA ATTTGATAAA	60
40	AAATTATACA CTTACGGCGA TAACTGGGGT CGTGGTGGAG AAGTATTATA TCAAGCATTT	120
	GGTTTGAAAA TGCAACCAGA ACAACAAAAG TTAACTGCCA AAAnCAGGTn GGCCTGAATG	180
	GAACCAGGAG GAANTTGAAA ATATGCTGGG GATTACATTG TGAGGTACAAG TGAAGGTAAA	240
45	CCTACACCAG GATACGAATC AACAAACATG TGGAAGAATT TGAAAGCTAC TAAAGAAGGA	300
	CATATTGTTA AAGTTGATGC TGGTACATAC TGGTACAACG TCCTTATACA TTAGATTTCA	360
	TGCGTAAAGA TTTAAAA	377
50	(2) INFORMATION FOR SEQ ID NO: 713:	

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 528 base pairs

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713:	
	AATGAAnCGA AAAATGACTA TAAAAAGTTT AAAGTGTTTT CACTTATTTC AACACTTGTC	60
10	ATTGTCATTT TAGCAATTAT AAGATTTGTT CATAAAATGA TGTAATTAGA GTGAGACATT	120
	GTTTTATGTC TCAGGATCCA GTTATTCATT ATATCTACAA TATTTACGAT TATATAAATA	180
	ACCCGAGATT TTAGTATGAT TCATTtCACT AAAATCTCGG GTTTCTATTT GATAATTTTT	240
15	AATGGGATAT GGCATGTATA CGTTCTTGCC TTTTATCTCA TTTCCAATGA TTAATCTGGA	300
	TATTGTTCTA AAAATGCTTT CGCTTCTTTA TTAACTGTTT TAAAATCAAT ACCTTGTTGC	360
	ATCGCTGCAA AGACACATCC ACAATAACAC TGCCTAAAGA TATTATAGTC ATTACACATT	420
20	TCTATGGAAC GCTCATAACC TTTACTTTTC YTAAAATCAC TTGGCAAATA GTTCACATCG	480
	TATATTTTT GGACATCCAT ACCAAGTTCA TTGATTAATT GTGCGTTC	528
25	(2) INFORMATION FOR SEQ ID NO: 714:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 731 base pairs (B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714:	
35	TTTAATGGCA TGAAGTCACA GTATATAAAG AATCTGGTGT GACAATCAGT ATGACTAAGT	60
	ATATAAAAAA AGAGCAGGTG CGAAATAATG GCGAAAGAGT CGAAATCAGC TAATGAAATT	120
	TCACCTGAGC AAATTAACCA ATGGATTAAA GAACACCAAG AAAATAAGAA TACAGATGCA	180
40	CAGGATAAGT TAGTTAAACA TTACCAAAAA CTAATTGAGT CATTGGCATA TAAATATTCT	240
	AAAGGACAAT CACATCACGA AGATTTAGTT CAAGTTGGTA TGGTTGGTTT AATAGGTGCC	300
	ATAAATAGAT TCGATATGTC CTTTGAACGG AAGTTTGAAG CCTTTTTAGT ACCTACTGTA	360
45	ATCGGTGAAA TCAAAAGATA TCTACGAGAT AAAACTTGGA GTGTACATGT TCCGAGACGT	420
	ATTAAAGAAA TTGGGCCAAG AATCAAAAAA GTGAGCGATG AACTAACCGC TGAATTAGAG	480
	CGTTCACYTT CTATCAGTGA AATAGCTGAT CGATTAGAAG TCTCAGAAGA AGAAGTGTTA	540

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GAAGCAATGG AAATGGGACA AAGTTATAAT GCGTTAAGTG TTGATCATTC CATTGAAGCT

GATAAAGATG GTTCAACTGT TACGCTATTA GATATTATGG GGCAACAAGA TGACCNTTAT

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	(2) INFORMATION FOR SEQ ID NO: 715:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 830 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715:	
15	TTTTAGrGGa AAGCGaATTA GtCaTATwCg CaGCAGATwG aATGATTGAA AAmGaAATTG	60
	attcgattcc aattgtaaga aaaaaagata atcaaaagta tgaagtaatt ggaagaattt	120
	CCAAAACAAC AATAGCTAAG TTATTAGTAG CATTATATAA AGAATAGGTG AGAAGTAATG	180
20	GAAAAATTA AAATTATCGT AGCTTCAGAT TCTATAGGTG AAACGGCAGA GTTAGTTGCT	240
	AGGGCAGGTA TTTCACAATT CAATCCTAAG CAATGTAAAA ATGAATTATT AAGATATCCA	300
	TATATTGAAT CTTTTGAAGA TGTTGATGAA GTGATTCAAG TTGCAAAAGA TACAAATGCT	360
25	ATCATTGTTT ATACACTTAT TAAACCTGAA ATGAAGCAAT ATATGAGTGA GAAAGTAGCA	420
	GAATTCCAAT TGAAGTCTGT CGATATCATG GGGCCATTAA TGGATTTATT ATCTGCTTCG	480
	GTTGAAGAAA AACCTTATAA TGAGCCAGGT ATCGTTCATA GATTAGATGA TGCATATTTC	540
30	AAGAAAATTG ATGCGATAGA GTTTGCAGTT AAATATGATG ATGGTAAAGA TCCTAAAGGA	600
	TTACCTAAAG CTGATATTGT TTTACTTGGT ATTTCGAGAA CTTCAAAGAC ACCATTATCT	660
ac.	CAGTATTTAG CGCATAAGAG TTACAAAGTT ATGAATGTAC CGATTGTACC AGAAAGTGAC	720
35	ACCGCCAGAT GGCTTATATG GATATTAATC CAAAGAAATG TATCGCACTT AAAATAAGTG	780
	AAGAnAAATT AAATCGCATT AGAnAAGAGC GACTAAAACA ATTANGACTA	830
40.	(2) INFORMATION FOR SEQ ID NO: 716:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1159 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716:	
50	ngaagaacaa gtttancatc taaatgcccg tttaaaacta caactacttg acgatgttaa	60
	ATCAGTGTTT AANTCTCAAA TGACGCAAAA TAGTGATTTT AATGAAGAAA AGAAAGTGTC	120

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	AGAACGTATA	AAAAAATACT	TTAATAAGCA	ACTCACTGAG	CAAATTGCAC	CAATCGTTCA	240
	ACAATTAGCA	GATTTACATG	TCATTATTAA	TCCTCAGTTT	AACTTTGAAT	CAGCTAATAT	300
5	AGAGCAACCA	TTATTGCACA	TCGATTTCAA	CGATATGCTA	AATGCATTGC	CTAAACAATT	360
	AACAAAACGT	aaaattttga	ATCCAAATGG	GCAAAGAGAT	ATACATGAAT	CAATTTGTCA	420
	AAGTACGTTA	GGATTATTAC	AACCACAAAT	GGGATTATTG	AGGCAACAGC	TTGAATTATA	480
10	TGTAAAGCAA	ATGGCTGTAG	AAGCTGAATC	GCAATTTGAA	AGTTTTGAAG	CTAATATTCA	540
	AACGCAAATA	AACGATTTAT	TAGCATTTGA	TTTAGATACA	ACACTTATCA	ATCAATTGAA	600
15	AGATAAACAT	CAACAACTGA	AAACTATTT	ATATTAAGAa	AGAAGGAACG	TTTTAAATGC	660
15	СТААТААААТ	ATTACTTGTA	GATGGTATGG	CGCTATTATT	TAGACATTTC	TATGCTACAA	720
	GTCTTCATAA	ACAATTTATG	TACAATTCAC	AAGGTGAACC	TACAAATGGA	ATACAAGGAT	780
20	TTGTGCGTCA	TATCTTTTCG	GCAATACATG	AAATACGCCC	TACACATGTA	GCTGTATGTT	840
	GGGATATGGG	ACAATCAACT	TTTAGAAATG	ATATGTTTGA	tGGTTATAAG	CAAAAkCGTT	900
	CTGCACCACC	AGAAGAATTG	ATACCACAAT	TTGATTATGT	TAAAGAAATT	TCAGAGCAAT	960
25	TTGGCTTTGT	AAATATTGGC	GTTAAAAACT	ATGAAGCGGA	TGATGTTATA	GGTACATTAG	1020
	CACAACAATA	TTCAACTGAT	AACGATGTCT	ATATTATTAC	GGGCGACAAA	GATTTACTGC	1080
	AATGTATTAA	TGACAATGTT	GAAGTTGGCT	AATTAAAAA	GGTTTAACAT	TTATAATAGA	1140
30	TATnCATTAC	ATCGTTTTn					1159

(2) INFORMATION FOR SEQ ID NO: 717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717:

GATTTAATCA	ATGCAGTTGC	AGAGCAAGCT	GATTTAACTA	AAAAAGAAGC	TGGTTCAGCA	60
GTAGATGCTG	TATTCGAATC	AATCCAAAAC	TCACTTGCTA	AAGGTGAAAA	AGTACAATTA	120
ATTGGTTTCG	GTAACTTTGA	GGTACGTGAA	CGTGCTGCAC	GTAAAGGTCG	TAACCCTCAA	18
ACTGGTAAAG	AAATTGATAT	CCCAGCAAGT	AAAGTTCCAG	CATTCAAAGC	TGGTAAAGCA	24
TTAAAAGATG	CTGTAAAATA	ATTTTACTTA	AAAAGCCCTG	AATAAGGGCT	TTTTATTTTG	30
СТТТТААТАС	TTACAACCTG	TACATAAATT	GTAATGTTCT	TCTAAGTTTT	TAATCTTTGG	36

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,	AACTACAAAA TATACATATG aATATTGAGA TTAATTGTTA GCGTTGAATT TACTTAAAAG	480
	GTAACCATGT CTACTATAGT ATTTTACGTT ATTTAAAAAG ATGAATAATG TAAATGAAGT	540
5	AAAGGTTATT ATGAGAATTA CAAAAGCTAC ATAA	574
	(2) INFORMATION FOR SEQ ID NO: 718:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 493 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718:	
	AAGATATTGA AAMTGMAATG GAGCACGCCC TTATTTGATA GAAGTAAAAG ACATTTAATT	60
20	CTTACCGATG CAGGTCAAAT TTTTTATGAG AAAAGTAAAG AAATTGTtGC ACTGTATGAT	120
	TATTTACCAT CTGAAATGGA ACGCTTGAAT GGACTGGAAA CAGGACATAT AAACATGGGC	180
	ATGTCGGCAG TCATGAATAT GAAGATTCTT ATCAATATTC TTGGTGCATT CCATCAACAA	240
25	TATCCAAATG TTACATATAA TTTGATAGAA AATGGCGGTA AAACAATTGA ACAGCAAATT	300
	ATCAATGATG AAGTAGATAT AGGCGTGACC ACTTTGCCAG TCGATCATCA TATTTTCGAT	360
	TATACTACCC TAGATAAGGA AGATTTGCGA CTTATCGTGA GCAGAGAGCA TCGACTCGCA	420
30	AAATATGAAA CTGTTAAACT CGAAGATTTA GCAGGTGAAG ACTTCATTTT ATTTAATAAA	480
	GACTTTTACT TGA	493
	(2) INFORMATION FOR SEQ ID NO: 719:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1257 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	· · · · · · · · · · · · · · · · · · ·	
•	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719:	
45	GCATTGCCAA AACAATACGT TTATATTATT GAGGAACTAC TGTATAAAAG TAATGAATAT	60
	CAAAATAAAA AATCATATTA CGAAACACTT GTTAACCAAG TAATTGAACT TAAACAGGCA	120
	GATGATTTAA TTATTGGACT CGCTTATTCC GTACAACGCT TAGTCGTCGA TCATTTACAC	180
50	GTTGTCGGTG ATATTTATGA TCGTGGACCA CAACCAGATA AAATTATGGA TACACTGATT	240
	AATTATCATT CCCTAGATAT TCAATGGGGT AATCATGATG TGCTTTGGGT TGGAGCCTAT	300

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a comment

	GATATTATCG	AAGACGCTTA	TGGCATTAAT	TTAAGACCAC	TGCTTACTTT	AGCTGAAAAA	420
	TACTATGACG	CAGATAATCC	TGCTTTTAAG	ССТААААААА	GACCTGACAA	ACACGAACGT	480
5	TTAACTCAAC	GTGAAGAAAG	TCAAATTACT	AAAATTCATC	AAGCTATTGC	GATGATTCAA	540
	TTCAAGTTAG	AAATACCAAT	TATTAAACGT	CGTCCAAATT	TCGAAATGGA	AGAACGTCTT	600
10	GTGCTTGAAA	AGGTTAATTA	TGATACAAAT	GAAATTACAG	TTTATGGTAA	TACATACCCA	660
10	TTGAAAGACA	CATGTTTCCA	AACTGTCAAT	CGTGATAATC	CAGCAGAATT	ACTACCTGAA	720
	GAAGAAGAAG	TCATGAATAA	ACTATTATTG	TCATTCCAAC	AATCTGAAAA	ATTACGTCGT	780
15	CATATGTCTT	TCTTGATGCG	TAAAGGCTCT	CTTTACTTAC	CATATAATGG	CAATTTACTC	840
	ATTCATGGTT	GTATTCCAGT	TGATGAAAAT	GGTGAGATGG	AATCATTTGA	AATTGATGGT	900
	CATACTTACA	GCGGCCAAGA	ATTATTAGAT	GTGTTTGAGT	ATCATGTCCG	TAAATCATTT	960
20	GATGAAAAAG	AAAATACTGA	TGACTTATCG	ACGGATTTAG	TTTGGTATTT	ATGGACTGGG	1020
	AAATATTCGT	CACTATTTGG	TAAACGTGCC	ATGACTACGT	TTGAGCGATA	CTTTATTGCA	1080
	GATAAAGCTT	CTCATAAAGA	AGAAAAGAAT	CCGTACTATC	aTCTTCGTGA	AGATGTGaAT	1140
25	ATGGRTCGTA	AAATGCTCaG	TGaTTTCGGA	TTAAATCCAG	ATGAAGGACG	CATTATTAAT	1200
	GGTCACACAC	CAGTGAAAGA	AATCAATGGC	GAGATCCTAT	CAAGGCTGAT	GGAAAGA	1257
	(2) INFORM	ATION FOR S	EQ ID NO: 7	20:			

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720:

TGAGCACATG	ACAGTGGCTG	AAAACATTAA	AAATTTTTTAA	TCACTTTGTA	AAAATCCAAT	60
TAACGATACA	ACTATCAACG	AATATTTACA	GCAATTAAAC	TTTGATGATA	CGTCTGCCAA	120
AGTATCTACA	TTGTCCGGTG	GGAATAAACG	TAAAATTAAT	ATATTAGTAG	GTTTACTAGG	180
TCAACCTCGA	ATTCTCATTT	TAGATGAACC	GACAGTTGGT	ATTGATTTAA	AATCTAGACA	240
TGACATCCAC	CAACTACTTA	ACATCATGAA	ATCTAAATGT	TTAATTATAT	TAACTACCCA	300
TCATTTAGAT	GAAGTTGAGG	CACTTGCAGA	TGGTTATCAA	GTTAATTGGG	CCAGGTnCCC	360
TTTTnTTCAA	CAGTTTTTGG	GGGCCAACCA	TGGGCTTATA			400

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(2) INFORMATION FOR SEQ ID NO: 721:

5	(A) LENGTH: 570 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721:	
10	CTTATTTATA TTATAATATA AATATTTTAT TTTTCAATAC TTAATTTTAA AAATCCCCTA	60
	TGAAAATGTT GATGAGCTAC ATCTTTAAAT CTTATTATAC ATTGTATAAA ATTATATTGC	120
	GAGGTAGTAA ATTGATATTA TACACTTTTG GTTGTGTATG CATCTCACCT ATCTTTTTTG	180
15	CTTTTTCAA ATAAGAAAGT ATTAAAAATY AATGCCTATA CAGGAACAGA CATGGCTAAA	240
	CTTGATTTAA ATAGTCTTGA CGACGAGCAC GTAAAATTAT TAATAAATGA ATTAAAATAT	300
	CCAGAAACTC ATATCGATGT AAATGAATTA AAAACAATAG TTGCTAGTCG AATAAATGAA	360
20	AGGCAAGÄAA TAATAAGTTT TAAGTTAGGA ATAAAGTACT TATTAACAAT AAAAAGAGGG	420
	AACATAGAAA AAGATAGGTT TTCAATTTCA ATCATTTTCA AAGATACCTA TCACACCCTA	480
25	GTTAGAATAG ATATTAACGG TGGTACTCAC GATAATCCAG ATGGAACAAT CGCTCCGAAA	540
25	AGTCATATTC ACATATATAA TGATAAGTAT	570
	(2) INFORMATION FOR SEQ ID NO: 722:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722:	
40	ATTTTAGTCT TAGGTGTTGA TTGCATGATG AATGCAGAAG TTATACCTGC AGCCATATTA	60
40	GCACCTTCAT TATTGTGTAT AATTTGAATA TTATTTGCTT TTAAAGTATG TCCAATTAAG	120
	TTTGAAGTCG TTGTTTTACC ATTTGTTCCA CTGATAAATA CAATATCATC AACTTGCTCT	180
45	GCTAATTTC TTAATATATC TGTATCCACT TTTCTAGCGA TTTGTCCAGG TAAATCTGTT	240
	CCTCTTTTAC CTACTGCTCT ACTTGCTTTA CGCGCCAATT TCGCTAGATG GATTGCCGTC	300
	CACTGTCTCA TGTGTTTCCT CCtCAAATTt CCACTCGCAT CATTATAACA TGACAAGGCA	360
50	ACTTCAAAAA AGTTTCTCAA TCACAAATnG ATACCAGTGT	40
	(2) INFORMATION FOR SEQ ID NO: 723:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1113 base pairs	

, participal or order

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723:	
	GATTATATGC TGTTGGCAAA ACAATATACC CAGATGAATT TTTATTTTTA GTAATAGTAT	60
10	AACCATGCTT TGTCTTACTA ACTTTGACAG CTTCTAATGA ATTTGAAGCG TCTTTAAGCG	120
	TGGTATAATC TTCGCCGTAT ATCCCTTTTA AATTTACTCG ATACTTACCT TTAGGCAATG	180
	ATAATCTAAT TCTATCTGGA GCTTTAATGC GTATCGTTAC GGGTGTTACA ACGCGTCGAT	240
15	ATTTATAAGT GAGTTTATTT CTTTCTTGTG TATATTCATT CACTTTAACA TCATGAGCTT	300
	TATCCGGCGA AAGTAATTCT AAATCCATTT CAAAATACAA ATCTTTAAAT TGATTAGAAA	360
	CTGATTTTGG CAACTGTACA GTTAGACCAC CATTATTTTG TTTAACTTGT AATAAATGTT	420
20	TTGTAGGAGA TTGCCAGGCT GCACTATITA ATTTAATTGT TGAATCTGAT AGTAAATTTT	480
	TATTGGCTTT AAAATGTGTA TTAACATCTT TAATATTGTT AGAAACAATC CCTTGCAACA	540
0.5	TTGCTTGTTC TTTATCTAAT GGAGATTTTA ATTCTTTATT GGAAAAGACC TTATTTGTAA	600
25	TATGTGCACT TGGATAATGG ATGGTATTTT TAGAATGAAT CCAACGAACT TTATTGTCTT	660
	TGTGTTCAGA CTTAATTTTA AATCCATATG GLAAGTTGTC ATCATGATLC ACTCTAATTC	720
30	GATCATTAAC ATTCCAAAGT GATAGTAAAT TTGACGATGC CAAGTAATCT ATAAGTGCTG	780
	TTTTTATCGA TTGGCATATT AATTTGGAGT GTCTTGTCAT AATATTTTAA AATGTCTCCA	840
	TTAAAAATAC TAGAATATAA TGAAATGCCA TTATAATGAT ATATAAATGG TGAATTTAAT	900
35	GCATAGTCTG ACATATAATC AATGCGATTA AATGAGCCTG TTGCATTTTG ATTTATCTTT	960
	TTTATAAGCT GGTTTACATA GTTACTATGG TAATCATGTT GTTTCAACGT TGATAATGAT	1020
	TGTTGATAAG GTTTGATTGC CATGTTTTTG TTGTTATCTA AAATGACGAT TTGTTGAATC	1080
40	ATAACGATTA ATACTAATAT TGCAACGGTT AAT	111
	(2) INFORMATION FOR SEQ ID NO: 724:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 464 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724:	

TGCCGTTTAG CAAAATCTAG TATCGCTTGA TGATCAGATT CTGAAATTTC AGTGTGTACT 60

	GATTGATTAA GTTTATATGC AAGTGCATGT TCTCGTCCAC CAGCACCAAT TACTAATACA	180
	TTCATTTATG TTACGCCCCT TTAAAATTAG TGTTTAAAAT GTCGAGTGCC TGTGACTACC	240
5	ATTGCAATAC CATGTTTATT AGCCATATCA ATTGAATCTT GATCTTTAAT CGAACCACCC	300
	GGTTGGATAA TTGCCTTTAT ACCATGTTGT GCTGCAAGTT CAACTGTATC TCCCATAGGG	360
	AAAAATCCAT CAGATACTAA CGGCTACATG ATCATTGATT TCAATAGCTC TCTCTAACGC	420
10	AATTTTAGCA GCACCGACAC GATTCATTGG CCAGCANCTA TACC	464
	(2) INFORMATION FOR SEQ ID NO: 725:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1440 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725:	
	GTTAAATnCA nTATTTNAAA TATATTACCT TATTAGAAAA AGTCGTAATA TGAGGTGTAC	60
25	AAATGACGCA AATTTTAATA GTAGAAGATG AACAAAACTT AGCAAGATTT CTTGAATTGG	120
	AACTCACACA TGAAAATTAC AATGTGGACA CAGAGTATGA TGGACAAGAC GGTTTAGATA	180
	AAGCGCTTAG CCATTACTAT GATTTAATCA TATTAGATTT AATGTTGCCG TCAATTAATG	240
30	GCTTAGAAAT TTGTCGCAAA ATTAGACAAC AACAATCTAC ACCTATCATT ATAATTACAG	300
	CGAAAAGTGA TACGTATGAC AAAGTTGCTG GGCTTGATTA CGGTGCAGAC GATTATATAG	360
35	TTAAGCCGTT TGATATTGAA GAACTTTTAG CAAGAATTCG TGCAATTTTA CGTCGTCAGC	420
	CACAAAAGGA TATTATCGAT GTCAACGGTA TTACAATTGA TAAGAACGCT TTTAAAGTGA	480
	CGGTAAATGG CGCAGAAATT GAATTAACAA AAACAGAGTA TGATTTACTA TATCTTCTAG	540
40	CTGAAAATAA AAACCATGTT ATGCAACGGG AACAAATTTT AAATCATGTA TGGGGTTATA	600
	ATAGTGAAGT AGAAACAAAT GTCGTAGATG TTTATATAAG TTATTTACGA AACAAGTTAA	660
	AACCATACGA TCGTGACAAA ATGATTGAAA CAGTTCGTGG CGTTGGGTAT GTGATACGAT	720
45	GACAAAACGT AAATTGCGCA ATAACTGGAT TATTGTTACC ACGATGATTA CGTTTGTCAC	780
	GATATTTTG TTTTGTTTAA TTATTATTTT TTTCTTGAAA GATACACTGC ATAATAGTGA	840
50	GCTTGATGAT GCAGAACGAA GCTCAAGCGA TATTAATAAL TTATTTCATT CTAAGCCTGT	900
50	TAAAGATATA TCTGCaTTAG ACTTGAATGC aTCTTTAGGT AALTTTCaAG AGATAATTAT	960
	TTATGATGAG CATAATAATA AATTATTTGA GACATCGAAT GATAACACAG TGAGAGTTGA	1020

	ATATTTAATT ATTAAAGAAC CAATTACAAC GCAAGATTTC AAAGGGTATA GCTTGTTAAT	1140
	TCATTCACTA GAAAATTATG ATAACATCGT AAAATCATTG TATATCATTG CGCTGGCATT	1200
5	TGGAGTGATT GCAACAATTA TAACTGCCAC AATCAGTTAT GTATTTTCAA CACAAATTAC	1260
	TAAACCGCTT GTCAGTTTAT CAAATAAAAT GATTGAGATT CGACGAGATG GTTTTCAAAA	1320
	TAAATTGCAA TTAAATACAA ATTATGAAGA AATAGATAAT TTAGCAAATA CGTTTAATGA	1380
10	GATGATGAGC CAAATTGAAG AATCATTTAA TCAACAAAGA CAATTTGTTG AAGATGCGTC	1440
	(2) INFORMATION FOR SEQ ID NO: 726:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726:	
	TGATATTCCG ACTTGCGAGG ATTATTGCGC ATTAAGGATT AACGCAGTAT GAGTCCAAAG	60
25	ACGCGCGACA CCTGGAAAAA GGATTACCTA ATGCCTTATT TACAGTAACC TTGTATGATA	120
	AAGATCGGTT AATTGGTATG GGTAGAGTGA TTGGCGATGG CGGAACTGTT TTTCAAATTG	180
	TTGATATTGC AGTTTTGAAA AGTTACCAAG GTCAAGGTTA CGGCATCTAA TTATGGAGCA	240
30	TATTATGCAA TATATTAAAG GTGTGGCTGT TGAGAGTACA TACGTTATCT GATTGGCAGA	300
	CTACCCAGCG GGnTAAATTA TATACCAAAT TTGGGTTTNA TACCTACCGA ACCAGANTCC	360
35	AGGCGGTGAT GTATG	375
	(2) INFORMATION FOR SEQ ID NO: 727:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 471 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727:	
	TAAAAAACTT AGAGATGAAA ATCATATTAT TTATCTGTTT TTGGGACAAT TTTTTACTAA	60
	AAATGAAGAT CCATGGCATC AAATACTTAA TGATTTAGAA GTTACAAATT CTGTTGATAA	120
50	TTTTTTAAGG TCAATAAGTA ATAAGGCCAA AGAAACAAAA AAAAGAGCTT TTATTATTAT	180
	TGATGCGCTT AATGAAGGTG AAGGTAAAAG GTTATGGGGA AATTATTTTC AAAGCTTTAT	240

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	AGATGTTATA T	TACCCAAAA	ACGCAATACA	AGATAACAAT	ATTGTAGTAT	TTCAGCATGA	360
	AGGTTTTAGT A	AGGAAGAAA	ACTATAATCC	AATTGTATCT	TTTTGTGATT	TTTATGGATT	420
5	AGAGCTACCT A	AGTTACCTA	TATTAAATCC	AGAATTCAAC	AATCCATTAT	т	471
	(2) INFORMAT	ION FOR SE	Q ID NO: 72	:8:			
10	(A (B (C) LENGTH:) TYPE: nu	ACTERISTICS 1750 base p cleic acid NESS: doubl : linear	pairs			
15							
	(xi) SE	QUENCE DES	CRIPTION: S	SEQ ID NO: 7	728:		
	TAGGATGTTC C	ACCCTgGCA	ATTGCTCTAA	GACATCTACa	GCAGTAGAAT	ayCCTGTTTT	60
20	CGTCtTTTTA A	TAACAGGTA	ATTGTAATGT	CTCAAACAAT	ACAACACCTA	ATTGCTTAGG	120
	AGAATTTATA T	TAAAATCTT	CACCAGCTGC	ATCATGGATA	TTTCGAATCA	AGACGTCTAA	180
	TTTTTCTTGA A	TTTCTTTTT	CCATTTCTTC	TAAATCATGA	ACATCTGTAA	ATATACCAAT	240
25	TTCTTCCATT T	CACTTAAAA	TCTTAGCTAG	CGGTAGCTCT	AAATCAGCCA	AGAGTTCTAC	300
	CTGATTGTAT T	CTTCTAATT	GTTTATCCAT	ATTTGGTTTC	GCAAAGTAAA	TTGCATCAGT	360
30	AATAGAAGCA A	CATATGGAT	TTAAAACATC	ATCTTCAGGT	ACCTTAAATT	TCTTACCTTT	420
30	TCCATATATA C	TCACATCGT	CTTTCACAAA	ACTTTGACCG	TACAATGAAA	CAACTGATTG	480
	AACATCACTA A	TCGTACGAG	ATGGATCAAT	TATATAACTG	GCCAACATAA	TATCGAAAGA	540
35	AATATTTTGA A	TATCAATCC	CCAATCTATG	TGATGCTACA	TATGTTTTT	TAGCATCATA	600
	TACGACTTTT T	TCGAATTCG	GATTTTCTAA	CCATGAAACT	AGTTCGACAT	AATTATTTAT	660
	GTCATCCGCA T	TAATTACAA	TATGTTTCTC	ACCTGEAAAT	aAAGAGAATT	TTAAAALATT	720
40	ATTLCGCAAA T	AGLTACCAC	CGtCTAATTC	GAAATGGATG	GCCGCTTCTT	TCAATGAAGT	780
	AAAATCCAAT A	TTATCAAAA	GACGTTTCcA	ATTTCAAATG	TCTTtTCTAT	TGCATCTTCA	840
	ACGCTTGCTG A	TTGaTCAAT	GTCAGCCAAC	AATTGTTTGA	ATTCTAACTT	CTTAAACAAT	900
45	TCGATTTTTT C	TTGTTGTTC	ATCTtGAkGA	GTCATTAACG	TATCTTCaAG	TTTTACTTCa	960
	ATCGGACTAT C	TACATTAAt	CGTTGCTAAT	TCTTTACTCA	TTAATGCATC	TTCTTTGCTA	1020
	TTTTGAAGTT T	TTCTTTTAA	CTTTTTACCT	GAAATTTCAT	CTAAATGTTC	ATAGACACCT	1080
50	TCTACTGTGT C	AAATTGGTT	TAGCAATTTT	ATTGCTGTTT	TCTCTCCAAC	ACCTGCAACA	1140
	CCTGGTATAT T	ATCAGAAGT	ATCTCCCATT	AATCCTTTCA	TATCAATAAT	TTGATTAGGT	1200

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	_	
	CCTTTTTTAG TGTAATAAAT GGTTACATTA TCCGTTGCAA GTTGTGTTAA ATCTCGGTCT	1320
	CCCGTAATAA TAATTGTCTG AAAGCCCGCT TTATCTGCTT CTTTACTTAA AGTTCCGATA	1380
5	ATATCATCTG CCTCATAGTT ATCTAATTCA TAACGTTTAA TATGATAAGC ATCTAATAAT	1440
	TGGCGAATAT AAGGAAATTG CTCACTTAGT TCAGGCGGCG TTTTCTGGCG TCCACCTTTA	1500
	TATTCACTAT ATTTTTCATG TCTGAAAGTC GTTTTACCTG CATCAAACGC TACTAAAAAA	1560
10	TGATTTGGCT TTTCTTCTTT TAAAATCTTC TCTAGTAACA TTGCAAAACC ATATACTGCA	1620
	TTGGTATGAA TGCCTGCTTT GTTTGATAAC AAAGGTAATG CATAAAAAGC TCTAAAACTT	1680
15	AAGCTATTAC CATCGATTAA TACTAATTTA TTCACAATTT TAACCTCCAG AACTAATTTA	1740
	TATATnTGTG	1750
	(2) INFORMATION FOR SEQ ID NO: 729:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 439 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729:	
	AAATTAATTT TAACATCCTT TCAAAATAGT TTTAACGGAT CCTCCCAAAA CGTAAACTCA	60
30	CATCAGTTAC TTGTAACATG CATTTTCTCC TTTTTTTCAT TCGATATTCT AACGGAAGAA	120
	TTATATCATA TTATCGTCAC AGTTTCGACC TCATATAAGT TGTAATGATA GAATGACTCA	180
35	CACATGTTAT AATAATAAAG AATACAAGAA TCGAAGGAGA ATAAACATGG CATTAGACAA	240
00	AGATATAGTA GGGTCTATAG AATTCCTTGA AGTAGTAGGG TTACCAAGGT CAACTTACCT	300
	TTTAAAGGAC CAACGGTGAA ACGTAAAGTT AAACCAATCA GAATGAACGT GATGATTGAA	360
40	TTAGAAGTAG GGGAGNATAT AGTTCCTCAT TTATCCAACC GGTCAGGTGG ATTATTGCAC	420
	TCAAATATGC ngnTATACG	439
	(2) INFORMATION FOR SEQ ID NO: 730:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 481 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50		
	(vi) SEQUENCE DESCRIPTION: SEO ID NO: 730:	

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	AGTTTAGGAT TGATGACAAA GCCATTACGA CCAACAAATC CTAAACCTGC ACGTTCTGCT	120
	ACTGCCCTAT CTGATAATAC ACCCGTATCT ACCATAGATT TGATTTCAAC ATCTGGAACT	180
5	TTAGATTCAA TAAATGCAGC TAACATGTCT AATCGTTTAC GCATAATTGT ATGATAATCT	240
	TGACCCCACG ATGCTCTAGC AAATAAGCCT CTGCGATCAC CTCTAACACT CTTAGGTGCA	300
10	CCTTTCAGTT TGTTAGGATA ACCAACTGCA ATTGCTATGA TTGACCTTGC TGTTGGTAAG	360
	GATAATTTAG GCTCCGTTCG TAAAGCAATA TCAGATTCTT CAAATCCTGA GGCATAACCA	420
	TTTGCATGAT ATGCTTCTAG CTTTTGCTTC AATTCATCAA AGGGnTCGGC AGTAGTAAAT	480
15	c	481
	(2) INFORMATION FOR SEQ ID NO: 731:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 828 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731:	
	GTGATGAAAA ATCTTTTCT ATTGATTGAG AAAATAGTTA TTTATATAGT TTTTAAAGAA	60
30	AAAAAGTGAT AATATTTAGC TAATCTAATG AAAATTGATT TATTGGACAA AAAATACATT	120
	TTAAATGAGT AGAGGAGGCT GCAAWTGGGT TACAGAACTT TAAAAAGTAT TTTTCATGAA	180
	CACAATGAAA GTAAAATGAA GGAAGAGTAT ATTAAAAGAT TTAATTCTTT mGCTTCTTTC	240
35	AATACTAATA TTAATATCAT ACCTATGGAA AATGGAAAAA AAGTTAATGA TTTGGAATAT	300
	CCTCTATTCT TTATGGTGAC TAAAAATCTA TCAAAAAAAC AAGAATTAAT ATCAATTAAT	360
	AGTAGAAAA TTGATAGAGC ACTTAATTCT TTACCATATG CAGCTAGAGA ACAATATTTT	420
40	AATGATTTAT TAATCGATGA ATTACAAAGT ACTAATGAAA TTGAAAATGT ATTTAGTACT	480
	AAACAAGAGA TTGCACATGC GTTAAATAAC CAAGCATCAG AATTTCTTAA GTTCAGAGGC	540
	CTCGTGGATC AATATAAAGA GATAGAACTT AATAAAAAA TTAAAGTTGA TAATGTAAGA	600
45	GACATTAGAG CGATTTATGA TAAATTAGTT TCAAATGAAA TTAACGAACA AGATAAGTTA	660
	GATGGAGAGC TATTTCGTAA AAATTTTGTC GGTGTGCATG ATGGGTCAAC GAATAAATAT	720
50	ATACATGTTG GGTTACAACC TGAAACCAAA ATTGTTGAAT TTATAGGTGA AATGCTAACA	780
	TTTTTAAAAT ATTTTGATGC GCCTCAGCCG TTCAAAATCA TGGCTAGT	828
	(2) INFORMATION FOR SEQ ID NO: 732:	

1632

والمناورة فالأراب وولاء ويتوار ويراوي

(A) LENGTH: 1622 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732:

10	CGTATGTTTC	GAATTTTATG	nATTGCATTG	GATAATAGTA	CCAGTTAAAA	GAACTAAGAT	60
	TGTAATTATC	CCCCCTTAAA	ATTCAAGAAT	ATATTTTCTT	AATCTATCAG	CAAGAGGTTA	120
	TATTTCAAAG	TGTTTATTTT	TAAAACAACA	TCTAAAAGCC	ATTTCATAAt	AAwGTTAAAT	180
15	CaTTAGaATG	TATAAAGATT	CCaATTAATA	AAAATAGATA	AAATGCAATA	AAGTTCCAAA	240
	TACTTATTAT	TATTCATCAC	AAATTACGTG	ATGCCCTCTA	CAACACTAAA	TCAAGGATGA	300
	TATTTATTTT	ATATACATTA	GCATTCATTG	TTTGCTTACC	CACATTATCC	TGTTTAGTCT	360
20	TTTTTATAAC	TCTAGTCTTG	AATGTCATAT	TTACAAAGAA	AAAAACACTA	AATTTTAA	420
	AACTAACACT	ATTTATTCAC	TTTGTTCTTT	TATAGCACCT	TTTATGTTTA	TTTTCTTGTA	480
25	TTCAATAAAT	AGTATGGAGA	TGATAATTTA	AAGTAGATAT	ATTTGAAGTA	TACTATAGAG	540
	TAAATTATAT	TGGGGAAATA	TGTAAACGAA	CCGGTTGATT	TTATAGTGGA	TTAACACTTC	600
	ATAGAGAATA	TAATCAAGAA	CAAAAACAGT	CAATAGGTGT	GAATTTTTT	AAAGACGGAT	660
30	CTGTTGCTAC	TAAAAAAAGA	AGTATACAAT	TCAATAGTTA	AACCTTAAAA	CAAGAAATAT	720
	TATTCAAAAT	CAATGAATTT	CCTATCTTAT	TAGTTTTAAC	AATATTTATT	CTCATAGAGT	780
	TTGTCCAATT	AAATATAGAT	GATTCAAATA	TTTATAAGCA	TACAAAAGAG	CAGTAAGACA	840
35	TTTTCTAATA	GAAAATAACT	TTACTGCTCT	TTGTACATTA	CTCATCAACT	ATTGTAAATT	900
	AAATAATAAA	TAACTACCTA	TTTTATTATT	CAGCTAAAAA	ATGCTCTGCT	AAATATTTTG	960
	CTGCGCCATC	CTCTTCATTC	GTGTATGCCG	TTACATCTGA	AGTTAATGCT	TGGATTTCAG	1020
40	GGCGTGCATT	TTTCATAGCA	ACTGTATAAT	GACCAAATTC	AAACATTGCT	CTATCATTGT	1080
	CGCTATCTCC	AATAACTAAC	GTTTCTTCTT	GATGAATACC	AAAATGTGCA	ATCATTTCTT	1140
45	TAATGCCTGT	ACCTTTATCA	GTTTGATAAG	CCATTGTTTC	CGCATTAAAT	CTTGATGAAT	1200
	TTGATACACT	AATCTGTAGT	TGCACATGAT	TTTGCTTTAA	TTCATCTCTA	AATGCTGTTA	1260
	TTTTTTCTAA	ATTAGAACTG	AATAGATAAA	TTTTTGAATA	TTCACCTTCA	GGAAACTTAG	1320
50	TTACCCAATC	TATCTTACCA	GCAAGCGCAT	CTTGTCTTGA	AGACCATTCA	CTATGACTTA	138
	CGCCATTAAT	AGGATCTTGA	CTACGAATCA	TATCTCGCAT	CCATGTTTCA	TCTTCTTTTA	144
	AACAAACTCT	ATTACCTTCA	AAAGGAAATA	ССТСАТААТА	AATTTGTTGG	СССТТАССТА	150

55

	CTACTTCTCC AATTGTTCCA TTTGAACTAA TGATGCCATT AACCGCAAAA TCTTGAGGTA	1620
	CA -	1622
5	(2) INFORMATION FOR SEQ ID NO: 733:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 472 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733:	
	AATGCCANAT AAATCCAAAT TCTTTTAACG AACAAGAGTG CCCAAGTTAT TGCTGATCGT	60
	TATGCCAGAT ANGCATATCA ATGATAATTA TGGTTTAGAA AGAATTTCTA AGACAAATCA	120
20	TGGATATAAT TATGTGTATT CCAATGATAA TTCAACTAGT AAGCAACATG TAAGTATTTC	180
	AAATCAAGGC ATAATAACGA AATAATAGAT GGAACAGTGT ATTCTAATTG GATATACTGT	240
	TTTTATTTTG CAATAATTTA ATTTAAAAAG GTGAATTCAA CTTATAAAAT GATGTAAATG	300
25	TTATGTCAAA ATCAACCAAT CCGTAATGTA TTTTAAAATG TTAATATAGT TCTGAAGAAG	360
	TATAAATGAG GTGTTGAAAT GGCTAAAAAT AAGAAAACGA ACGCGATGCG TATGCTTGAT	420
	CGTGCAAAAA TTAAATACGA AGTTCATAGC TTTGAGGTAC nTTAAGAACA TT	472
30	(2) INFORMATION FOR SEQ ID NO: 734:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 519 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734:	
40	CATAGCCCCA AATTTTTCT ATTATTTGTT CACGAGTAAA GATTTGCTTA GGACGTGCTG	60
	CAAGCATAAA TAATAATTGA AATTCCTTGT TCGGTAACGT CATCGTTTTA TTAGATACTT	120
45	GGAGTTCCAA ATAGGATTGG TTTAGCGTTA AGTTGCCAAT AGTCATTTCT GAATTTGAAT	180
	TGATATTATA TCGACGTAAT ACAGCACGAA TTCTAAAAAT AAGTTCCTTA ACCTCAAAGG	240
	GTTTGGTTAC ATAATCGTCA GTACCGCTTA TAAACGCACG CTCTTTGTCA CTAAGTGCAT	300
50	CCCGCGCTGT TAACATAATA ACTGGTATAT CATAATCATT TTTTAATGTA TTACATAATT	360
	GAAAGCCGTC CATACCATCC ATCATAATAT CTACCACTGC AATATCGaCA CGCTGTTTTT	420

	GTTTTGTMAA ATGGGCTAGC TATAATAATT TAGGGGATT	519
	(2) INFORMATION FOR SEQ ID NO: 735:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735:	
15	ACTIGAAAAC GATAAACAGT ACTITCCAGC TACACATTGG AAAGCTATAA ATGGGATACC	60
15	TTATGCAGGC AGTAGTGATA TTGATGGATT GCCTCAAGAC GGTATCATTT CGGTAAATGA	120
	TAAAAATAAA TTAGATAATT TAAAAATAGG CGAACAGGAA TTATTCAAAA TAGCATTGTA	180
2 [.] 0	CAGAAATCCC CAAACGGTAA ATTGTGGAAA ATAACAGTTG ACGATAGTGG GAAACTTGGT	240
	ACAGTGCTAT TTTATTAGAA AGGAAGGTGC ATTATGGAAA ATTTGTATTT AATAAAGGAT	300
	TTGGGAGCTT TAGCAGGTCG AGATTATAGA GCTAAGGAAA TACAAAACTT ACAAGGAATA	360
25	GGCATTGCGC TGGGCTGACC ACCAGGGTTT AnGTGnCCnC	400
	(2) INFORMATION FOR SEQ ID NO: 736:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 780 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736:	
	CTTTTTATT GAAAAAGTGG TATTTGATTA TCTATTTACT ATTTATATTA GCGGCACTCC	60
	TTATTACATT AACGACAATC CAACATGTAA CAGAAGATGA CAATCATnTT AATATAGGTG	120
40	TCGTAGATAA AGATCAATCA AGTGAAACGA AATTAATCTT AAACTCTATT GGTAAAGGGA	180
	GTAACCTAGG AAAAAACGTG AGCATTAAAG CATATGATGA TAAGCAAGCA CATACTTTGT	240
45	TAAAAAAACA TAAACTTCAA GGCTATTTTG TTTTTGATAA AGGTATGACC AAGGCATTTT	300
	ATAAACAAGG CGAACTACCA ATTTCAGTAT ATACATATGA TCAACAATCC ATGAAAAGTG	360
	TCGTGCTATC TCAGCTAACA GATTCTGTTT ACCAACGTCT TATGCGATCA ATGGGTGGCA	420
50	TCTTAGCTTT TCAAGACTTA GCACCGAAAG CATCACATTC TGACAGTATC AATGTTATGA	480
	CTGATTTGCT GATLACAGGA TTAAACCGTT CAGGTGCALT TAACTTAGAA CCGATTCATT	540

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CACTATCTTT ATTTACAGTT TTGAAAATGA ATCAAGATAC TGTATTGAAA GCGCGATTGA	660
AAATGTTTCA TTTTTCTAAA GAGCGTTTAT TAATCATTCG TACGTTGATT ACATGGTTTT	720
ATACTATGTT ATGGGNGTAT CGNTGGTGTA GTTTGGAATG TGGTTCAGTA TTCCGAATNA	780
(2) INFORMATION FOR SEQ ID NO: 737:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 946 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737:	
TATTTAATTT CTTnATTnTG GTTTTTAATT nTAAGATGAC CATAAATGAA TTTCTTCTGC	60
TGTCATAGAA TTAGAGCAAA ATACGAGCAT AAATTTAACT AATTTCTTGC TTGTCTTATA	120
GTCTTGATTG CCTTGTAAAA ATGTTAGTAT TAATTGCTTC ATCGTTTCGA ATTGTTGTGT	180
TGATTTAATA GCGATTGCTA AACCTATATT TTTTTCGAAA AGCTTTTCAA AACATCTATT	240
TAACAGGTTG TAATTCGTTT GGCTAATCTC AATATCGTGA ATATCGTCAA TGAAAACGAC	300
AGGTTTTGGT AAGTGCTCAA AGTTAATATC GTAATATTCA TTGAAAALAA ATTGAAATAG	360
TTCATTGAAA TTACTAAATC GAACAAATAC TTTGGCACGC TGACTTCGAT CTTTCGGATT	420
AAAATCATCT ATATGAATAT CTGTTGTATT TGTAGCCAGT TGAGCTGTTA AATCAATTGT	480
TGAAATTAAC TCAGTGAATT GTGATACGTT ATCTTGTTGG AAGTGTATTT GTGGTGGTTC	540
AGTAATCTTG GAAACGAGTG AACGGAACTG TTTAGGACTA AAATGCAAGT AATTCTTAAA	600
TTGATTTGCA AAATTTGTAT GACTGTTAAA ACCGGCCAAT TCAGAAACAG TTGTAATAGA	660
ATGTTTTGTA GAAAGTAATA AATTGATGGC GTTAACAAGT TTAATACTTG TAAAATAATC	720
TTTAAAATTC ATACTCAAAT ATCGAACAAA AAGATTAGAA CAATATGATT CAGAGATGTT	780
GCAATGCATC GCTATATCTT TTAAAGACAA GTGCGCATCA ATATKGTCAT GAATATAGTT	840
TACACAGTCT ATGAACACCG GATTGCTTAA AGCAATATTT GGTAAATATT CATGATCTAT	900
TCTTATAAAA GCTTCTTTAA GTAAAGTGTC TATNATACTT TGACCT	946
(2) INFORMATION FOR SEQ ID NO: 738:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 397 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738:					
TTTATTTGAT GATGTACTAA AGCAAGATGA AAGATTTGTT ATTGTAGTTC AAGCATTAGA	60				
AGAAAAGAAC GGACAATTAT TAAAGAGAAC TTTAAGGGAA TATCCCGGTT TAAACCATAA	120				
ACAAATGAAT GATTTATTTA TGCACTTAAA GGAATTATTT TCCGAAGAAT CATTTGCTGA	180				
AAACCAATCA GCGTTCAGTA TTACAGTTTA TACAAATTTA GATTATACTG CTGACCAAAT	240				
ATATGCTCAT GTAAAACGTT TCAGAGGTAA GCATGACTGG ACACAAACAG CTAAATAAAA	300				
TCAAGATGCT TGCAGTGGAT TKTAACmATT AATGETAGAT GTCmCyGcAT TTTTAATGCC	360				
ATTCGGTAAT TAATCCGGAT GGTCCAATTT AATTAAC	39				
(2) INFORMATION FOR SEQ ID NO: 739:					
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 915 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear					

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739:

CAAGGTATTT CATTGACCC ATTCACACCA TTAATAGTGG CAGCAGCATT ATACTTTGTC 60 TTAACATTTG TACTTACACG CATTATGAAC ATGATTGAAG GGAGATTGAA TGCCAGTGAT 120 180 TAAAATAAAC AATCTTAATA AAGTTTTTGG AGATAATGAA GTTTTAAAAS ATATCAATCT TGAAATCAAT CAAGGGGAAG TAGTAGCAAT AATAGGTCCA TCTGGTAGTG GTAAAAGTAC 240 ATTGTTAAGA TGTATGAATT TATTAGAAGT ACCTACTAAA GGTCAAGTGA TTTTTGAAGG 300 CAATGACTTA ACGGAAAAAG GGACACAAGT AGATAAACTA CGTCAAAAAA TGGGTATGGT 360 ATTTCAAAAC TTCAACCTAT TTCCACATAA AAAAGTTGTC GATAATATTA TTTTAGCTCC 420 TAAATTATTA AAGAAAGATA ATAACGATGA ATTACATAAG GAAGCATTGT CGTTATTAGA 480 TAAAGTGGGA TTAAAAGAAA AAGCAGATGT ATATCCGAAT CAATTATCAG GTGGTCAAAA 540 ACAAAGGGTA GCAATTGCAA GAGCTTTAGC AATGCATCCA GATGTTATTT TATTCGATGA 600 ACCAACTTCA GCATTAGATC CTGAGGTAGT TGGTGATGTA TTAAAAGTAA TGAAAGACCT 660 AGCCAAAGAA GGTATGACCA TGGTGGTTGT GACACATGAA ATGGGATTTG CCAAAGATGT 720 AAGTGACAAA GTCATATTTA TGGCAGATGG CGTTGTCGTA GAGTCAGGCA CnCCAGTCGA 780 AATATTTGAA CAACCGCAAC ATGAAAGAAC ACAAAATTTC TTAGCAAGAG TATTATAACA 840 ACCTAACGAG GCTTGAATAT ATGATACGCA CCACAAAGTT ATATCATATA TTCAAGCTTT 900

(2) INFORMATION FOR SEQ ID NO: 740:

 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 435 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740:	
AGTAAATGCG ATGTTGCATG GAGGCTATAG CAATGAGCAA TAAAGCTTGG GGCGGTAGAT	60
TTGAAGTACA ACCTGAAGAG TGGGTTGACG ACTTTAACGC ATCCATTACT TTTGATCAAA	120
CGCTCATAGA TCAAGATATC GAAGGCAGCA TTGCACATGC AACTATGCTT GCGAATCAAG	180
GCATTATTAG TCAACAAGAC AGCGAACAAA TTATACAAGG ACTAAAATCT ATTCAACATG	240
ATTATCATCA AGATCAAATT CAATTTAGTG CATCATTAGA AGATATTCAT TTAAATATTG	300
AACATGGAAT TAATTAAACG TATCGGTGGA TGCTGGTGGT AAGTTGCATA CTGGACGCGT	360
AGLAAACGAT CAAGTTGCAA CAGACATGCA CTTGTACACT GAAGAAACAA GTGCAAGnnn	420
TCATCGCATT GGATG	435
(2) INFORMATION FOR SEQ ID NO: 741:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1198 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741: AATATCAȚAA CCAAAGCTTG TCATTACTTA TATGTAAAGA TTAGAGGCTA ATTACATAAT	60
	60 120
AATATCATAA CCAAAGCTTG TCATTACTTA TATGTAAAGA TTAGAGGCTA ATTACATAAT	
AATATCATAA CCAAAGCTTG TCATTACTTA TATGTAAAGA TTAGAGGCTA ATTACATAAT CCTAACTTAT TTAACAGGAA GTCATGAAAA CTATATTACA ACTAAAAGTA TAACTTTCCA	120
AATATCATAA CCAAAGCTTG TCATTACTTA TATGTAAAGA TTAGAGGCTA ATTACATAAT CCTAACTTAT TTAACAGGAA GTCATGAAAA CTATATTACA ACTAAAAGTA TAACTTTCCA TCACCAAAGT CAGAATTTAT TGAAACACTC AACTGATAAT ATAGAAGGCT AATTATAAAA	120
AATATCATAA CCAAAGCTTG TCATTACTTA TATGTAAAGA TTAGAGGCTA ATTACATAAT CCTAACTTAT TTAACAGGAA GTCATGAAAA CTATATTACA ACTAAAAGTA TAACTTTCCA TCACCAAAGT CAGAATTTAT TGAAACACTC AACTGATAAT ATAGAAGGCT AATTATAAAA ATACCTGGCG ATTAATAAAC TGTTTCCGTT TTTTAGCACT TAATATATTT AAAAAGACAA	120 180 240
AATATCATAA CCAAAGCTTG TCATTACTTA TATGTAAAGA TTAGAGGCTA ATTACATAAT CCTAACTTAT TTAACAGGAA GTCATGAAAA CTATATTACA ACTAAAAGTA TAACTTTCCA TCACCAAAGT CAGAATTTAT TGAAACACTC AACTGATAAT ATAGAAGGCT AATTATAAAA ATACCTGGCG ATTAATAAAC TGTTTCCGTT TTTTAGCACT TAATATATTT AAAAAGACAA ATAGAGCCCT TTCAGGCTCT ATTTnCTGTA TCCTTAACAA CAGAAGCTGT TAAAACTACC	120 180 240 300
AATATCATAA CCAAAGCTTG TCATTACTTA TATGTAAAGA TTAGAGGCTA ATTACATAAT CCTAACTTAT TTAACAGGAA GTCATGAAAA CTATATTACA ACTAAAAGTA TAACTTTCCA TCACCAAAGT CAGAATTTAT TGAAACACTC AACTGATAAT ATAGAAGGCT AATTATAAAA ATACCTGGCG ATTAATAAAC TGTTTCCGTT TTTTAGCACT TAATATATTT AAAAAGACAA ATAGAGCCCT TTCAGGCTCT ATTTCTGTA TCCTTAACAA CAGAAGCTGT TAAAACTACC CGTCTTTTCA CAACCAAAGC TACAAAAAAG ATGGCTAGTT ATTCTTTCGT CACCCGCTGA	120 180 240 300 360
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740: AGTAAATGCG ATGTTGCATG GAGGCTATAG CAATGAGCAA TAAAGCTTGG GGCGGTAGAT TTGAAGTACA ACCTGAAGAG TGGGTTGACG ACTTTAACGC ATCCATTACT TTTGATCAAA CGCTCATAGA TCAAGATATC GAAGGCAGCA TTGCACATGC AACTATGCTT GCGAATCAAG GCATTATTAG TCAACAAGAC AGCGAACAAA TTATACAAGG ACTAAAATCT ATTCAACATG ATTATCATCA AGATCAAATT CAATTTAGTG CATCATTAGA AGATATTCAT TTAAATATTG AACATGGAAT TAATTAAACG TATCGGTGGA TGCTGGTGGT AAGTTGCATA CTGGACGCGT AGLAAACGAT CAAGTTGCAA CAGACATGCA CTTGTACACT GAAGAAACAA GTGCAAGnnn TCATCGCATT GGATG (2) INFORMATION FOR SEQ ID NO: 741: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1198 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double

TGAATATITT	TTGTTTAACT	CTTAAATTTC	GGGTTTAACT	TCCTCTATTT	CTAACAGTTA	660
TACTCCAGGA	TTAGTTTCTT	TAGAATCCGT	ACCGATTAAT	TTAACAGTAT	GGTTTTGCCA	720
GTCAACTTCA	TAAGTAGATG	TAAACGTTAC	TGTATTTTGA	TnTTTGTAGT	TATTTCCAAC	780
CCAGTGTAGT	CGATTCCATT	GATTAGTATA	TCTATCCATT	TCTCTTTGGT	AAGTTACTTT	840
GATTTTAGAT	TtTTTTGTAT	CATTTTGTTT	ATGAGAAAGT	ACGCTTATAA	ATTCTGGGTT	900
AAAGTTACCA	CGCGCCAATA	AAGGCATTTG	ATGTGTTGGC	AAGAAATTTT	GACCAGCATT	960
TGAACTACTT	TGTCTACCAC	CTAAAAACAG	TTCATTACCA	TATGTTGGGT	CATAACTATC	1020
TCTACCATAT	GGTCCCCAAC	CATTATTCAT	AATTTTGTGC	GCCTCAACAC	CCCAGCCAAT	1080
TGATTTATGA	TTTGTTTTTC	TATCAATCGT	AGTTCTGTAA	CTTTCTTGTT	TATTAATTTAT	1140
CGTTTCTGAA	AATGATTTTG	ATCCATTTAA	TCCACCTGAT	AAGCCATTAG	ATATATTA	1198
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(2) INFORMATION FOR SEQ ID NO: 742:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 818 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742:

GTGGCATATn CAAACTACTA CTGAAAGATC AATTACATAC GTACAGATTT TGCAAAATGA 60 TCAAGATTAT CCAACAATTT TTAGATGAGA CAAAACGTAA ATCTGTAATT AATTCAGATG 120 TTAATGTAAC GGTAAAAGAT AGAATAATGA CTTTATCAAC GTGCGAAGAT GCATATAGTG 180 AAACGACGAA AAGAATTGtT GTTGTCGCAA AAATAATTAA GGTAAGTTAA ACAGAAAMGA 240 GGATAATTAT GAAATTTATG GCAGAAAATA GGCTGACGTT AACaAAAGGA ACAGCAAAAG 300 ATATTATAGA ACGATTTTAC ACGAGACATG GGATTGAAAC ATTAGAAGGC TTTGATGGCA 360 TGTTTGTTAC ACAAACTTTA GAACAAGAAG ATTTTGATGA AGTGAAAATT TTAACAGTTT 420 GGAAATCAAA GCAAGCTTTT ACGGATTGGT TAAAATCTGA TGTCTTTAAA GCAGCGCATA 480 AACATGTTAG AAGTAAAAAT GAAGATGAAA GTAGCCCGAT TATAAATAAC AAAGTAATTA 540 CATATGATAT AGGCTATAGT TACATGAAAT AATTGAATTT AAAGAGGTTG CAGTACTTGT 600 TATGACAATT GGTATTGTTA GCTTTTGTAA CGACCATACA TGATACCGAT GATGGTCGTT 660 TTTTTAATGA ACACAAACAT GCTAACAACA AATTGCTAAA ACATAGTTTG aTTTGAATGT 720 GGCTTTGGAA AATAATCATC CALTATATCa TTLTGGATTn TATTTTGGAA GAAGAAAAGA 780

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(2) INFORMATION FO	OR SEO ID NO: 7	43
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(i) SEQUENC	E CHARA	CTERI	STICS:
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- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743:

TGCTGGTAAA TCTTCCCTTA TCAAGT	CTTT AATTGGTGAA	TTTAATGCTA	CCGGTACTAA	60
ATTGTTATAT AACAAACCTA TACAAC	AACA ACTGCAACAT	ATTACATATA	TTCCACAAAA	120
AGCACATATT GATTTAGATT TTCCTA	TAAG TGTGGAACAA	GTGATTTTAT	CAGGTTGCTA	180
CAAAGAAATT GGATGGTTTA GACGAC	CTAA TAAATCAGCA	AGGGATAAAC	TCAAACAGTT	240
ATTAAGCGAT TTAGAATTAG AATCTT	TACG TCATCGACAA	ATTTCAGAAT	TAAGTGGTGG	300
ACAATTACAA CGTGTGCTAG TAGCAA	GAGC ATTGATGTCC	GnAAGTGAAG	TTTATTTTCT	360
AGATGAGCCG TTTGTCGGAA TTGATT	TTAG TAGCGAAAAA	tTAATCATGA	CAAAAATcGA	420
GAACTTAAAA CAACAAGGAA AACTTA	ATTCT TATCATCCAC	CATGATCTAT	CAAAAGCAAA	480
GCAATACTTT GATCGCATTA TTCTAT	TAAA TCAAACATTA	CGATACTTTG	GTGATAGTGA	540
AGAGGCTATG AGTGTCACTC GCTTAA	ACGA AACATTTATG	AGTAGCACTG	ACTGTAGTGA	600
CCCTAGTCAA AGGAGCAATA TAACAT	GTTA GAGTTTGTCG	AACATTTATT	TACATATCAA	660
TTCTTGAATC GAGCATTGAT AACTTC	CAATT ATTGTAGGGA	TAGTTTGTGG	TACAGTTGGT	720
AGTTTAATTG TATTACGTGG TCTTTC	CATTA ATGGGAGATG	CAATGAGTCA	CGCAGTATTA	780
CCTGGTGTTG CCCTATCATT CTTATT	TTGGT ATTCCAATGT	TTGTAGGCGC	ACTTATAACT	840
GGTATGATCG CAAGTATTTT TATCGG	STTAT ATCACATCTA	GTAGTAAAAC	GAAACCTGAC	900
GCCGCTATTG GAATTAGTTT TACCGC	CTTTC TTAGCTTCGG	GGATTATTAT	TATTAGCTTA	960
ATAAACACTA CGACAGATTT GTACCA	ATATT CTGTTTGGTA	ATTTACTGGC	AATCACAAAT	1020
AGTGCATTTT TAACAACTAT TGTGAT	TTGGT TCAATCGTCC	TTATTCTAAT	CATTATTTTC	1080
TATCGTCCAT TAATGATTTC TACATT	CCAACGTTTA	GTAGAATGAG	TGGTCTAAAT	1140
ACGACGTTAT TACATTACTT TGTGAT	GTTG LTACTCTCAT	TAGNAACAGT	AGCAAGTALT	1200
CmAACGGTA				1209

(2) INFORMATION FOR SEQ ID NO: 744:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 675 base pairs

(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744:	
	CCGCCTTTCG TAAACCTAAT ATAATACGAA ATTTTCGTAT TGTCAACATT AAATACGTTT	60
10	TTTTCGTAAA AAACTTTACT ATGATATGAA AATTTCGTAT AATAAGAAAA AAGGAGGTAA	120
	GTAATATGAA CAAAGAMAGM AATATTATTA TAGCCAAAAM CATTAGAAAA TTTCTCAACG	180
	ATTCAAATAT GTCTCAAAAG AAACTTGCTG AaCTCATTAA CATAAAACCA TCTACTTTAA	240
15	GCGATTATTT AAATTTACGT TCCAACCCCT CTCACGGCGT TATACAAAGG ATAGCTGATG	300
	TTTTCGAGGT TGGTAAAAGC GACATAGATA CTACATACAA AGACGATAAC GACATCACTT	360
	CCATATACAA CAAACTCACA CCTCCCCGCC AAGAAAACGT ACTTAACTAT GCAAATGAAC	420
20	AATTGGAAGA ACAGAATTCT AAAGGAGATA ACGTTGTAGA TATTAATTCA TATAAACAGG	480
	AGAAAACTCC AGTTAACGTC AATGGTTGCG TCTCTGCTGG TGTAGGAGAA CGTTTACACG	540
05	ATGAAACGCT ATTTACTGAA ATGGTTAAAG GACCTATCCC CACACGCAT TTAGCGTTAA	600
25	AAGTAAATGG TGATTCTATG GrACCTATGT TTAAAGATGG CGAAATCATA TTTGTGGAGA	660
	AAACTCACAA TnTGA	675
30	(2) INFORMATION FOR SEQ ID NO: 745:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 924 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 745:	
	CAGGTGTCAT AGTTGAACTT GGtGGTTTTG GACTAATCGT TAAATCATCA ATTTGTGTCA	60
	TCCAAGGTTG GAATTTACTG CCTTGTGTCT CCAGTGCGCT GAAAATACCT TTATCTTGAA	120
45	ATAAGTCAAC TAACTCTTGG ATACCTTTAA TTAATGCTGG GTTACCACCA GAAATTGTAA	180
	CGTGGTTAAA TAAATCGCCA CCAATTCGTT TTAATTCATC ATAAATTTCT TCAGCGGTCA	240
	TGAGTTTTAT ATCGCCTTTA GCACTACCAT CCCAAGTAAA TGCAGAATCA CACCAGCTAC	300
50	AGGATAATCA CATCCAGCTG TTCTCACAAA CATCGTTTTT CTACCGATTA CTCGACCTTC	360
	ACCCTGAATG GTTGGACCGA ATATTTCGAG TACAGGAATT TTAGCCATTA GTTACACCTG	420
	TTCCTTTGGT CTAAATACGA CATAACTTGT TGGTGTTTCT CTTACAAATA CTTGAATACA	480

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	TACGATTTCA GTTGAAGGGA TTTTGTTTTT AAAAGCAGGT AAGTTATTTA ACAGTTGATG	600
c	GTCAAATTTA CCGTGTATCA TCTTTTTCAA ATGGCTAAAG TTCACTAAGA AGCCAGTGTC	660
•	ATCTAGTTTA TCACCGACAA TTGTTAAAya CAAAGTAAGT ATGACCATGG ACATTTTGAC	720
	AAATACCTGC TTCTTCACAT GGAATGTGAT GTGCAGCCGA AAAATTAAAA TCTTTATTTA	780
0	ATTCGAATTG ATATGGATGC GTTGTACTAG GATAGATTTG TTGTAACATT TTAAAGCGCT	840
	CCTTTACTTT CAAGATATTG ATTTAGTCCA CGTTGACGTA AATGACAAGC TGGACATTCA	900
	CCACAGCCAT CCCCAATGAT ACCG	924
5	(2) INFORMATION FOR SEQ ID NO: 746:	
eo	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 971 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 746:	
	ATCTTTTGGG TATTTTCTAT ATTAGCTGTT GTTTTCTTAG TATTATTTAG TTTTGCTGTT	60
	GGTGCATCAA ATGTACCAAT GATGATTTTA ACATTTATAT TACTCGTTGC AACCTTTGGA	120
30	ATTGGATTTA CTACAAAGAA AAAATATCGA GAAAACGATT GGCTATAAGT TATATCGACA	180
	ATAACACGCG TTGATTTAAG ACCACACATG TTCATGATGA ACATTTAACT GGTTTTATAT	240
	TGGCGCGTGT TTTTATTATT TAAGGTATAA AAGCGTAATA TGTTACCTAA TTGTTAGGAC	300
35	TACATATTAC GCTTTTGGTA ATTATTTTGA TTTTCTTTTA AATCGTTGTT CATGTAATTG	360
	TATTAACGCA TCATGGTGGG GCTCTAAaTA ATCATtGCTA ATTCTTGATG GAGACCmCGA	420
10	TTECCAACTA rGATKGAATT KGGACCMCTA ATKGTTAATG GTCcECCTAG TAAATTGGAA	480
10	GCTTGTCCAT TACTTCCATA TAAALAACCA ATCCGCCAGC AAALCCCCAT GGTKGAAGTC	540
	TTGGCGTCAT ATATGCTTCT AAaTTACCTG TAGCAACTGA AACGATTTCA AGCGCTGCAC	600

TACCATATGC CCTTGCACTT CTAGAATCAT TAACAATTTC TTTAAAGATT TCTCCTAAAA

TTGGTTTAGT TAACCAGTTC GGATTGATCC CAATAATGCT TTGTCTTAGA TTAGAATCAT

TCAATGGTTT CAAGGGTTGG CTACCACGAT ATGCACCTTC CCCTACTTTA GCATGATATA

AGACATCAGC CATAACATCA TATACAAAAC CTGCATAAGG TTTACCATCG ATATAAATAC

CAATTGAAAT TGCGAAATTT TCTTGTTGAT GAACAAAATT CAATGTACCG TCTATTGGGT

CAACAATCCA TACCGTACCT TTGGAAGTAT CGATGTCATG ACCATGCCCT TCTTCACCTA

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(2) INFORMATION FOR SEQ ID NO: 747:

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 865 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
o	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 747:	
	TTCTCGTCAC TGTACGTTGT ATTGCGGCAT CATCCATTAT GATACGTTCA GACATATTCT	60
5	CACCCTTTCA AAATTTAGAA ACAAAAAACC TCATGTCTTT AATATCGACA TGAGGTTTAG	120
•	TATATACAAT CAGCCTATTT ACATAGAAGA ATCGTAGTAT TACTACTTAT TCTTGCATAT	180
	GTGAAAGTGT TATGATCATT TTAGTATATA TCTATATTTT CATGTCTTTG ACGTCTCTCT	240
20	GGACGCTCAA TTAAAGACTC TTTATGTTGT ACTTAAACTG TTATAAGGAT AATACTAATC	300
•	AGGCGCTTTG TCAATCTATA TTGAAAAATT AACCATACTC AGTAAAAATG TTAACCTTAA	360
	TCTATTTTAT AATGTGTTTT CATTTAAAAA AAACGAAAAC GATAAACACT TATAGTTTAC	420
?5	ATAATAATGT TATCGTAATT ATAGCACGAC ACAATTATGC ATCTCTTTTT CGAATTGTAT	480
	CTAATAAATC TTCAAAGTCT TGTGGTAATT CAGCATGTCT TTCAATATAT TCACCTGTTA	540
	CTGGATGTTC GAATCCAATA AGTCCAGCAT GTAGAGCTTG ACCACCAATA TCCAATGTCT	600
3 <i>0</i>	TTTTCGGTCC ATACTTTGGA TCACCAACTA ATGGGAAGCC AATATATTTC ATGTGAACAC	660
	GGATTTGATG CGTACGTCCT GTTTCAAGTT GACATTCAAC AAGCGTATAA TCTTTAAAAT	720
	GTTCTAGTAC GTTAAAATGT GTCACTGCTT CCTTACCATC ATCANCAACA GCCATAGATT	780
35	GACGATCATT TTTGTTTCTA CCAATTGGCG CATCGATTGT ACCGTAATCA TGAGGAATAT	840
	TCCCGTGGAA CTAAAnCGAT ATAGT	865
40	(2) INFORMATION FOR SEQ ID NO: 748:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 818 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	·
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 748:	
50	ATAACATTGT GGAGCCTATG ACATTGATTT ATGTCTCGGT CTCAAATGTT CTTGTAAAAA	60
	AACTAAGTAT AGTTGAATTT TAAGTTAAAA AAATTGTTTT TGCAAAAATA AAATAATCCA	120

TTTTAGGTTC	TTCGCCTCTA	AAAATCCTTG	CGaTATTAGA	GCGATGTCTA	ATTATCAATA	240
TGATTGAAAC	TAAGAAACTA	ACGACTAATA	AAATATAGTC	TTGAATGATA	AGCGAGCCAA	300
TCACACAGCA	AATTGCTGCA	ACGATACTTG	CTAAAGAAAC	ATATTTAAAA	ATCTTCAATA	360
CAATAAAGAA	GATAATTGCA	AGTATTAGTA	AAAGTATCGG	ATTGACTCCC	AAGACGACAC	420
CTGCACTAGT	TGCAACAGCT	TTGCCACCTT	GGAATTTTAA	ATAAACAGGA	TAAACGTGTC	480
CAAGTATAGC	GAATAAGCCA	ACAATTAAAC	CATTTGTAAA	AAAAGTACTA	ATAGGGCCAT	540
CTGCGTGAAC	TTGTAACCAT	AAAGGGAAGA	AAACAGTTAT	GAACCCTTTG	AAAATATCTA	600
GAAATGTTAC	CAAGAATCCT	GCAGGACGAC	CTAATACTCT	AAAGCTATTA	GTAGCGCCAG	660
TATTACCACT	ACCAAATTGT	CTAATATCTT	TTTTGAAAAA	TAATTTTCCA	ATTACGAATC	720
CACTTGGGAA	AGCGCCGATA	AGATAACTTA	GTAGTAACAT	GACGATTATC	ATCATAAATA	780
TTACACATCC	TTTAATATCT	TAGGACTATT	TTATCATA			818
(2) INFORM	ATION FOR SE	EQ ID NO: 74	19:			

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 971 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 749:

AIAICCAAIA	ACTGTTCATT	GTCTTGATAT	TCCTTAAATG	TTTCATAATG	CTCATTAGAA	60
ATGACAATTT	CAAGCAACCA	ACCCGTGCCA	CTTTCCTCTT	TATTAATTAT	TACGCCATCT	120
TCTAATTCAT	ATTCTATAAT	TCTGCCGTGT	TCATTCACAA	TTTGAAACCT	TACTGCTTTA	180
AAAGTTTTCA	TATTCCCACA	TCCCATTAGT	TTAATATTTA	TGATTTTTGA	ATTATTTAGA	240
AGATTTAAGG	TCATTTCATG	ACTAATTTCT	TTAAATATAA	CAAATAACGA	GATGCTATAG	300
CTATTAATTA	TTTAAAATTT	GcCATTTTGa	CCATTTTTAA	GCTAGTAATT	AAGATATAGG	360
CATAGGAGGT	GAATCACACA	CTACATGCTA	AATAAAATCG	TAATTGTCGG	GAGCTGACGA	420
AAGACGCACA	AATATTTGAA	AAGGAGGATA	GAAAAATTGC	AACGTTTTGT	GTTGCAACGC	480
ACCGAAATTA	TAAAGATGAA	AATGGAGAAA	TCGTCTGTGA	TTACTTATTC	TGTAAAGCAT	540
TTGGCAAGTT	AGCTTCTAAT	ATAGAAAAAT	ATACTAATCA	AGGTACATTG	GTTGGTATAA	600
CTGGTCAAAT	GAGATCAAGA	AAGTATGATA	AAGACGGACA	AACACACTTT	GTCACTGAAT	660
TATATGTTGA	AACAATAAAA	TTTATGTCCC	CTAAATCCCA	AAATAATGAA	ATTCTCTCAG	720

TCCAATTATC CTAAACATCC TTAATATACA TTTAATCCAT CCTAAATTTT TTATAGATCT	840
AATTAACTTG AAATATACTC ACTTAAAAAC GACTTACATG ACCTAGTACT GTTGGTAAGG	900
TCGnCTTTG GTGTAGTTTT CCTAATAGAN AATAGACNTA GGTTGCCAAA CCGATTACAT	960
AAAAATTGC C	971
(2) INFORMATION FOR SEQ ID NO: 750:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 832 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 750:	
ATAGATTACT CTTTTGATCT GTAGATCCTA CTGTAACGAC ATTGTCCATA GATGCAGGAA	60
CATCTTTCAC TTCGCCATTA CCTTGATATT CACGCTGTAA TTTTAGTTTC TGTTTGTCAT	120
TGACATCAAT ACCATCATTA CCAGCTGCAG CAACAACGAT AGATTTTTTC TTCTTGGCGT	180
AATTGATTGC TTTCTGTAAC GCATCGTATT CTACTTTTTC ATCTTTTCTA AATGTTTGAT	240
GGTCATTTTT GTCCAAAATA ATATAACTAC CAACACTAAT ATTAATGACT TGaTTTCCAT	300
CATTTGCAGC TTGAACAATC GCTTTTGATA CCCAAAGCAG TTCTGTTTTT TTACTACCAA	360
ACACGCGATA CATTGTAAAT TTGTTATTCG GTGCAACACC TATTAACTTA CCATTAGCAC	420
TCGTTTGACC CGACACCATC GTGCCATGTC CTTTCCTATC ATTGACATCG TGAACATCAC	480
CTGTTTCCTC CGGTTCAGTA CCTCTAAAAC CGTTTAAAGG TACTAAATTT TTAGAATCAG	540
TCGAGAAATT ATTTTCAAA TCGTCATGGT TTTTCATCAC ACCTGTATCT ATGATTGCTA	600
TTTTGGTGTT AGCATGTTTT GGCAAATCAT CATACGATGC ACCATTATTG GTTATTTTAT	660
TCATATCCCA TTGTCTTGAA AATAATGACT CATTTGATGT TCTGTCTATT GTTTTCTCGC	720
TAGTAATACA AGTTGAACAT GTGGCATTGA TATATTTAAL ATCATTTTTA TAGTTTGCTA	780
AAGCATTAGC ATGCATTTTC GTCATTTTAA TCTGTGCCAC ATGGAATTCC GG	832
(2) INFORMATION FOR SEQ ID NO: 751:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 475 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

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GTAATATCAA	TCTCTTCATA	AGCTGAATTA	TTTTCATGCA	CTTCTTGATG	TGATGATTTG	60
TCACGAACCG	CTACAACTAA	CATTTTATCG	TCTAAAATAA	GTTGTTTATA	TTTTTCTAAT	120
TCATCAGGCG	CTAAGTTGTA	GCGTGATAAA	ACTGCATGTT	CACCATCTTC	TCCTGTTAAC	180
AGTTTAGTCA	TTCTATCACT	AAATGTTCCA	CTTGTTGAGA	TAAGGGAGAT	TTCAGAGTCG	240
TGTAAGTCAT	TTAGGTGTAA	TTTACTTTTA	CTAATAATTG	TTAGCTCTGA	TTCTAAATAA	300
CCTTCAGATT	TCTTTTGATT	GATTACGTTG	TATAATTCGC	CAGTGTCATT	TACTACAGTA	360
ATATCTGCCA	TAGTTGTCGC	CCCTTTAAAA	ATTTGTTTAT	tTAATCTTTT	ACCCTTCTTA	420
TnATAAAGTA	AAACCCTTAC	ATTATTAAGT	nATAAGTCTT	CATTCGCATT	AAACG	475
(2) INFORM	ATION FOR SI	EQ ID NO: 79	52:			

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1019 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 752:

GCGACACTTG	TGAGTTCTCC	AGCAGCAAAC	GCGTTATCTT	CAAAGGCTAT	GGACAATCAT	60
CCACAACAAA	CGCAGTCAAG	CAAACAGCAA	ACACCTAAGA	TTCAAAAAGG	CGGTAACCTT	120
AAACCATTAG	AACAACGTGA	ACACGCAAAT	GTTATATTAC	CAAATAACGA	TCGTCACCAA	180
ATCACAGATA	CAACGAATGG	TYATTATGCA	CCCGTAACTT	ATATTCAAGT	TGAAGCACCT	240
ACTGGTACAT	TTATTGCTTC	CGGTGTAGTT	GTAGGTAAAG	ATACTCTTTT	AACAAATAAA	300
CACGTCGTAG	ATGCTACGCA	CGGTGATCCT	CATGCTTTAÁ	AAGCATTCCC	TTCTGCAATT	360
AACCAAGACA	ATTATCCAAA	TGGTGGTTTC	ACTGCTGAAC	AAATCACTAA	ATATTCAGGC	420
GAAGGTGATT	TAGCAATAGT	TAAATTCTCC	CCTAATGAGC	AAAACAAACA	TATTGGTGAA	480
GTAGTTAAAC	CAGCAACAAT	GAGTAATAAT	GCTGAAACAC	AAGTTAACCA	AAATATTACT	540
GTAACAGGAT	ATCCTGGTGA	TAAACCTGTA	GCAACAATGT	GGGAAAGTAA	AGGAAAAATC	600
ACTTACCTCA	AAGGCGAACT	ATGCAATATG	ATTTAAGTAC	AACTGGTGGT	AATTCAGGTT	660
CACCTGTATT	TAATGAAAAA	AATGAAGTGA	TCGGaATTCA	TTGGGGCGGT	GTACCAAATG	720
AATTTaATGG	TGCGGTATTT	ATTAATGAAA	ATGTACGCAA	CTICTTAAAA	CAAAATATTG	780
AAGATATCCA	TTTTGCCAAC	GATGACCAAC	CTAATAACCC	AGATAATCCT	GATAACCCTA	840
ACAATCCTGA	TAACCCTAAC	AACCCAGATG	AACCAAATAA	CCCnGACAAC	CCTAACAACC	900

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CAATTAAGTT CGTCTAGATA AAATAGGAAG CAAAGTCTTA GCAACGTAAA ATATTTTGA 1019

	(2) INFORMATION FOR SEQ ID NO: 753:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 533 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 753:	
15	ATTCTTATCC CAGGTAGGTG NTTTACTTCT TATATTAGGT GCAATAACTC ATGCCACTCA	60
	TCTTGTGGCA CAACATGAAT CGCATTTTCA AAAATTGCAT GTCCTGCTTG ATCAGTCAAA	120
	CCGGCAGCAT GATCAAAATG CATATGTGTC ATTAGCACAT AATCAATATC CTTTGGCGTT	180
20	AAATTATAAT TTGCCAAATC AGCAATTATA TGACTTTCTT CATCTACTCC AAAATTACGT	240
	AATTGCTTTT CAGATAATTT ACCATTACCA ATACCTGCAT CTATAATCAA ATTATATTGA	300
	GCCGTTTGAA TCAAAATTGG ATGTGTCGGT AAATTGATTT GATTTCGTTC ATTTGCATTG	360
25	TATTGCTTTG ACCACAACGG CTTCGGAACA ACACCAAACA TTGCACCGCC ATCCATTTTT	420
	GTATTGCCAC CATTTAGATA ATGAATAGAT ATATCCCCGA TTTTCATAAC ATCACCTATT	480
	CTTTCTGTAT TCGTTATTAC AATTAGCATG TGTTTATTAC ATCATATCAC TAT	533
30	(2) INFORMATION FOR SEQ ID NO: 754:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1225 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 754:	
	ATCCCCTGCA AGTGATAAAA TTATTGAAAA AGGCGACATG ATTACATTAG ATTTTGGCGC	60
	GTATTATAAC GGCTATTGTT CAGATATTAC TAGAACATTT GCTATTGGAG AACCAGATCC	120
45	TAAACTGAAA GANATATATC ANATAGTACT TGAATCTCAA ATGAAAGCAA TTAATGAGAt	189
	TAGACCTGGC ATGACTGGTG CAGAAGCTGA TGCCATTTCA AGAAACTATL TAGAGTCAAA	24
	AGGGTATGGA AAAGAATTTG GACATTCACT AGGACATGGT ATTGGTTTAG AAATCCATGA	30
50	AGGGCCAATG CTGGCTCGTA CGATACAAGA TAAACTTCAA GTTAACAACT GTGTTACAGT	36
	AGAACCTGGT GTTTATATAG AAGGTTTGGG CGGTATAAGA ATAGAAGATG ATATTTTAAT	42
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AGCGTGTAAA	ATGAGGAGGA	AACTGAATGA	TTTCGGTTAA	TGATTTTAAA	ACAGGTTTAA	540
CAATTTCTGT	TGATAACGCT	ATTTGGAAAG	TTATAGACTT	CCAACATGTA	AAGCCTGGTA	600
AAGGTTCAGC	ATTCGTTCGT	TCAAAATTAC	GTAATTTAAG	AACTGGTGCA	ATTCAAGAGA	660
AAACGTTTAG	AGCTGGTGAA	AAAGTTGAAC	CAGCAATGAT	TGaAAATCGT	CGCATGCAAT	720
ATTTATATGC	TGACGGAGAT	AATCATGTAT	TTATGGATAA	TGAAAGCTTT	GAACAAACAG	780
AACTTTCAAG	TGATTACTTA	AAAGAAGAAT	TGAATTACTT	AAAAGAAGGT	ATGGAAGTAC	840
AAATTCAAAC	ATACGAAGGT	GaAACTATCG	GTGTTGAATT	ACCTAAAACT	GTTGAATTAA	900
CAGTAACTGA	AACAGAACCT	GGTATTAAAG	GTGATACTGC	AACTGGTGCC	ACTaAATCGG	960
CAACTGTTGA	AACTGGTTAT	ACATTAAATG	TACCTTTATT	TGTAAACGAA	GGTGACGTTT	1020
TAATTATCAA	CACTGGTGAT	GGAAGCTACA	TTTCAAGAGG	ATAATCTCTA	ATTTGTTAAC	1080
AAATAGCTTG	TATTCACTAT	ACTGATTTAA	CGTAAGAnAT	TCTAAATAAG	TCTCATAAAG	1140
CTATTGCCTA	AAATGATTAT	AGGTTATATG	CTGATATGAG	GCTTTTTATT	AATAAAATTT	1200
TTTTTAAAAT	ATAAAACGAA	TCGTC				1225
(2) INFORMA	עדוראן ברסף פב	O ID NO. 75	· • ·			

INFORMATION FOR SEQ ID NO: 755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 755:

ACAAACAAAT CACTTAGTTA AAATTGACAG TGCATTATAT TCCGATAAAT TATTCAACAT 60 TGTAGAAAnn AGAATTGATA CACCAGATAT TGGCTATAAT ACAGTGGTTT TATCAGAAAA 120 ATGAGTGTAG AAATTAAAGG GATACCTGAN GTGTTGAATA AATTAGAATC GGTATACGGT 180 AAACAAGCAA TGCAGGCTAA GAGTGATAAA GCTTTAAATG AAGCATCTGA ATTTTTTATA 240 AAGGCTTTAA AGAAAGAGTT CGAGAGCTTT AAAGATACGG GTGCCAGTAT AGAAGAAATG 300 ACTAAATCTA AGCCTTATAC AAAAGTTGGT AGTCAAGAAA GGGCTGTTTT AATTGAATGG 360 GTAGGTCCTA TGAATCGCAA AAACATTATT CACTTGAATG AACATGGTTA TACAAGAGAT 420 GGAAAAAAT ATACACCAAG AGGTTTTGGA GTTATTGCAA AAACATTAGC TGCTAGCGAA 480 CGTAAGTATA GAGAAATTAT AAAAAAGGAG TTGGCCAGAT AAATGAATAT ATTAAACACC 540 ATAAAAGGAA TTTTATTATC TGATGCAGAG CTCAAAACAC ATATAAATTC TAGAATATAC 600

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	TATGATTTGC	CTTCAGACTT	TATGTCTGAT	AAATATCTCA	GTGAAGAATA	CTTAATTCAA	720
	ATAGATGTAG	AATCTTCAAA	TAATCAGAAA	ACAATTGATA	TAACAAAACG	AATAAGATAC	780
	CTGTTATATC	AACAAAATTT	AATTCAAGCA	TCTAGTCAGT	TAGATGCTTA	TTTTGAAGAA	840
	ACTAAACGTT	ATGTGATGTC	GAGACGATAT	CAAGGCATAC	CCAAAAATAT	AAATATTATA	900
	AATCAGCGCA	TCGAATAGGT	GTGCTTTTTA	ATTTTTAAGG	AGGAAATAAG	CAATGGCAGA	960
	AGGACAAGGT	TCTTATAAAG	TAGGTTTTAA	AAGATTATAC	GTTGGAGTTT	TTAACCCAGA	1020
	AGCAACAAAA	GTAGTTAAAC	GCATGACATG	GGAAGATGAA	AAAGGTGGTA	CAGTTGACCT	1080
	AAATATCACA	GGTTTAGCAC	CAGATTTAGT	AGATATGTTT	GCATCTAACA	AACGTGTATG	1140
	GATGAAAAA	CAAGGTACTA	ATGAAaGTTA	AGTCcTGaCA	TGaGTaTTTT	CaATATTCCa	1200
	AGTGaTGaTT	TAAaCACaGT	TaTTGGaCGT	ACTAAAGATA	AAAATGGGTA	CATCTTGGGT	1260
-	AGGAG						1265

(2) INFORMATION FOR SEQ ID NO: 756:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1111 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 756:

CATATACCCG GGTTCCAAGA ATCCTCTATC CATATGGTCC CCCAATTTTG ATTCCACCAT 60 ATTGTTAAAT ATCACTTTCC CAGCCTACTT TTTTATnCAG TTGGGCTCTC TAAAATTGTT 120 TTGAAATCCA GGTTGAACAT ATTTCCAGTG TATGACCAAT CGAAACATTT GCACCAATAA 180 GGCCGCCAAT TTTTCCTGTA TCATCACCAG TAACATTACC GTTGAATCCA TAAGTTAAAG 240 TACTCATATA CTCTTTTGTA TCAATCGAAT TTCTTGGATA GTAATCAGAT ATTTGAGCTA 300 CTTCATTATC AGGTAGTTGC AACTGTACCT TAAAGGCTGA AGGCCAGGCT AAACCACTTT 360 TGTTAGCACC TTCTTCGCTA TAAACTCTAT ATTGACCAGC AATGGTACCT TTCGTTCTAA 420 TAACTAGCAG TTTTTTATTA TGATTTTTAT CATCGATAAA ACTATAAAAT ACTTTTTTGT 480 GCATGCCATT TTCTTTATCA TAAGTGACTA AATCACCTGT TTTTACTGTA GTATTGCTTC 540 CAATATCTGT AGTACCGGTT TTAATATTAA TATCAGAATC TGCGGCATTA GCGACAGGAT 600 TCATTAATAT GGAACCTAGC AATAGTGTTG TTGTTACTGA GCTGACTATA CGTGTTTTCA 660 TTTTCATCAT CCTTCTATTT TTTAAAACGA TTTGAGGAAA CAATAATCAA TATGTCAATT 720

	GTAGCAACTG ATAAATTACT GAGTGATGAT GAGTGATTAT TTTAAGAATA TGTTTTTAAC	840
	TTTTATTTAA AATTTGAAAG GAAGCATTTC AATTTCGAGG GTTAGTCAAA GTTGAATAAA	900
5	TTCTTTATGA AACAAGGAAA AGACATAGCT AATTTLATTG ATTAATTTCT TTAAAACTAA	960
	TGATTTGTTT GATTTAAAAA TGTAATCGAT TACAATATAA AAATACAAAT ATCTTAGAAT	1020
	TAAATCAATT AATTAACTAT TAAATAAAAA TTAACTATAT ATTAACTAGT GTAAATTAAT	1080
10	AAATAGAAAT AGAGAAAAAG GGTATTAATT A	1111
	(2) INFORMATION FOR SEQ ID NO: 757:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 466 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 757:	
	TATCTATTGT ATGTAACAAT AGGTACATAA TATTTTTAGG GTGGGTTATA TGAGCATAAT	60
25	TACAAGATTG TTTAATAACA GTGATTTTGA AAAATTAAAT CAACTATGTA AATTATATGA	120
	TGATCTAGGT TATCCAACAA ATGAGAATGA TTTAAAAAAG AGACTAAAGA AAATAACGAA	180
30	TCATGATGAT TACTTCCTAC TGCTTTTGAT AAAAGAAAAT AAAATAATTG GTTTAAGTGG	240
50	TATGTGTAAA ATGATGTTTT ACGAAAWAAA TGCAGAGTAT ATGAGAATCC TTGCGTTTGT	300
	TATACATTCT GAATTTAGGA AAAAAGGTTA TGGAAAGAGA TTATTAGCTG ATTCTGAAGA	360
35	ATTTTCTAAA CGGTTGAATT GTAAAGCMAT AACACTAAAT AGTGGTAATA GAGATGANAG	420
	ACATCTGCAC ATAAACTATA TAGTGATAnT GGGTATGTTA GCAATA	466
	(2) INFORMATION FOR SEQ ID NO: 758:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 402 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758:	
	CGTACAGCAT AACCAAATAC ATATCTGCCA AAATCGCCAT ATGCCCCAGT TCCTCTTCCA	60
50	TATTCCGTTG TCATTGAGTT TTTAATTTTA TCGATAGAAA AATGTAAATG GCTATCTAAT	120
	TTGTTTTTTA AAGATTTTAT GTAATCECTA TATTTAAATT CGAATATTCT TTTTTATACC	180

	AACTAATATA TWCAATTGTA TGCCTAGCAT AATCTCTCAT TAAAATATGA GGATATACCA	300
	TTTCTTTATC AAATATETCT TCATAAATAT AATTAGCAAT CTCTATATGT ATTECACAAA	360
5	TGTCGATTCG AAGTGTCGCC CCTAAAACAG YAGCATATAA TC	402
	(2) INFORMATION FOR SEQ ID NO: 759:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 338 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759:	
	AAGTTACTCA ACAGCCATTT GACACGTCTC GATTAGAGCG ATTAGGTATA ACCGAGCGCC	60
20	AAACTAAAGA CATGTATCGT TTATTAGGAC TAGCCAAATA TGAAGATCGA TTTGTTATTC	120
	CAACATCACA CAAAGAAACC TATTTAGATA CGTATCACGC ACAAGGTAGT ACAGGATACA	180
	ATTACGGCGG CGAGCATTTT GGAGATAACT GTGAAGGCTG TGGCGTTGCA GTAGGTTCAG	240
25	GGAAAACTGG TCAAGAAATT TATAATGGAG AATTCTATGG AGGGATTTCC GTGGTTAATT	300
	TCGATAATTT AAAAAATATC CAAGAAAGTT TGGGTnnn	338
	(2) INFORMATION FOR SEQ ID NO: 760:	
<i>30</i>	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 399 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760:	
40	CTCTATTATA TITAGAGTTA TAGCTATTGC AGTTGTTTAT TTATTGAAAA TAAATGTACT	60
	ATCATTAGET TTAGCAAGTG TATTAGGCAG TTTGGTATCE AGGCTACTAT TATCTATTAT	120
	TITAAATTTA CCTGTGTGGG TAGTGTTGTT AAACGCGATT CCAGGCGTAA TATTCACTTT	180
45	AATTGTAGCT ATTCCTTTAT ATCTCACATT GAGAAAAAGA ATGGCAGTAT TACTAAGATA	240
	ATAAATCAAA ACACGGTCGT CACAATTACT GTTGGCGACC GTGTTTTACT AGCTATTTAT	300
	TGTTTTCAGT TTCTTTTGTA TCTAACAATT TCACTTTGTG ATTTTCCCAA TCAATTTCAT	360
50	ATGTTGATTT AAATGTTCTA GTTTTAAAGT TTTTATAAT	399
	(2) INFORMATION FOR SEQ ID NO: 761:	

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5	(A) LENGTH: 639 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 761:	
10	GCATATnCAA AACAATAGCT GCTTTAGGTG CGGGGGCTAT TAGCGTTATT TCTGCACTAA	60
	CAGGAGGTTT AGTTGGCGCA GGTGTTGGTG GTTTCCTTGG ATCTATAGCT GCATCGAATA	120
	TTGATACTAG TAAGGGAATA TATATAAAAT TAAAAACTAA AAAGTATGCA GCCGGGGAAT	180
15	ACGTTCTGAC AGGAGAAAAA TGGGGATATC AGTAAGGGTG ATTTTATGGA TAGATTAAAA	240
	TATTCACTTA AAGTTGGAAT TTTAGCATTA TTATTATTTT GTACTTTAAA TTATTTAGTT	300
	CCAATGCAAA GCAATGCTTT TTCAATAATT ATATATTCGG CAATTTTTGC TGTGTTACTT	360
20	ATGCTTTTAG TTTATATATT TTTAGGAATT TTAAAGAAAT GACATGAAAC AAATTAGCAT	420
	TGGCTATGAA GAAATCTATG GGGATAGAAT TTTTCATAGC CATTTTTTAA AAGAGCATGA	480
25	AGTAAAAAT TGGAAAACCG TCAATCAAAT AATTGAAAAA GAACACTTGG ACAAAAATGA	540
	ATATGNAAGC GGAACCGCCG TTATTTTCT TTTGCAGGAT CGTTAGATTA GATTNCGGTT	600
	GTATAGTATA ATGAAAAATA TTATAATAAA TTTATAAAA	639
30	(2) INFORMATION FOR SEQ ID NO: 762:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 852 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 762:	
	nTGTTCGTTG TCTGGATCCA ACGTAAACAG TCGCTTCATC TAATACAATG ATAGGCGCAT	60
	CTTTTAATAT CATTCTTGCA ATAGTGACTC GTTGTTTTTC ACCACCAGAC AATTTATCTC	120
45	CCACTGTACC AACATTCGTA TCATATCCAT CTGGCAACTT TTCAATAAAT TCATGACATT	180
	GTGCTAACTT GGCAGCTTTT TCAACTGCCT CATCCGTAGC TTCTGGATTG CCAAGTTTAA	240
	TATTTTCTTT AAAAGTAAGA TTTAATAAAA AGTTATCTTG TCCAACAAAA CCAACTAAAT	300
50	CGTTAAGTTG TTTCGATTCA ATATCTTTTA TATTTATACC GCCAATCGTA ATTTCACCTG	360
	AAGTCACATC CCAGTATCGT GATATAAGCT TGGCAATGGT TGACTTACCG CTACCAGATG	420
	CCCCGACGAT AGCTGTGAAA TTATTTTCTG GTACTGTAAA TGATAAATGC TTAAAGACCA	480
<i>55</i>		

	•	
	GAGGCTTCTT AAATTTTGTT GACAATACTA ACTCTTCTAG ACTTAATATT TGATTCACTT	600
	CAGTTAATGC GTATTGTATA GACTTTAAAT GATTTACATA ATTAGTAAAA TTCTTAATCG	660
5	GTGCTACTAC ACCTAAAGAT AATACGATGC ATAGGAAAAA TTCCGCATAG TTTAATTGGT	720
	TGATAGATAT CAAATACATG CCGACCGGTA AAATCCCTAA AAATGTTGAA GGTAATACAC	780
	TAGCTCCTAA ATTCATATAC CCCCATGTAT TTTTAAACCA ATTCAAAGTG TGAATCTTAT	840
10	AATTATCTAC TG	852
	(2) INFORMATION FOR SEQ ID NO: 763:	•
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 852 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
20 .		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 763:	
	CTCTTCATGC GTCATACGTT GTGTCGATTG ATCAGTTGTT TTGTCTAAAT CACTAGCTTT	60
25	AAATTTAGAT TGATTTGATT GACGTGTCGT AAATnGTTGT TCCTTTTGTT GGCGTTTGCC	120
	TTTTTTTCTT GATCTTATTA AAAATAAATT GATAACCCCA ACAATAATGA GCGCTAAAAT	180
30	AATGTAGCTA ATAATGAAGG TCGTAGTCAT TTAATGACCC CCTTAATTTT TATGGATTTT	240
	TACTTCAGCG TTCaTTCCaG GAACAACTTG TTTAGACGGT TCTGATTCTA GAGTGATTTT	300
	AACAGGTATT ACTTGAGAAA CTTTAGTGTA GTTACCATCA CTATTTGATG ATGGCATTAA	360
35	TGAAAAgtTG CAGCAGTTGC TTTTCCAATA CTATCAACTT TACCTTTAAT AGAAGCTTTT	420
	TGACCGTCAA TAGTCACATC AACATCTTTA CCTACTTCAA CATCTTTAAT ATCTTTTTCG	480
40	TCAATATTTG CTGTTACATA TAAATCATCT AAATTGTATG CATAAGCGAT TGGGTTACCA	540
40	GCTTGCACCA TTGAACCTTC CATACCATCT AATTTGGCAA TTGTACCTTT TTGAGGCATT	600
	TTAAGATCCA TATCTTTCGT TTCGCCATCT TGACCTTGTA CAGTAACAAT TGCTACTTTG	660
45	TCACCTTTAT CGAGTTTGTC ACCTTGTTTA ACATTAAGTG ATTTAATTTG TCCAGATGCA	720
	GGACTTGCTA TTTTAATTTG ATCGCCATTT ACTTTTGCAT TATCAGTTGT TACATAGCTT	780
	GTTGTTTTAT TCCAAAAATA AAAGCCAGCA ATCCCAATGG CTAACnGTAC AACAACCGTA	84
50	ATGACATTNA AT	85
	(A) TUROPUS MICH BOR CEO ID NO. 264	

(2) INFORMATION FOR SEQ ID NO: 764:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	(xi) SEQUENCE DESCRIPTION: SEO ID NO: 764:	
	ACATATTCGA CATTCATTTT AAATTGCATA TAACTACATT AACCATTCAT TGTGCAGCGC	60
10	CTGTTGTTTA GATGATCATT TATTGACTTT TTGCTCTTAT nCCAngCaAT TTTTTGATTT	120
10	ATTGCTTATA ATACATTTTA AGACAAATGT TTGTTTCAAC ATCGCATGCG ACATCATTAA	
		180
15	YTATTCATTT AAATTTATCC AGTTTCTATT TGTCTGCAAT TGCTGAAAAT TAAAGGAGCT	240
	TATTTTTAAT AATGGAACAA ATTATCACTG AATTTATTAG CCGTTTTGGG TATGCAGCCA	300
	TTTTTATATT AATTTKATKA GAAAATGTAC TACCTATCGT aCCATCGGGA AATTATTCTG	360
20	ACATTTGCTG GTCTTATGTC TGTTAAATCA CATTTATCAA TTTTAACTTT ATTTATTATT	420
	GCAACTATCG CATCGTTTAT AGGGCTGTTA ATTTTATATT ATATCTGCCG TTTGATTTCA	480
	GAAGAACGTC TATATCGTTT TATTGATCGA CACGGTAAGT GGATTAAATT GAAAAGTAAG	540
25	GATTTAAAGC GAGCAAATGA TTGGTTTAAA AAGTATGGCG TATGGGCTGT ATTKATCTGT	600
	CGTTTCATAC CTGTATTACG TGTALTGATT ACCATTCCAG CTGGTGKaAA CCGCATGAAT	660
	GTTGTGACAT TEACCGTTAT TTCATTAATA GGTACTACAA TCTGGAATTT CGGTTTAATT	720
30	TTACTAGGAC GCACTTTGAG CGATAGC	747
	(2) INFORMATION FOR SEQ ID NO: 765:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 820 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 765:	
	TTTACCTTTT AACCAATCAT GCATTAATGC AATGTGTACT GTCTTAACAA ATGTTGCATA	60
45	TECATCTTCT GCACTCCACT TTTTCAATTC CTGTTGATTA ATGGCATGTT TTTCTCCATT	120
	TTCCAACATA TTGACATACA ATTTATAATG TTTTTCAACT GCCTGAATAA AAGCGAGTTG	180
	ATTITIATIT AAATGIGATI TTAACTITIC TAAATCIGAA TTAATAAAGT CTTCTATAGT	240
50	CGAATAAGAC ATATCTTGGT ATTCAACTAC TGCATTAATT TCATCTAATA ATTGCGATTG	300
	TGATTTTAGC GTTATATAAC TCTCGTCTCC ATAAGATATT TCTGTAGTAG CTGCTGTAGT	360

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AGGATTTGGA GAACTGACTA AAATATGCTC GCCTAATAAT GCATTTATCa AACTACTTTT

	
TGTTTCGTGG ATATCTTGCT TTGTACGCTT GAACAAAGGC ACATCCGAAA TTATATCAAG	540
CGCTTTTTGA ATATCTATAG ACATATTTGT TGTAGCTGTA TTTTGATTTA GCTGCTGATT	600
ATCACGATTA TCCTGAGCAT TATCAGTAGC CACTTGATAT GTTGTCTCTT GTCGACCTAT	660
TAATTTATCT AGAGATTCAT CTAAATGAAT ATAGTAGTGA CGATAATTCT TAGTCGTCAA	720
TGACTGACGC AGCTCATTTA ATTCTGTATA ACGTTGATAT TCTTTTAAAT CATCACTTTC	780
TTCTGTTGGn AATTCATCTG CCTGCACATT TTCTATnATT	820
(2) INFORMATION FOR SEQ ID NO: 766:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 672 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 766:	
TCAACATGAC ATTAATTTAA TAGCGATGCA TACAAATTTA GATGTAAATC CGTATGGTGT	60
CAATATGATG TTGGCGAAGG CGATGGGTTT GAAGAACATT TCAATAATAA ATAATCAACA	120
AGATGTATAC TATAAAGTTC AAACATATAT ACCTAAGGAT AATGTTGGAC CATTTAAAGA	180
TAAGCTTAGT GAAAATGGAT TAGCGCAAGA AGGTAATTAT GAATATTGTT TCTTTGAAAG	240
TGAAGGAAGA GGGCAATTCA AACCAGTTGG TGAAGCTAAT CCAACAATAG GACAAATTGA	300
TAAAATTGAA TATGTAGATG AAGTTAAAAT TGAATTTATG ATAGATGCAT ATCAAAAGTC	360
AAGGGCTGAG CAATTAATTA AACAATACCA TCCATATGAA ACACCGGTAT TTGATTTAT	420
TGAGATAAAA CAAACATCCC TTTATGGACT TGGCGTTATG GCAGAAGTGG ATAATCAAAT	480
GACATTGGAA GATTTCGCAG CTGATATTAA ATCTAAATTA AATATCCCAA GTGTCCGTTT	540
TGTTGGTGAK TCTAATCAGA AAATTAAACG TATTGCAATT ATTGGTGGTT CAGGTATTGG	600
ATATGAAKAT CAAGCLGTCC AACAAGGCGC AGATGTCTGT TACGGTGATA TTAAACATCA	660
GATGCCTAGA TG	672
(2) INFORMATION FOR SEQ ID NO: 767:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 403 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	GAAAAAGTTA AACCTACTGT AACTACAACA AGCMAAGTTG AAGACMATCA CTCTACTAAA	60
_	GTTGTmAGTA CTGaCACAAC AAAAGATCAA ACTAAAACAC AAACTGCTCA TACAGTTAAA	120
5	ACAGCACAAA CTGCTCAAGA ACAAAATAAA GTTCAAACAC CTGTTAAAGA TGTTGCAACA	180
	GCGAAATCTG AAAGCAACAA TCAAGCTGTA AGTGATAATA AATCACAACA AACTAACAAA	240
10	GTTACAAAAC ATAACGAAAC GCCTAAACAA GCATCTAAAG CTAAAGAATT ACCAAAAACT	300
	GGTTTAACTT CAGTTGATAA CTTTATTAGC ACAGTLGCCT TCGCAACACT TGCCCTTTTA	360
	GGTTCATTAT CTTTATTACT TTTCAAAAGg AAGaaTCTAA ATA	403
15	(2) INFORMATION FOR SEQ ID NO: 768:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 483 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768:	
23	TTCAATGCTC GTTTTGCTTG CGTTAGTAAT TTCTAACATA TTCATTCACA TTTTGGAGCC	60
	TAAACTATCA ATCACCACTC AAATCATCAT CGTTTTGATT TTAATTGAAG CACTAATTGG	120
30	ACTGCGTTTC TTGAAAGCGT ACGATGTTAA GCGTGGCAAA GATAAAGAAA ATAAGAAAAA	180
	TAGTAAGGAT TTCGTTAAAC TAAAATCAAT TTTAGTAGCA ATTTTATTTA CATCATTGGC	240
	GCTGACAGCA GGTACTGTAG CTGATATATA CGGTTTCACT GACTTAGGAA ATACTAGAAG	300
35	TGATTTAATC GTTTGGAGCA TAGGTGGTAT TATATTTGGC CTCGTATGTT ACACAATGGA	360
	AGATAAAAGA TAACGATAAG GAGCTGGCGA TTATAAAGCT AGCTCCTTTT TTAACTTaTA	420
	TATGTAAAGA aCTATCCTAA GGGKTTTTAA TCATATGTCA ATAATTTCTA TAATACATTA	480
40	TTA ()	483
	(2) INFÖRMATION FOR SEQ ID NO: 769:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769:	
55	ATTATATGTC TGATGTATTT CATGTCGTTA AAAATAAAGG TACGGAAGAT TTTAAAGAAG	60
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	GGATGATGCT TGAAGGTGAA AAAATCAAAG CTTTTTATGA AGATATGCCA CCGTATCAGA	180
	CTGTCAAAAA AGGAACGATA CAAATTAAGC GTGATGGCAC ACCTATTATC CTATTAAATG	240
5	TCATTATACG CTmGTAGCTA CCCGCAAATC GGTACAATCG CAGTTATCAT TTACGAATTA	300
	GCACAAAACC GCAGGATCAC GTTGAATTCC ATTATAGTAT TTACGGCTGA AGACTGTAAG	360
10	nTANACTGGT AACCATATCA TGGATGATTG ATCATAGATG	400
	(2) INFORMATION FOR SEQ ID NO: 770:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 750 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770:	
	ATCTCTTCTA CTTCTTTTAC AAATTGAGAA CGTCTTAAAA TGGCTTTCAC ACGGGCAACA	60
	ACTTCTCTAG GTKAAAAAGG CTTAGTCATA TAGTCATCGG CACCTAATTC TAAACCTAAT	120
25	ACCCGATCAA ATTCATCATT TTTCGCCGTT AACATTAATA TAGGGACTAA ATTTTTATTT	180
	GTTCTTACAG TCTTACATAC GTCAATGCCA TCTTTTTTAG GTAGCATAAC ATCTAAAATA	240
30	ATTAAATCTG GCTGTTCACT TTCTACCTTT TCTAAAGCCT CATCACCATC AAATGCGACA	300
	ACAACTTCAT AACCAGCTGK TTCtArGyTA TATTTAAGTA ATGGTTACGA TTGAATGtTC	360
	GTCATCTACT WCCaACACTT TTTGCGACAT GGLATGCCTC CCTAACLLAK AATTATATTT	420
35	CATTATAACC GAACTATTTA TAAAAATAMC ATCCTACACA TTATCTTTAC ACATTTTTTA	480
	CATTACTTTA CATATAAATA AAATACTTCT TATATTTCCT TCTmTCATTT GCATGACTTA	540
	CTCTGGGACA ACGAAATAAA TTTTGTAAAA ATAGCATTTC TATCCCACTA CCTATGCATG	600
40	AGTITTACTC ATTTATTCCT AAGCTTATGT ACATATTCGC TTTGTCTAAT GTGTAAGAAA	660
	CACTACATAA TCAATCATTG GTGACTCTTT ATTATTTCTA TCCTGTTGCC AACTTCAATT	720
45	CATTTAAAAA GGCGAACCTA GCAATTAAAG	750
45	(2) INFORMATION FOR SEQ ID NO: 771:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1462 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

	ATTTAATTAT	TATTTTTCCA	AATCAATACG	ATATAATTTT	ATGTTTTTAT	CTTTTGGTGC	60
_	TGaGGCAAAT	TGATAAGt CG	TTTTGCCTTT	TTCAATATAT	CCAAAATTAC	CAGCAACTTT	120
5	GCTATATTCC	GTATGTGTTA	CTGCTTTGCC	AACATAATTT	TTAACAGCTT	GATATGTTGG	180
	ACCATTAGCA	TCATTATACA	TCATTGAAAT	ATGAGTTACT	TTACCATTGT	TTTTCTTACC	240
10	ATCAGTAGTT	ACTAATAACA	TACCTTTTTT	AGTATGGAAT	TCGTAATAAT	GTTCAGTTCC	300
	ATCTTCATTG	TAAGAATACA	TCGGATTTTT	GTACTTAGTT	AAAACATCTT	TAATAGATTC	360
	GCCAATTTTC	ACATTTTCTA	ATGACTGATC	ACCCTTAATT	AATTGTTTAA	CAGTATCAAT	420
15	AGAGTTGCCA	CTTGCTGCTT	CGGCACTAGT	GTTCACTAAG	CCTACTCCCA	TTACAACAGA	480
	ACATGCAATT	ATACTTGCCG	TTAGTAGCTT	TTTCATAAGC	ACTCTCTCCT	TTTATTTATA	540
	TCGTCTTGTG	CTCACAACCA	TTATACAACA	ATCATTTCTA	AAACAACAGT	CATATTACAA	600
20	TTATATTACA	AATAATAATT	ACTACTTTTA	TATTTCACTT	ATCACTAAAA	ATTAAACATG	660
	CTTTTCATCG	TGATGTTTGT	TGATAAATGC	AGCTGTATCT	TCGACGAATC	TTTCTTGCTC	720
25	TTCAACAAAT	GGGAATGCAC	TTGATTCTTG	ATATACTTCA	AAGTCCGCAT	TTTGGATTAA	780
23	ATCAGCTACT	TCTTTAGCTT	CTAATCTTGT	TGTTCTTTCA	CCGAATTCTC	CTGCAATAAT	840
	TTTTGTCGGT	ACTACGACAT	TTCTATAAGT	TTGAGAAATA	TCAGCGTTTT	TGAATACCTC	900
30	TTTAACTGCT	TGAATTTCTT	CTTTAGTTGA	TATTTCATTT	GTATCTACGA	CATGTTTGAG	960
	GAATCGATTC	ATTTTTCTCG	GACGATAATA	CTTACGCTTA	TTTAAAAATT	TAWCYTGtTT	1020
	TTCaGGATCC	CaGTTtCGAA	TAATATGGGC	ATATTTTCTA	AATAAACGTT	CTTCCGGTAA	1080
35	TTCACCTTCA	ATAGATGTTG	GATTTACCAA	CGTAAGTGAT	GATGTAAATT	CAGGATAACG	1140
	TACTGAAATA	TCCGCACCAA	TGATTCCACC	CATTKCATGG	CATACAAATG	CAACTTCTTC	1200
	AAATATATAA	TATTTAAGTA	ATTCAACAAT	GTCATCAGAA	AAATCTTTTA	TTTCAATGTG	1260
40	ACGAGGTTTA	TCAGAATAGC	CATGTCCACG	TAAATCAATT	AACACAACTT	GAAATGATTT	1320
	TGCTAATTCT	GCTGCTAATT	TATTAAACAC	AGAATAATTA	TCAAGTACAG	TATGAATCAA	1380
45	TACGATAGGA	TAGCCTTCAC	CTAAnGTACT	GTAATGTATC	GATGTTCCAT	CTTTTCTAGT	1440
	AAATAGATCC	ATAATTTTCT	CC				1462

(2) INFORMATION FOR SEQ ID NO: 772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 772:	
	ATTATTATAA GGAGTTATCT TACATGTTAA ATCTTGAAAA CAAAACATAT GTCATCATGG	60
5	GAATCGCTAA TAAGCGTAGT ATTGCTTTTG GTGTCGCTAA AGTTTTAGAT CAATTmGGTG	120
	CTAAATTAGT ATTTACTTAC CGTAAAGAAC GTAGCCGTAA AGAGCTTGAA AAATTATTAG	180
10	AACAATTAAA TCAACCAGAA GCGCACTTAT ATCAAATTGA TGTTCAAAGC GATGAAGAGG	240
	TTATTAATGG TTTTGAGCAA ATTGGTAAAG ATGTTGGCAA TATTGATGGT GTATATCATT	300
	CAATCGCATT TGCTAATATG GAAGACTTAC GCGGACGCTT TTCTGAAACT TCACGTGAAG	360
15	GCTTCTTGTT AGCTCAAGAC ATTAGTTCTT ACTCATTAAC AATTGTGGCT CATGAAGCTA	420
	AAAAATTAAT GCCAGAAGGT GGTAGCATTG TTGCAACAAC ATATTTAGGT GGCGAATTCG	480
	CAGTTCAAAA CTATAATGTG ATGGGTGTTG CTAAAGCGAG CTTAGAAGCA AATGTTAAAT	540
20	ATTTAGCATT AGACTTAGGT CCAGATAATA TTCGCGTTAA TGCAATTTCA GCTAGTCCAA	600
	TCCGTACATT AAGTGCAAAA GGTGTGGGTG GTTTCAATAC AATTCTTAAA AGAAATCGAA	660
0.5	GAGCGTGCAC CTTTTAAAAC CGTAATGTTG ATCCAGTAGA AGTA	704
25	(2) INFORMATION FOR SEQ ID NO: 773:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 427 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 773:	
	GACCACGACA CCACAAGCTA TGAAGAATGC CYTTGTTAAG CCGCCTTTGA ATtGCATAGA	60
	GATGAAAATA CCAATATTAA TAAAGAAGTT ACAGAAAATA CCTTTTGTAA AAATATTCAA	120
40	CCATGTTGAA TCAACAGTCT TTTTCTGAAC TAAAGCTGTT AAAGCTTGTG TCATTTCAGG	180
	TGTCATGACA TGCGCAAATT TCATTAAGAA AAATAACACA AACCCACCTA AAATATTTCC	240
45	TAAGAAACAA TATAATAAAA TCCAAGTCAT CTTCTTAACA GAAACGACTT TATAATACCA	300
	GCCTACTGTA AAGTACATGA AGTTACTTGT TAATAATTCA GAGTTAGTTA ATACAACTAA	360
	AATCAAACCT AAACTAAACG CAATGGCTCC CATTAAATTG ATAAGTCCAT CTACGTGAGT	420
50	ACTCGCA	42
	(2) INFORMATION FOR SEQ ID NO: 774:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs	

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	(vi) SEQUENCE DECORTORION ORG. TO MA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 774:	
	AGGTGAGCAT TATTAAATAT TGCCAAGAAA TCAAAACTAA AAACTATGCA AAAGATGTAG	60
10	ATATATTATT TATTCTTGGC GGTGATGGCA CGGTTAACGA ACTTATAAAC GGTGTTATGA	120
	CACATGACCT TCAACTCCCT ATTGGCATTT TACCAGGCGG TACTTTTAAT GATTTTACAA	180
	AAACGCTAAA TATAGCACCT GAATCATAAA CAAGCTAGTG AACAAATGGA TTTCTGCACA	240
15	AGTTGGTACA TACGATGTAA TTGAAAATGA AATGAATCAA TATGCACTCA ACTTTGTGGG	300
	CTTAGGTCTC ATGTTCAAAA CGCGGAAAAC GTACAAGAGG TTCAAAAGAT GTATTGGGTA	360
	AATGGAGTTA TATTGGGTCC ACCGTCCAAA ACnCGGCnAA	400
20	(2) INFORMATION FOR SEQ ID NO: 775:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 484 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 775:	
	AATTATTCCT CAATAGGAGC ATTACCCGCT CTCTCACCAA TTCCCAAAAA TGTAGTTTCT	60
	ATTTGCTTTG CACCATTTAA AATTGCAGCT AATGTATTTG CAGTAGCCAA CCCTAGATCG	120
35	TTATGACAAT GAGCAGAAAA AATTATGTTA GAATATTTTT TTACAAAGTA ATTAAAAATA	180
	TCTCCGTATT CTAATGGTGT CGAACATCCT ACAGTGTCCG CAAATGTAAC TGTTCTAACT	240
	TGATATTTTG AAATAATTTC CATGTATTCT TTCAATTTTT CTCTAGAAGT CCTTGTTCCA	300
40	TCTTCAAAAC AAATATCTAC TCCTTTTTA TCTTTCTT	360
	ATTTTCTGAA TATAATATTT ATTTGAAAAA TTAAGCTTTT CTTTTATATG CAAGTCAGAT	420
	ATTGGCAATA GTATTTTTAC CACTAAATTA TGAATTTTCA ATTTGACTAT TTTTGGTATG	480
45	TCnT	484
	(2) INFORMATION FOR SEQ ID NO: 776:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 788 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
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	(X1) SEQUENCE DESCRIPTION: SEQ 1D NO: 776:							
	CGCAAGATGA AGTTAAAGAA CTTAATCGCT TATTAGGTAA AGTCATTCAT GCATTTGATG	60						
5	AAACAAAGGA AAAATAATTA ACTTTTGTCA TGACAATTAA AGTAATGTTT AGAATTTATT	120						
	AAGAATAGAA AAACAATTAG CACGCGTAAC TTGTTAGTnA AAAAACTGCT TGAAAGGTTT	180						
	CTTAGCCTAT CAAGCAGTTT TTTTATGCAT TATATTGAAT CATATTCCAT AAAGCACCTT	240						
10	GATTAGCTAG TAATTGTTGA TAGTTTCCCT TTTCAACTAT TTTACCATTT ATCATCACAA	300						
	TGATGGTCTC AAAACGTGAC AATAAAGTTA AATCGTGTGT AGCAACAATT AATGTTTCTG	360						
15	CATGTGCTTC AATTAAATCC ATAACTTTTA AACTATTTTG TTTATCTAAT GCAGTTGTTG	420						
	GTTCATCTAA AATCCATGTT GATGCAGTAT CTTTTAATAA CATCCTCGTA ATCGCTAAAC	480						
	GCTGAATTTC TCCGCCAGAT AATGTATGAC CATCTAAGTC AATTTGACGT tCTAGTGCCA	540						
20	AATGTTCTAA ATCTAATTGC TTAAATATTG CTTGCACCGC TTCATCTTTT TCATCGGTAA	600						
	ATAAATTTTG ACGTATTGTA CCATCAAATA ATTGTTGAGA TTGTAGCAAG ACATTTAACG	660						
	ATTCAAACTT ATCTTTGTCA TCTATTTCAA ACATATCCAT ATTTTCGAAA CGAACAGAGC	720						
25	CACTATCTAA TTGATATAAC CCTGCCATAA TTTGTAGTAA TGTACTTTTT CCTGAACCAG	780						
	AAGGACCC	788						
	(2) INFORMATION FOR SEQ ID NO: 777:							
30	(i) SEQUENCE CHARACTERISTICS:							
	(A) LENGTH: 1145 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double							
35	(D) TOPOLOGY: linear							
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 777:							
40	TTACAAAAGA AATGCAACAA AATTTTTGAA TCATTACATT TTTTTATAAA AATTTCACTT	60						
	TAGATTCACA ATAATTACTT ATTITGTCAA TTTATTTAAT GTCAATATGT TGATTAATTA	120						
	ATAGTGTTGT CTAATGTATA TAATATTTAG GTCATCGTTA TAGTCAACAA TAATAAGGTA	180						
45	TTTCGAGTTG AAATTTATCT TATTATTTTT CCACTTTTAC GTGCTATCCC ATTACACAAA	240						
	AACAAATAAG TAAAGATATT AAGTACAAAA AAGTGGAACA CCTTGTAGAT GCTCCACCTC	300						
	AATTATATA AGTTATATTA TTTTGCTGCT TGGTATAATT CATCAACTTT TTTCCAGTTA	360						
50	ACAATGTTCC AAAATGCAGT CATATAGTCT GGACGTTTAT TTTGATATTT CAGATAGTAG	420						
	GCATGCTCCC AAACATCAAA TAGTAAGATT GGTGTTTTGC CTTCTGTTAA TGGATTATCT	480						

	GATCCAAATA	ATGTTGTTGC	TTTATTTGCA	AATTCATTTT	TAAATTCATC	TAAAGTGCCC	600
	CACTGCGcTT	TGATGTCATC	TATTACGCCA	CCTTTTTCTT	CAGAATTAGG	.TGATAGTATT	660
5	TCCCAGAATA	ATGAATGGTT	AAAATGACCA	CCGCCATTAT	TACGGACTGA	CATCCTCATC	720
	GCTTCCGGTA	CCTTGTCTAA	GTnAGCAATC	ATATCCGCTA	GTGATTGATG	CTCTAACTCT	780
	GTTCCTTCAA	CTGTTGCGTT	TAATTTCGTC	ACGTACGTAT	TGTGATGTTT	GTCGTGATGA	840
10	AACTCCATTG	TTCTTTGATC	TATATATGGT	TCCAATGCAT	CATATGCATA	TGGTAAATTT	900
	GGTAATTTAA	ATGCCATAAG	TATATTCCTC	CTTTTATGAA	TATACTTTTA	TAATAATTAA	960
15	TTTTGGGTGT	GTTTTGCAAT	TTATTATTAA	TATTTGTTAT	ATCCAATTAT	ATAAAATTTA	1020
	AATATTCGAA	ATTGATATAA	TATTTAATAT	TGAATGCAAA	AAGGCATTTA	ACTGCTTTTG	1080
	TTTCCCGCTT	TTAAAGAGAA	TTAAAAAAGA	CAACTTCCAT	TTTTCAATAA	GAAATTGCCT	1140
20	TTTCT						1145

(2) INFORMATION FOR SEQ ID NO: 778:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 902 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 778:

60	CTCCACTTAC	CCTTTTTCTT	CGGAAGATTC	AATATACGGC	CAATATTATC	AAAAGAGGnC
120	ATTATCTTCA	GCATTAAATA	GGTGCTATCC	GTTATCaATT	AATGGTGTAT	TAAGCCCATC
180	TTTATTGAAT	CTTTACCATA	CCAATAATGT	CGCTTTTTCT	CAAAGCTATT	ATTGTGGTAT
240	CATTCTTATA	CTACAATTGC	AACAAGGTTA	AAATGGAATT	AAATCAACAT	GCACCTACTA
300	TCTAAATGGA	TACCTTCTTW	AAAGCTTTAA	TCGCCAATTT	TATAAGAAGG	AATTGTGGTA
360	ATCTATAAAG	TTAAACTTAT	AATATAATTG	TAGCTCTGCA	AGCGATATGA	GTTTCTATAA
420	AATTACTGCA	GTACGAAACT	TAGTAACTAT	TCCGTCTACA	CAGGTATCTG	TACACATATA
480	TGGATTTGAA	ATACTAACAC	TTCCCGATAA	ATAAGACCTT	AATATAAACT	AAATGCCATA
540	TAACGTTAAT	СААТААТААА	ACGACACTAG	AGATGGATGA	CLATCCATGT	AATATCTTCG
600	AATAATGAAA	TCTCATCATT	ATCCAATTCG	ACCATCATAT	AATAGAAACC	ATGGATATTA
660	ATATTTTACA	TATCAATAAC	CTACCTATGC	AAATGATAAA	TAAGTACTAT	AATAATAA
720	AATAACACCC	AAAAAGCTAA	GGTGGCCATA	CAATTTAAAC	GATCATTTT	ACTTTAGGTG

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	ATACTATAGA TAAACATCAT TAACCCTAAA GAAATTATTG ATACTCCCCA AAAAATAAAT	840
	CCTATTTTGT ATCGCTTTTT AATTGTTAAC AATAATGTAA CCAAAATAAC TGGGAAAAAT	900
5	AT	902
	(2) INFORMATION FOR SEQ ID NO: 779:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 779:	
	GGAATTAGTT TCCTAATGAT CAAACCATAA CCATTAGCTT TTAATGATGT TACGCCTTTA	60
20	AAGATTAGAG GATGATGACT AATAATAGTA TTATAACCTT TTTCGATTGC TTCATTTACT	120
	ACTTCCAACG TACAGTCTAA TGCTGTTAAA AGACCAGTAA CTTCAACATC TTCATCACCT	180
	ATTAACAATC CTACATTATC CCAAGATTCA GCAGTACTAA ATGGCACATG ATGATCTAAC	240
25	AATGTCATTA AATCAGCTAT TTTCATaCTA TAACACCCTT TCAATTACaG CAATTTCGTC	300
	aTTAATTTGa GCTAAACGTT GAKGAKGTTG TTCAGTAWTG AGtTTCGATT TAAtATGATA	360
	AAGTGCYTCL AACTCLCTTT GCCATTTLTT TATAAAATAT	400
30	(2) INFORMATION FOR SEQ ID NO: 780:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 557 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 780:	
	GTTCCTGTTT TAACATCAAT ATCTATCTTT TTAATATCTT GAACATAAAG CAGATTCAGT	60
	TGGCTAATAT TTGAATTTAT GTTAATCACT TTTTTCGTTC CATTTTTAAA ATGTACTGTG	120
45	TAAGInGCIT TITTIGCATA TITTAATICA CGITCCCCGA TACCTCTATC ATGCTTCAAT	180
	ACTGATTTAA CTTTTTTAGA GATATCTTTG TAGCCTACAC GTGGGTCACC TGTAAATTTT	240
	AAATCTGaTA AAATTGGTGT TGATGTGCCA TTTACTGCAA TTGTGTATGG TACATATCTG	300
50	TCTGCTTTCG CTTTAGTTCC TGTTTTAACA GTAATTTCAA TTCTCTTAAC ATCTTTCGCA	360
	TGAACTAAGT TTGCTGTGTA ATTTTTTGAA TTCAACTGTA AGATTCTTTT ACCACCATTT	420

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	CTATCATGCT TCAGTACTGA TTTTATTTGA CTAGTTAAAT TTTTGTAATT TGTCCAAGGT	540					
	TTATNTGAAA ATGAAAG	557					
5	(2) INFORMATION FOR SEQ ID NO: 781:						
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 475 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 						
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 781:						
	TTCTGATAAC ACAACTTTCT TGGACCAAGT GACAATGGTA AAGTTGATAT TCTCAAAAAA	60					
	TATATTTAT TGAAAAGGTA ACTATATCGA CCGCTCTGTG CGACTTGCTG TGTAGAAACA	120					
20	TCAAGCCCAG CTTGAAACTT CATATAAACT AATAACTTTT GATAAATGCT ATTCCCAATT	180					
	TGTTCATACT GCTCCAAGTT ATCATTAATT CTAAATTTAA TACTTACTTC ATTTTTAACT	240					
	GGAATAAAAT GTACATCACT CGCTTTCATT TCTATCGCTT TATTAATTAT TTCTTGAAAT	300					
25	AGAATCTTCA AAAAAACACC TCCTACATAT AATCACGTAG GAGGTGTTTT TATTACTTCA	360					
	ATTTAACCGT GTAAAAATGG ATTTAATTGT TCATCATCAA CCGTCGTATA TGGACCATGT	420					
30	CCAGGGAATA AAGGTAAATC GCCTTCTAAT TCAAATATTT TATCTTGAAT AGAAT	475					
	(2) INFORMATION FOR SEQ ID NO: 782:						
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 						
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 782:						
	ATGAATATCG GTGCAGGACG TATCGTTTAT CAAAGTTTAA CTCGAATCAA TAAATCAATT	60					
	GAAGACGGTG ATTTCTTTGA AAATGATGTT TTAAATAATG CAATTGCACA CGTGAATTCA	120					
45	CATGATTCAG CGTTACACAT CTTTGGTTTA TTGTCTGACG GTGGTGTACA CAGTCATTAC	180					
	AAACATTTAT TTGCTTTGTT AGAACTTGCT AAAAAACAAG GNGTTGAAAA AGTTTACGTA	240					
	CACGCATTTT TAGATGGCCG TGACGTAGAT CAAAAATCCG CTTTGAAATA CATCGAAGAG	300					
50	ACTGAAGCTA AATCCATGAA TNAGGGCATN GGCCATTTGC ACCGGGGCCT GGCCGTAATA	360					
	AGCCAAngga CCGGGCCAAC CGTTGGGACC GGGAAGAAAA	400					

(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 810 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear							
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 783:							
10	GATTAATGTA CTCGTGTACA TAACGTTTGA AGTATGATAA ATAGATATAG AAATAAAGTC	60						
	ATATGTGACA TCAATTAAAT GATGTTCAAA TGACAAGATA CAATAGAGGA ATGTTTGTAA	120						
15	TANAAACGCT TCATATAAAG GTCGAGTCAA TATATGATAC GACTTTATAT GAAGCGTTTT	180						
	ATTTGCTATG AGCTAGTATA TTTTATAATA ATTTTTCTAT TTCTCTTTCG ATTTGAACAG	240						
	GTTTTTTTG AGGTGCAAAT CGTTTAACAA CGTTACCYTC GCGATCCACT AAAAACTTAG	300						
20	TGAAATTCCA TTTGATTTTC TCATTAAAGA ATCCGTGTTG TGCCGCAGTC AAATATCTAA	360						
	ATAAAGGTAA TTGATGTTCC CCTTTTACGT CTATTTTTTG ATGCATAGGG AAGGTAACAC	420						
	CATAGTITAA TITACAGTIT TGAGCTGCTT CTTCGCCTGA ACCAGGTTCT TGGCCACCAA	480						
25	ATTGATTACA AGGGAAACCT AGAATTACAA ACCCTTGATC TTTGTATTTC TCGTATAATG	540						
	ATTGCAAACC TTCAAATTGT GAAGTAAAGC CACATTCGCT AGCTGTATTA ACAATTAGCA	600						
30	TAACGTCACC CTTATATGCA TCTAATTTGT AAGTAACACC TTTATTTGTT TCTACTACAA	660						
	AATCATAAAT TGTCTCCATT GTATCATCCT TTCGATTTAC TTAAAATGTA CCACAAAATC	720						
	GTGTAALAGT CTKTACTALA ACTCTATGAT AGAATACTTT GAGTAGGATT TTATTAAGGA	780						
3 5	GATGTATAAC ATGGnTCAGC AACAAATTCA	810						
	(2) INFORMATION FOR SEQ ID NO: 784:							
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 788 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 							
45								
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 784:							
	AAATTCATTG CAGAAAACAT AGATAAATAA ACAAATTGAC TTTAAACGAG CGTTGCAACA	6						
50	TATCTCGAAT TGTAAAGGAG CTTGAAAATG AATAAAAATA TAGTCATTAA AAGCATGGCA	12						
	GCATTAGCCA TTCTAACCTC AGTAACTGGA ATAAATGCTG CAGTCGTTGA AGAGACACAA	18						
	CAAATAGCAA ATGCAGAGAA GAATGTTACG CAAGTTAAAG ATACAAATAT TTTTCCATAT	24						
<i>55</i>								

ACCAATAAAC	ATGTATCAAA	AGATTATAAA	GTTGGCGATA	GAATTACTGC	CCATCCAAAC	360
GGTGACAAAG	GAAATGGTGG	TATATATAA	ATTAAAAGCA	TTTCTGATTA	TCCGGGTGAT	420
GAAGACATCT	CTGTCATGAA	TATTGAAGAA	CAAGCAGTCG	AACGTGGACC	AAAAGGCTTT	480
AATTTTAATG	AAAATGTCCA	AGCATTCAAT	TTTGCGAAAG	ATGCTAAAGT	TGATGACAAA	540
ATTAAAGTTA	TTGGTTACCC	ATTACCTGCT	CAAAATAGTT	TTAAACAGTT	TGAATCTACA	600
GGAACTATAA	AAAGAATSAA	AGACAATATT	TTAAATTTTG	GATGCCATAC	ATTGGAACCC	660
GGGGAATTCA	GGGATCACCA	GTTCTAAATT	CTAACAATGA	GGTCATAGGT	GTGGTGGTAT	720
GGGCGGGTAT	TGGGAAAAAT	TGGGTTCTGG	AATAATAATG	GGTGGCCGTA	TACTTTACGC	780
CTCCAnAT						788

(2) INFORMATION FOR SEQ ID NO: 785:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1023 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 785:

CAATATTTTA	GAAACAaTAA	TTAACTTGCG	ATGAACAAAC	TATTAACAAT	AATCTTGAGT	60
ATTATATTA	TCTTAATTAA	TAATATATT	ATTTAAGATT	ATGTTACTTC	CAACTTTCAA	120
AGTAGAAAAA	CGGTATAATT	TGTTGATGGG	TGTTTATTGA	TAAACTGCAA	AAAATACAGC	180
CTACAACCAC	ATAGATTGTA	GACTATATTT	AAAATAATAG	GTATTTATCA	TATCTCGTAA	240
ACTTAGTGCC	AATTTTTATA	CTCGTGGTGC	TGGTAAGCTA	CCCTTAAATT	CAGGAACGTA	300
GTGTGTaGGG	CTATAACTTG	GAACAGCATA	TTGATAATTT	ACATTTTTGA	TATTTAATGA	360
TGGTTTCCCA	ATTTTATAAC	CATTTGATTG	TGAAAATGAG	AAATAKTTCT	TCACACCTTT	420
AACTACTTTA	TAAGAATAGA	AGTATTTATÀ	GTCATATGCT	TTATTTACTT	TAGCATTTTG	480
ATGTGTTGCT	GTTGTGTTAT	TTTGGAAACT	TGGTACATGC	ATACGATGTG	AATTGTGACC	540
ATATGGTGGA	ATTACCTTGA	AACTATTTAT	TTGTGGCACA	ACACAAAAGT	GATTAATTTT	600
AATGCTAGCA	TGCCCTGGTG	TAACAAATTT	ATGCGCGTGA	TATCCAGGAA	CTGCAAAATG	660
ATGCTTGATA	ATTAAAGATT	gAGATGGATG	TGTATATCTA	GGCGATTCTG	ATGGTTTAAC	720
AATAAAGTGT	TTATTAATAG	AATCCTTTGC	ATGATTTACA	TGTTTATGTA	CATGTGTTGA	780
TTTGTATGAA	GTAATAACTT	TCTTGTAGTG	GGTTTGCGTA	GTAATGAAGT	GGTGGTTTAC	041

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	TTGTTGTGAA GCTGGATTGT TTGTTGCTAC ATTCACGCGA TTATTGATTT CTTTGTACTC	960
	TGGCACAATG TTTCCTAACT TTGATTCTGG NACGACAAAG TTTTTATCTA CAATTTTACT	1020
5	AGC.	1023
	(2) INFORMATION FOR SEQ ID NO: 786:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 487 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 786:	
	TCAAGTTTAT TCGCTTGTTG GAAAGCTTTA ACTTGATTTT CTAAAGCTTT ATCAAATTGC	60
20	GTTGATTCAT TATCAACTTT ATAACCTAAA GCTGATAAAC CAATTTTAAT AGTTTTAATA	120
	TTTTTATCAT CGTCTCCAAC TTTAAATGTT TTCGTATTAG GAATGACATT TAAAGATTGA	180
	TATTTAGGTG TGTCAATAGT AACGTCTGGT TTAATGCCTT TACCGTGAAT ATAATGACCA	240
25	TCTGGCGTTA ACCATTTCAT TTCAGTATAT TTTAACAATG AACCATCCTT AAACTCTCTT	300
	GTAGTTTGTA CGACACCTTT GCCGAATGTT TTTGACCCAT AAACTTTAGC TTTATTATAG	360
30	TCTTTTAGCG CACCAGTAAA CACTTCAGAA GCGCTAGCTG AACCTTCATT CACTAAGATG	420
	GATATATCCA TGTCTTTCGC TTCTTTTAAC GCATCATTAG AAGTEGAATT GCTCAGTACT	480
	TTACCTT	487
35	(2) INFORMATION FOR SEQ ID NO: 787:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 803 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	•	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 787:	
,,,	GNAAACNATA TTTANAATTA AGTGTTCGAT TTGCAGTAAA TTCATACAGA AAAGCTAAAA	60
	TTAAAATGAT ACAGTGGAAT AATGTCACAT TCTCCATAAA TAATTGACCG AAGAAGCATA	120
50	AAACATAGAA TAGTACAGTA ACACTTACCG GCTGCTTTTC TTTATATATA ATTGCATTAA	180
	TACAATAATA AATAATAAAG AGTGAAATTA GTGTTGATGT CGCATAATTA TAAAATCCTG	240
	CARACCACCC ATTATCTATCT CORTANATAC CACTTCCTAN ARTTACATT ARAGRARATG	300

	TGCCCATACT AATGAGGCCA TATGAAAGCC AACGTAACCA GCTTACATGT ACAGCTATAA	420
	TTTCAAAGAT ATTTCCGATA TAGCGACCAT TAAGTGATGC AAATCCTACT TTTAAAATAT	480
5	CAGTATTATA ATTGCTAAAC CATTGTAAAT CATCGTGCAT GAGTGGTAGT AAGATACCCA	540
	TAAAAGTATA AAACAATAAT ATCGCAATTA ATATCAAAGT TGTCTTGTGT AATTGAATTG	600
10	TTTTCACTTT GCTAATCCTC AAATCTAGTT AAATTTTCCT CAACTTGTAG GTCGAAAAAT	660
10	TAATTCAATA TTTTTAATGT ATTTCTAATT TTCACCTATG CATGTTTCCT CAATCAAATT	720
	AGATAAACAA GGTATTTAAT ATTACTTTCA ACAATTTATC TAAATCGCCC CTCGTCTTTT	780
15	TCTATGaCGA ATGATTACAC TTG	803
	(2) INFORMATION FOR SEQ ID NO: 788:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 788:	
	GAAAAGTTGT ATTATGAATA AAGTTAATCA AGGTGCTCAG GAAGAGGCAA TGGAAGAGTT	60
30	ATTAGTGACT TTTCAAAAAT TGATTAAAGA CTAAAGGAGT TTAAGATGAT ACATCAAAAT	120
	ACGATTTACA CAGCGGGAAT TGAAACAGAA GAACAAGTAA GTCAATTGAC AGAACGCATT	180
	TCAAATATGA TAGGTGTTCA TCAAGTGAAT ATTAATATAA TAGATGGTCA AGTAACTGTA	240
35	TCGTATGAGA CACCAGCAAA TTTGAATAGT ATTGAAAAAG AAATCTATGA TGAAGGATAC	300
	AAAATTGTAT TTTAGGGTAT AATGTAGAGT GCGCTATAGA TTTTAATTTT GAAAATAAAT	360
	TAAAAATTTT GTAAATGATG TAGTAAAGGT ATGTCGAATA	400
40	(2) INFORMATION FOR SEQ ID NO: 789:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 762 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 789:	
	GTTTAAAGAT GGAGAGATTA TTGATTTTTC AGCTGGAAAA GGTGAAGCGG TATTGAAAGA	60
	TTTAATCAAT ACTGATGAAG GTTCAAGAAG ATTAGGTGAA GTAGCATTAG TACCTGATGA	120

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	ATGTCATTTA GCGATTGGAT CTGCTTACGC CTTTAATATT CAAGGTGGAA CGGAAATGAC	240
	TGTTGAGGAA AAGATTGCAA GCGGATTAAA TGATTCAAAT GTACATGTCG ATTTCATGAT	300
5	TGGTAGTAGT GATTTGACTA TTTATGGCAT ATTCGAAGAT GGTTCAAAAG AACTAGTATT	360
	TGAAAATGGA AATTGGGCAT CAACATTTTA ATAAATGTTA TTTTGAGGTG CTGAGTAGGA	420
10	AATGAAACAT GTATTTAAAG GTCAAATACG TGATTAAAGT ATAGATTGGG AGATAAAATA	480
,,	ATGACAAATC AGGACAGACC AATGAAATCT ATGTCAGAAT CAAAATGTTA TAAAAATAGA	540
	CAAGTTTTCC CTCAAGATAC GAATCACCAT CATACAATGT TTGGTGGTAC ATTGATGGCT	600
15	AATATTGATG AAATTGCAGC AATCACAGCT ATGAAACATG CTGGTGCGCA AGTAGTTACC	660
	GCATCTACAG ACTCAGTAGA TTTCTTAAAG CCGATTAAAA CAGGGGACAT ATTACAATAC	720
	GTAGCGATGG TTTCATACGC TGGGACTAGT TCAATGGAAG TG	762
20	(2) INFORMATION FOR SEQ ID NO: 790:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 790:	
	TTTAATTTTA TCTTTTGGAT ATCACATAGA TGCTACTTTT CTATACTGTT CTAAATCTAT	60
	TATTICGICA CATIGATITG CAATAGCCAT ATCATGTGTT GCTAAAATCA GCACTITATI	120
35	TTCATCGACC AAACCAAATA ATGATTGAAT AATCATCTGT CCTGTTTTAG GATCTAACGC	180
	ACCCGTTGGT TCATCAGCTA ACATAACAAT CGGATCTTTT AACATCATTC TAATTAAAGC	240
40	GACACGTTGT TGTTCACCTC CACTTAGCGT ATGAACTTTT CTTTTTAAAC TGTTTGACAG	300
40	ACCAAACTGT TCLATATAAC GLATCTLLAT TTGTnCTTTT TCTTTCTTAC TTATTTTTTT	360
	ATATGCTAAT CCAATATCTA AATTTTCATT TACTGnCAAA	400
45	(2) INFORMATION FOR SEQ ID NO: 791:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 791:	

	AACGTAAAGC GGAAGTTGGG ATGGTTGAAG ATGCTGAATT TCATGCGCAA CTACATCGTT	120
	ATAATGCTTT TCTAGAGCAA CATCAAGATG ATAAAGTGTT GTATTTMGAA ATTGGAATTG	180
5	GTTATACTAC ACCACAATTT GTGAAGCATC CTTTTCAGCG TTGACACGTA AAAATGAAAA	240
	TGCCCTTTAT ATGACGATGA ATAAAAAGGC TTCGCATTCC GAATTCAATT CAGGACGTAC	300
10	CATACTTTAA CTGAGATTCT CAACTTGTTC AGCAGACTCC GGACGCAGCA CACGAAATAC	360
,,,	ACATGGGGGC AGAGTNACTT ATGGACCGTT GAATGNGATA	400
	(2) INFORMATION FOR SEQ ID NO: 792:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 678 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
?0		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 792:	
_	GTTCCGTTTG ATACAGAGAA GCGAATGTAA GCATAATCTT TAACAGTATC GTATGATALA	60
?5	ALTTAATTGG CAACTTTTTG TCACCTTCAT AAACTTCAAA TTTTCTCCAA AATTGACCTG	120
	ATTGTAATCC TAATTCAATT TCTGGTTTTG AATCAGTGAA AATAACTCTA GCAGGTTTAA	180
30	CAGAACTTGC ATAATGATAA AACTGTTGAG TTCCATCTTT CTTTTTCATT TCAAAATCAA	240
	TTGGACGAGA GTTTGGTGCG CTATGATCTT TGTCTTTTAT TGCAGGGTTT TTAATCGCTT	300
	CTCTAAGTTC CTGaTTCAAA ATAGGATATG TATTGTTAGT GGCYTTTGCT GCTGGTTTAA	360
15	CTTCTTTTGT TTCCTTAGGG GCTTTAACTT CTTTAACTTC TTTAGCTTCT TTTGTTTCAG	420
	AAGTAGGGGC CTCAACTTCT TTATTAGATA CTGAGACAGC ATTAGCTACT GGTTTAGTTT	480
0	CTGGAGCTTT TTCAGATGTT GTTGTTGGAC TTGCAACTGC TTCAGTTTTT GGTTGTGCTT	540
.U	CTGTATTTGT ACCACCTGTT TCTTCAGCTG CTGCTTGTGT TCGCCATTTG ACATTAATAA	600
	TAAAAGTGTA CTAATTGCTA CAGATGCAAC GCCTAGTGAT GACTTTCTAA TTGAATAAAA	660
5	TGATTTAAAT TCTTTTTG	678
	(2) INFORMATION FOR SEQ ID NO: 793:	
o	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 351 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

ACTGGCGGAT CCACGATGGC ATGTGTTAGT GAAGCAATTC ATTTATTACC ATATAATGTA	60
TTCTTCGTAC CAGCCAGAGG TGGACTAGGC GAAANTGTTG TCTTTCAGGC AAACACAATT	120
GCAGCCAGTA TGGCACAACA AGCTGGCGGT TATTATACGA CGATGTATGT ACCTGGATAA	180
TGTCAGTGAA ACAACATATA ATACATTGTT GTTANGAGCC ATCAGTCATT AAACACTTTA	240
GGACAAAATT AAACCAAGCA AACGTTAATA TTACACGGGC CTTTGGTGAT GCGCTGGAAG	300
ATMGGCGCCT CGGACGTCCA ATCACCTGGA AAAGGTCCTT GGAACCACTT C	351
(2) INFORMATION FOR SEQ ID NO: 794:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 794:	
GGGCGAGGCG TTCGCGCACC GGCCGAGCAG CAAATAGGCC GGGATGTCGC GTCTTGCTGC	60
AGGTCCGAAA AATATCAACT TGAAGAGGTA ACACCGnTAG ATATGTTTCC ACAAACAACA	120
CATGTTGAGA CAGTGGCATT ATTCAATTTG AAATAGCGCA CATGATTTGA GATAAAATTT	180
CGCCTTAATA AGTGAAGAAA GAAGTCGTAT ATTAAAATTT TATTACAGCC AATTTACTTT	240
CTTGATATGA ACTTTTTAAA TTAAATGTGA CATTGTATAC TATATTTAAA GAAGAATAAG	300
AATGTCATGA TCGGGAGGGT TGGTAATGCA TAAAATTGAT TTAACGACAA ATAATTTTCA	360
AATGCGAGGT TTATTATCCT GGCAACCTGG TTATTGCGTT	400
(2) INFORMATION FOR SEQ ID NO: 795:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 407 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 795:	
ATGTTCCAGG AACGTATTTT TACAACCGAC AATTAGCATA TGTCATAATG AGTTTTATAA	60
TTGTATTTTT TATTGCATTT TTAATGAATG TTAAATTACT GAGTAATATT AAAGTGCAAA	120
AAGGTATGAT TATAACTATC GTCTCACTAT TATTACTGAC GTTAGTAATA GGTAAAGATA	180
TTAATGGTTC TAAAAGTTGG ATAAACTTAG GATTTATGAA CTTACAGGCA TCTGAGTTAT	240

	TAAGTAAACC AAAATTAATt TTAAGTCCTA TTGTATTAGC ATTAGGTTGT ACGTTTTTAG	360
5	TTTTCCTACA AAAAGACGTG GGCAACATTA CTAATATTAA TNATNTT	407
5	(2) INFORMATION FOR SEQ ID NO: 796:	407
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1053 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 796:	
	CAGTAGGTAC ACTTGCAGCA TTTGTTGGAT ACTTAGAGTT ATTGTTCGGG CCTTTACGTC	60
00	GTTTAGTCGC ATCATTTACA ACTTTAACGC AAAGTTTTGC TTCAATGGAC CGTGTATTCC	120
20	AATTAATTGA TGAAGATTAT GACATCAAAA ATGGTGTTGG TGCTCAACCT ATTGAAATTA	180
	AACAAGGTCG TATTGATATT GATCATGTTA GTTTTCAATA TAACGATAAC GAAGCTCCAA	240
25	TTTTAAAAGA TATTAATTTG AGTATTGAAA AAGGAGAAAC AGTTGCTTTC GTAGGTATGA	300
	GTGGTGGTGG TAAATCAACA TTAATTAACT TAATACCGAG ATTTTACGAT GTAACTTCTG	360
	GGCAAATTTT AATAGATGGT CACAACmTTA AAGATTTTTT AACGGGAAGT TTAAGAAATC	420
30	AAATAGGATT GGTGCAaCAG GATAATATTT TATTCTCTGA TACAGTTAAG GAAAATATTT	480
	TaCTTGGTCg TCCaACAGCa ACAGATGAAG AAGTAGTTGA AGCGGCGAAA ATGGCTAATG	540
<i>35</i>	CACATGACTT TATTATGAAC TTGCCACAGG GATATGACAC TGAAGTAGGT GAACGAGGTG	600
00	TTAAATTATC AGGTGGTCAA AAACAAAGAT TATCGATTGC TAGAATATTT TTAAATAATC	660
	CGCCAATTCT TATCTTGGAT GAAGCAACAA GTGCACTTGA TTTAGAAAGT GAATCCATTA	720
40	TTCAAGAAGC ATTAGATGTG TTGAGTAAAG ATCGAACGAC ACTTATCGTA GCGCATCGCT	780
	TGTCCACTAT TACACATGCT GACAAAATTG TCGTAATTGA AAATGGACAT ATTGTTGAAA	840
	CAGGTACGCA TCGTGAATTG ATTGCAAAAC AAGGTGCTTA CGAGCATTTA TATAGCATTC	900
1 5	AAAACTTATA AAGTATTAGT TGTTTGACTT CAGTACAATC TTGAAGAGAA AATTTGTAAC	960
	AGGATGGTGG GGTCATAACA TAGAAAAAGC AGTAAGAGAT TTTCTTAGTT GAAAATAATC	1020
50	TINCTGCTTT TITAAATTTA ATTTCGnGAT TCA	1053
	(2) INFORMATION FOR SEQ ID NO: 797:	
55	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 544 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 797:	
_	AAGAGTGACT CCTGAAGTGA AAGAAGGGGA CCGTGTCGTG TTCCAACAAT ATGCTGGTAC	60
5	AGAAGTTAAA CGAGATAATG AAACATATCT GGTATTAAAT GAAGAAGATA TTTTAGCAGT	120
	TATTGAATAA TACAGAACTT AATTCATAAA TAAATTAAAT	180
10	CTAAACAAAT GGAGGTTTAT CATTTATGGT TAAACAATTG AAATTCTCTG AAGATGCACG	240
	TCAAGCAATG TTACGTGGTG TTGACCAACT TGCAAATGCA GTTAAAGTAA CGATTGGTCC	300
	TAAAGGACGT AATGTTGTAT TAGATAAAGA GTTTACAGCA CCTTTAATTA CGAATGATGG	360
15	TGTGACGATT GCYAAAGAAA TCGAATTAGA AGATCCATAT GAAAATATGG GGGCTAAACT	420
	AGTTCAAGAA GTCGCAAATA AGACAAATGA AATTGCTGGT GACGGTACGA CAACTGCAAC	480
	AGTATTAGCT CAAGCAATGA TTCAAGAAGG CTTGAAAAAT GTTACAAGTG GTGCGAACCC	540
20	AGTT	544
	(2) INFORMATION FOR SEQ ID NO: 798:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 372 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 798:	
	CAATTGCATA GATATTGCTG ATAGACGTAC GGCTTTGTTT ATCAACTTCT AATAATCCAC	60
3 5	GGTCAGCGAA TTTAACACCT AATTTCGTCT GTGTTTGGAC GACGACCTAC AGTTACTAAT	120
	ACATAATCAG CTTCGATTGT TTTCTCTTCG CCTTTAGCTT CATAAGTAAC TTTAACTCCG	180
	TTATCTGTTT CTTCAGCTGA TTTAGCCATA GCTTCAGTAA CGATTTCAAC ACCTTTTCT	240
40	TICATACCIT TITTAACAGG TIGTGTGCAT TIGNTTITTC GAGGCCACCT AAGATATCIT	300
	TAGCACCTTC AAGGGATGGG GTACTTTCTG nAACCAAAGT TAGCAAATGC TGTACCTAAT	360
45	nCTGGTCCAA TG	372
	(2) INFORMATION FOR SEQ ID NO: 799:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1182 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 799:	
5	AAACGACATT TGTTTAATTG GAAGAATTAG CACCATTTTT TGAGGCGGGT ATAGALTCAT	6
	TTAAAATCGA TGGTATTCTA CAAACGGAAG AATATATTAA TGTGGTAACG GAACAGTATC	120
	GTCAAGCGAT AGATTTGTAC AATGAAGATC CTGAAATCTA TGAAGATGAG AAATTTATGT	180
10	TGATGGATCC AATTGAAGAA ATTCAACCTG ATCATCGACC ATTTGACGAA GGTTTCTTAT	24(
	ATAAACAAAC AGTATATTAA GGAGGTTAAT CATGAAGACA ATAGAAGAGA TTAAATCAAC	300
	TCCTAAAACA GTTATGAAGA AACCAGAATT ATTAGCACCT GCTGGAAACT TAGAAAAGTT	360
15	AAAAATAGCA GTACATTATG GCGCTGATGC CGTATTTTTA GGTGGTCAAG AATATGGATT	420
	ACGTTCAAAT GCTGATAATT TCACGATGGA AGAAATAGCT GAAGGTGTTG AATTTGCGAA	480
	CCGTTACGGT GCCAAAATTT ATGTTACGAC AAATATTATT GCACATGATG AGAATATTGA	540
20	AGGTCTAGAA TCATATTTGC GTAATTTGGA AAAGACTGGT GCGACAGGTA TCATTGTTGC	600
	AGATCCTTTA ATTATCGAAA CATGTAAAGA AGTTGCGCCA AAACTTGAAA TTCATTTATC	660
25	TACTCAACAA TCACTTTCTA ATTACAAAGC TGTAGAATAT TGGAAAGAAG AAGGATTGGA	720
	TCGTGTTGTA TTAGCACGTG AGACCGGCGC GATGGAAATG CGTGAAATGA AGGAAAAAGT	780
	AGATATTGAA ATCGAAGCAT TTATTCATGG TGCTATGTGT ATCGCCTATT CAGGTAGATG	840
30	TACATTAAGT AATCATATGA CTGCAAGGGA TTCCAACAGA GGCGGTTGCT GTCAAAGTTG	900
	CCGTTGGGAT TATGAATTAT TAGAAGTTGA TGATAATGGT GAACTTGATG TTTTTTATAA	960
	TCAAGGTGAA GTTACACCGT TTGCGATGAG TCCTAAAGAT TTAAAATTAA TCGAATCAAT	1020
35	TCCTCAAATG ATGGATATTG GTGTGGACTC ATTAAAAATT GAAGGACGTA TGAAGTCAAT	1080
	TCATTATATT GCAACAGTTG TCTCAGTATA TCGTAAAGTC ATTGATGCGT ATGCGGCAGA	1140
10	TCCTGACACT TTAAGATTAA TCCGGAATGG TTAATAGAGT TA	1182
,,	(2) INFORMATION FOR SEQ ID NO: 800:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 989 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 800:	
	GTATTCTTCC AATAACACCT TTCATTTGGA AACCGTTTAG AAAGAATACA GTTACTTCAG	60
	TTTGGTTTGC TTTAAAATTC TCTaGTGCTT TGTCTTGGAT GTTTTCGLTG CAATCATCTG	120

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	TTTTCTTTAT	CTAACCAATG	AACACTCATT	TTATTCTTGA	ACCATGTCAT	TIGTCGTTIT	240
	GCATATTGGC	GTGAATGTTG	CTTTAAATCA	TTGACAGCAT	CTTCATAAAT	CATTTGTCCG	300
5	TTAATCACAG	GTATTAATTC	TTTATATCCA	ATAGCTTGCA	TACTTTGGCA	AGATTCATAG	360
	CCTTGTTCAA	CAAGTTGTTG	CACTTCTCTA	AATAATCCGT	GATCCAACAT	AATATCAACA	420
	CGTTTATTTA	TTCTTGAATA	TAATGTTTTA	CGCGACATTT	CAATCCCTAA	TAATAATGTA	480
10	TCATAATTTT	CAGTAAATTG	TTGCACTTTC	TTGCGATTAC	TCAAAAGTTT	TTTTGTTTTT	540
	TTATAATAAA	CAATAGCGCG	CAACACTCTT	TGGcGGTTGT	TAGGGTGAAT	ATTTTCTGaC	600
15	AGAAACCGaC	ATCAAATTGA	GCTAAATAAT	CGTGTAGTTG	CTGATTATCT	AAATGTTCTA	660
	ATGCAGATAA	CTTTTGTTTA	ACTATGGATA	ATTGTGCAGG	TGTACTGTTT	CATCTTCTAA	720
	TTCATAATTA	TATATTAATG	ATTGAATATA	TAAGCCTGTT	CCACCTGCTA	TGATTGGaAC	780
20	TTTACCTCTA	TTCGTtATAT	CAGTAATTAA	ATCTTCTGCT	AATCGCTTGA	ATTCATATGC	840
	TGAAAATGTA	TCATCAGGAT	TCAAGATATC	AATTAAATGA	TGTGGAATAC	CATCCATTTC	900
	TTCAGGTGTn	ACTTTTGCAG	TTCCAATATT	CATATGTCTG	TAGACTTGCA	TAGAGTCACC	960
25	GCTTATGATT	TCACCATTGA	TACGCTTCG				989

(2) INFORMATION FOR SEQ ID NO: 801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801:

CGTTAGATAT AGAATTAAAA GATAATATTA AATTTCAAAA CGGTCAAAAA TTGACTGCAG 60 AAAAAGTGAA ATCTAGCCTT GAAAATAGCA TGAAAAAAAG CGACTTGGTC AAATATTCAT 120 TACCAATATC ATCAATTACC GCTAAAGGTC AAAAACTGAC AATTAAAACC AACTCCGCTT 180 ACCCTGAACT TGTATCTGAA TTAGCTAATC CTTTTATGGC AATTTATGAT ACAGATGCTA 240 AATCAGATGT TAATCAAACT CCTGTTGGTA CAGGCCCTTA CCAAATAAAA GATTATAAGC 300 AATCTCGAAA AATATCATTG TCGAATTTTA AGGACTATTG GCAAGGTAAA CCGAAACTTG 360 ATCATATTAC TGTGACGTAC CAAGAAGACG GCAATAATCG CGTCAGAAAT TTAGAATCTC 420 AAAAGATGA TTTAATAACT GATGTCCCAG TTAATAAAGT TCAAGACATA GAAAATAATC 480 AAAATTTAAA AGTGTCAAAA GAATCTGGAT TTAGAACTTC TTTACTTATG TATAATCATA 540

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(2)	INFORMATION	FOR	SEQ	ID	NO:	802

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(1)	PEQUENCE	CHARACTERISTICS:

- (A) LENGTH: 1139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 802:

GCG	AATTCGT	ACACACATAT	ACACAAAGAT	AATCATAGTT	TTACATTGAA	GCACATGAAA	60
GAT	AATTCAT	TTAAAGGAAG	GTATTATCAA	TGACTAAAAA	AATGGGATTA	TTAGTTATGG	120
CTT	ATGGCAC	ACCTTATAAA	GAAAGTGACA	TAGAGCCATA	TTATACAGAT	ATTAGACATG	180
GTA	AACGTCC	ATCTGAAGAA	GAACTTCAAG	ATTTGAAAGA	TAGATATGAA	TTTATAGGTG	240
GTT	TATCACC	ATTAGCAGGT	ACAACAGATG	ACCAGGCTGA	TGCGCTAGTT	TCAGCATTAA	300
ATA	AAGCATA	TGCAGATGTT	GAATTTAAAC	TATACTTAGG	ATTAAAACAC	ATTTCACCAT	360
TTA'	TCGAAGA	TGCGGTTGAA	CAAATGCACA	ATGATGGCAT	TACTGAAGCA	ATCACGGTAG	420
TAC	TAGCACC	ACATTATTCT	TCATTTTCAG	TAGGATCATA	TGACAAACGT	GCTGATGAAG	480
AAG	CTGCAAA	ATATGGTATT	CAACTTACAC	ATGTGAAACA	TTATTATGAA	CAACCTAAAT	540
TTA	TGAATA	TTGGACGAAT	AAAGTCAACG	AAACATTAGC	TCAAATACCG	GAAGAGGAAC	600
ATA	AAGACAC	GGTATTAGTT	GTTTCGGCAC	ATAGTTTGCC	AAAAGGTTTA	ATCGAAAAGA	660
ATA	ATGATCC	ATATCCACAA	GAACTAGAAC	ATACTGCGCT	TTTAATTAAA	GAACAATCTA	720
ATA	TIGAACA	TATCGCGATT	GGTTGGCAAT	CTGAAGGTAA	TACAGGTACA	CCTTGGTTAG	780
GGC	AGATGT	ACAAGATTTA	ACACGTGATT	TATATGAAAA	ACATCAGTAT	AAAAACTTTA	840
TATA	TACGCC	AGTAGGTTTT	GTATGTGAGC	ATTTAGAGGT	GCTTTATGAC	AATGATTATG	900
AATO	TAAAGT	AGTTTGCGAT	GATATTGGTG	CGAATTATTA	TCGTCCAAAA	ATGCCGAATA	960
CACA	TCCATT	ATTTATCGGT	GCAATTATTG	ATGAAATCAA	GTCTATATTT	TAATGACGAA	1020
AGAA	GCGTGA	AACGTTGTGA	CTAAATCAGT	GGCTATTATA	GGAGCGGGGA	TAACAGGTTT	1080
ATCA	AGTGCA	TATTTTTAA	AACAGCAAGA	TCCTAATATT	GATGTAACCA	TCTTTGAAG	1139

(2) INFORMATION FOR SEQ ID NO: 803:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 989 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 803:	
	TATCCHAAAT AHAAATGTGC GCATTTATCA AAACCTTACA TACAATAGAG TTTTCCCTAA	60
5	CAGTAAATTA GATATTATTA CACCTGTTGA TATGTCTTCT AATGCCAAAC TGCCAGTTAT	120
	TTTTTGGATG CACGGTGGTG GTTATATTGC GGGTGATAAG CAGTATAAAA ACCCATTATT	180
10	AGCGAAAATT GCTGAACAAG GGTACATTGT TGTGAATGTA AATTATGCAT TGGCGCCACA	240
	ATATAAATAT CCCACACCAT TAATTCAAAT GAATCAAGCA ACTCAATTCA TTAAAGAAAA	300
	TAAAATGAAT TTACCTATTG ATTTTAATCA AGTAATTATT GGCGGTGAYT CTGCAGGTGC	360
15	TCAATTAGCT AGCCAATTTA CGGCAATACA GACGAATGAT CGCTTAAGAG AAGCCATGAA	420
	ATTTGATCAG TCATTCAAAC CATCGCAAAT TAAAGGTGCT ATACTATTTG GTGGTTTTTA	480
	TAATATGCAA ACAGTTAGAG AAACTGAGTT TCCAAGAATA CAGTTATTTA TGAAAAGTTA	540
20	TACTGGCGAA GAAGATTGGG AAAAGAGTTT TAAAAACATT TCACAAATGT CGACAGTAAA	600
	ACAATCGACA AAAAATTATC CACCAACATT TTTATCTGTT GGAGATAGCG ATCCATTCGA	660
	AAGTCAAAAT ATAGAATTCA GTAAGAAATT ACAAGAATTG AATGTACCAG TAGATACTTT	720
25	GTTTTATGAT GGTACGCATC ATTTACATCA TCAGTATCAA TTTCACCTTA ATAAACCTGA	780
	ATCGATAGAT AATATCAAAA AAGTGTTACT TTTCTTAAGT CGTAATACAT CCTCTAGTGG	840
30	TATTCAAACT GAAGAGAAAC CACAAATAGA AAATCCGAGT AATGAATTAC CGTTAAATCC	900
	TTTAAACTAA TGATAAACAG TAGTAATTTA TTACTTAAGC AACATTTAAG ATTTTCAAAT	960
	TAAAAACGAG AATTTAAAAC ATGTGGTGC	989
35	(2) INFORMATION FOR SEQ ID NO: 804:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 711 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 804:	
45	TAANCCCTGG TITAATGATT TIGATTACGT GTTTTTATAA TAAAAACATA TCGAACATTG	60
	ACTACGTTAT TAAGCTGCTT TTTTGTACAC TTTATAACCA ATAGCTTAAG ATTTAAAACT	120
50	AATCGGAAAG AACAATGATT CACCANAAAA ATATTTATGT TGCTATTAAA AATCAGTTAA	180
	TACGAATGTT AAAATACGTT TGATTTTCAT TAATAATGAT TCAAGTTTAT TTAAATGAGC	240

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GTTAATGTCA GTCTGTTTTG ATGCACCTTA TAATAAAGAC AGATAGTTCA AATTACGTAA

	AAAGCAACAT TAGCATTAGG AATATTAACT ACAGGTGTGT TTACAGCAGA AAGTCAAACT	420
_	GGTCACGCGA AAGTAGAACT TGATGAGACA CAACGCAAAT ATTATATCAA TATGCTACAT	480
5	CAATACTATT CTGAAGAAG TTTTGAACCA ACAAACATTA GTGTTAAAAG TGAAGATTAC	540
	TATGGCTCTA ACGTTTTAAA CTTTAAACAA CGAAATAAAG CTTTTAAAGT ATTTTTACTT	600
10	GGTGACGATA AAAATAAATA TAAAGAAAAA ACACATGGCC TTGATGTCTT TGCAGTACCT	660
	GAATTAATAG ATATAAAAGG TGGCATATAT AGCGTTGGCG GTATAACAAA G	711
	(2) INFORMATION FOR SEQ ID NO: 805:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 680 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 805:	
	ATCAGGAAAA ACAGAATAAT GTAAATCAAG CTGTTCAGCC TCAAAATAAT ACTAATGAAA	60
25	CATCAAAAGT ACCGGCTAAT TTTGTCAAAT TGAATGATAT TAAACCAGGT GATACTTCTA	120
	TACAAGGAAC AACTTTACCA AATCAATTTA TACTATTAAC TATTGATAAA AAAGATGTGA	180
30	GCTCAGTTGA AGATTCTGAC AGCAGCTTTG TTATGTCTGA TAAAGATGGG AATTTTAAGT	240
	ATGACTTAAA TGGTCGCAAA ATTGTTCATA ATCAAGAAAT TGAAGTGTCT TCATCAGATC	300
	CCTATTTAGG TGACGATGAA GAAGATGAAG AAGTAGAAGA AACTTCAACT GAAGAAGTTG	360
35	GTGCTGAGGA AGAAAGTACA GAAGCTAAAG CTACATATAC AACACCGCGA TATGAAAAAG	420
	CGTATGAAAT ACCGAAAGAA CAGCTAAAAG AAAAAGATGG ACATCACCAA GTTTTTATCG	480
	AACCTATTAC TGAAGGTTCA GGTATTATTA AAGGCCATAC CTCTGTAAAA GGTAAAGTTG	540
10	CTCTATCTAT TAATAATAAA TTWATTAACT TTGAGACAAA TGCTAtGGTG GtCCaAATAA	600
	AGAAGAAGCG AAATCTGGAT CAGAAGGAAT CTGGATGCCT ATTGATGACC AAGGATACTT	660
	TAATTTTGAC TTCCAAACGA	680
15	(2) INFORMATION FOR SEQ ID NO: 806:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 950 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

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GTATTTCATT	AGCCATTGGC	AATTGACATC	TGACAATGAG	GAATGGCTTT	TGCATTGGAA	60
TTCACAGTTG	GAGTGCATTT	ACTGGTTATT	TTGGAGGTCA	TTGTTGATAC	ĄTTATTAATG	120
GAGAATAACC	GAATTTGTTA	TGTTATTTCC	ATTTTTTA	TTTGCAATTG	TATTAAATGC	180
TGCACTTGGA	GATAAAATTA	AAAATCCTTA	TGGATCTGCC	ATAATTCTTG	TTCTAGTTAT	240
TATCGTATTA	AGTTGGGGAG	GTATTGACAA	GACTTGTTCG	TGGTAAAGTA	CTTCAAGAAA	300
AAGAAAATGA	ATACTTTTTG	GCAGCAAAAT	CAATTGGTAC	ACCCACATAT	TTTATTAAAA	360
TGAAACATCT	TTTGCCGAAT	ATATTAAGTG	TAGTTATCGT	ACAAGCAACA	TTGTTATTTG	420
CCGGTATGAT	TGTAGTGGAA	TCAGGTTTGA	GCTTTTTAGG	ATTCGGAATT	AGTAAAGCAA	480
TACCATCTTG	GGGTAATATG	TTGAGTGATG	CTCAAGAAGG	GGATGTTATA	AGTGGTAAAC	540
CGTGGATATG	GATGCCACCT	GCTATAATGA	TTACATTAAC	TATATTAAGT	ATAAACTTTG	600
TAGGGGAAGG	GATTAAAGAT	GCTTTTAATC	CTAGAGGTAG	ACGTTAAATA	ATAAAAGAGG	660
CACTAGTTAA	TTCTAGTACC	TCTTTATTTT	ATCTCTTACG	TCCTAAACCC	ATCGCTTTTT	720
CCATTTTTT	GACAGTTTTA	AATGAAACTT	TGTGTGCTYT	ATCTCTACCT	TGATCTAAAA	780
TATCAYCAAG	TTTATCTGAG	TTATAGAAAC	TTTCGTATTT	TTCTTGGAAT	TCTACTAAAA	840
ATGCTTTAAC	TATTTCAGCA	AGGTCACCTT	TAAATTTACC	ATAACCTTCG	CCCTCATATT	900
TTGCCTCAAT	ATCTTTAATT	GGCATGTCTG	TTAATCCAGC	GTATATTGAA		950

(2) INFORMATION FOR SEQ ID NO: 807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 807:

60	GAGTACCTCC	TTACCCATAT	GAAACATTGT	GACCTGTTAC	GAAGCTTTAC	GTTACCAGTC
120	ATAGTTTCAT	TTAAGATAGC	ATATACTTAA	ATAACTACTT	ATAAATACAC	TTAATAATT
180	GTGATATAAT	ACTGAGTTTT	AGTCAAAAAT	TTCACATAAA	ATGAATAATT	TTGAAAAACA
240	AAACATTTAA	TAAGTGAATG	TTTAGAGAAA	AGTATGATAT	GAAGTTATGT	TGTA GACTGT
300	ATCGTCaTGA	CCTATAGATA	AAAGAAAACG	ACATCTATTA	Tratgatact	AATTTTTATT
360	TTCTGATAAG	gCgTAAGtCa	GGkGaTTTAA	AcAtATAaTA	AGTTLACTCa	GTGTAAATTC
411	СТАСАСТА	ACCOTTTATG	а ттаа стта	CAAATAnTCn	GATATTTTAT	TTGTACCATT

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(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 842 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 808:						
10	AATGGCNATT AATCTTTAAT ACGATGCTTG AGGATTTTTC CTAATAAAAC CTTGATTTCm	60					
	AAAAGGGTTT AAATCMAATG AAACAATAAT AAAAAAATGW CGCAATATAA TAATAAGTAC	120					
15	AAATTTAATT AAGAAATTAA ATTGATTGTA TATGTATATT TTGGTAACGT AAAAGAGAAA	180					
15	TATACAAAAT AATTAATTAT TTATATGAAA AGAGAATATA AATGAAGTAT AAAACAGAGA	240					
	GACGTGAAGC GATGGGATAT TTAAMAAGGT TTGCATTGTA CATAAGCGTT ATGAYTTTAA	300					
20	TATTTGCGAT AGCAGGTTGT GGCAAAGGTA ATGAAACAAA AGAAGATTCA AAGGAAGAAC	360					
	AAATCAAAAA GAGCTTTGCG AAAACATTAG ATATGTATCC AATTAAGAAT CTCGAGGACT	420					
	TATACGACAA AGAAGGATAC CGAGATGGCG AATTTAAAAA GGGTGATAAA GGGATGTGGA	480					
25 ·	CGATATATAC AGATTTCGCC AAAAGTAATA AACAAGGTGG ATTGAGTAAT GAAGGTATGG	540					
	TCTTATACTT AGATAGAAAT ACACGGACTG CAAAGGGACA TTATTTTGTT AAGACATTCT	600					
	ATAATAAGGG CAAATTCCCA GATAGAAAAA ATTATAAAGT TGAAATGAAA	660					
30	TTATCTTATT AGATAAAGTA GAAGATACAA ATCTAAAAAA GAGAATAGAA AACTTTAAAT	720					
	TTTTTGGACA ATATGCAAAC CTTAAAGAAT TGAAAAACTA CAACAATGGT GATGTCYCAA	780					
	TTAATGAGAA TGTTCCAAGT TATGACGCAA AATTTAAAAT GAGCAATAAA GATGAAAATG	840					
35	TT	842					
	(2) INFORMATION FOR SEQ ID NO: 809:						
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 451 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear						
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 809:						
	TAAGACTATG CCATCTTGGC AACGCGTTGT CGCATATTCA TTATTAGTAA GTATATGCAA	60					
50	GCATGATTTT GCCATAACLT TACCLCLTTC TATATTTAAG TACCACTTTT ATCATTCCCT	120					
	ATAATATTA ACTTATTAA TTAAACGTAA ATTTAACACA ATACGAATAC CAAATCAAAA	180					

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aaaaatagat	GTAGTCAGTT	TAATTAAACT	ATCCAATTGA	AAACACACTA	CTTTTTAGTA	300
TTTTCAAAAT	AATTTTAAAT	GACCACATCT	ACAACGTATT	ACTATTATCT	TTTGTTAGTT	360
ATATATTCAT	TTTCAATTTA	raaataaaca	CTTAtTTAAA	TCACATTCTA	CTTTTGAGAT	420
GAGCTCAAAC	TAACATTAAA	TTGTTTATAT	T			451

(2) INFORMATION FOR SEQ ID NO: 810:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1499 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 810:

60	AGIIGCIIGA	GAACAGTATG	CIACITIGIT	AATCCAATTI	CITGITGICC	ACAITITGIG
120	ACGAGATTGA	GAGCAAAGTT	TGAGTATTTT	TTGTCCAACA	TACTCAGCAT	CCACGCATGT
180	TGCTTGTTGC	TACGACTAAC	TTAGGTGAAA	CATTnCCATT	TGTTTTTCAT	TTCAACACAC
240	GCCTAATTTC	CGCCTTTGAA	AATTTTTCTC	TTTAACTGCA	GCAATCCTGT	ATTGTCTTTT
300	AAGCGAAAGT	GCAATGGAAT	CCCATACCTG	TTTGAGGAAG	TCCCAGCACC	ATTAAACTTT
360	TTTTCCTGTG	TTACAATATT	TTTCTTCCAG	TTTAGATAGC	TTCGTTCTTC	CCTTCCATGA
420	AGCAACAGGA	CTACTGCTCC	GCACCAATAG	AGCGGAATAA	CTGCTGAATA	GCTGCATTTG
480	TTCTTCTTTT	TCTCTATAGC	AGTGCTGCAA	CATACCAGCT	ATAAAACTAC	TTAATACAAG
540	AGAAGCGCCC	TGTAATCACA	GCTACTGTCA	TTCCGCTTCA	CCTCTAGCTC	TTCTTTTGCT
600	TTTCATTTCT	TATCTTCTTT	GATAATTTCT	ATCACTTTTA	TTTTTTCAAA	TGAGTCATCA
660	TTCATCGATG	ATTTTAATAT	TCTTGATCCG	TTTTACAAAT	GATCAATTAC	TTGTAATGCT
720	AGAAGCCCCA	CAATTTTCCC	TCTCCCTTTG	TTTCTTGGCA	CGCTGTCACT	CTATAAACAT
780	TTTAACATTC	TATTTTCCAA	TTAATTAGTA	ACCACCATTT	TACCATGTCC	TAGGTATCTC
840	AATTTCTTTC	GCGTGTCAAT	TCTATAAATG	ATCTATATCT	TGAATGCTTT	GTTATACCTT
900	CCCCATTAAT	TTTGATAATA	TATAACTCaT	TGCATAATCA	CTAATTGAGA	ATTTTCGAAT
960	TTCGTCTAAA	TTGCGCCATC	GTTAATGATA	TACACTACTT	GTGGACCTAC	TTAGATCCTT
1020	GTCTTGACCC	CATCTAAGAA	GTTGTATCTA	ATCATCCATT	CGCTTACCGC	GAACTGACAT
1080	AGCTGTTAGA	TGTCATAATC	GACTTTTCAT	TTGGATAGAT	CTATTACACT	TCTATTGCAT
1140	AAGCTTGGCA	TATTATAGTA	TATCCCTCAA	GTCATGCACC	CTTTTGTCAT	TATTCAATAT

	CCACCGAGTG TACTCAATGG ACCTTTGAGA CCACTAATGA CTGTTGCAGC ACTACTATAG	
		1260
5	CCATTTTCCA TAGAATGTGC AGCTTTTTCA CTACTGTAGT AATTTAATTG CGCTATTTTT	1320
3	CCAAAGTTTT GAGCTATTTC ATCATACTTT TGACTTATGC TTTCCAATTC TTTTACAACA	1380
	TGTGCAATCG TTTCAGCTTT AACACTAATT TTTCCACTCA ACGTCATTAC TCCTCLGcTL	1440
10	TATLAATATG ATTTTCATCA GTATCGAATC CAAATAATTC TCGTGATAAA NGTATTGAA	1499
10	(2) INFORMATION FOR SEQ ID NO: 811:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 620 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 811:	
20	CNCGCTGCAC CGAAGAATGC TTTTGGTTTG TGTAAAGATG CAGGATCTAA ACCACCTGAT	
	AATGTACGAC CACTTGGTGG AATAACYAAG TTATAAGCGC GTGCTAATCT CGTTATAGAA	60
25		120
25	TCCATTAAAA TAATGACATC TTCCCCCAATT TCTACTAAAC GCTTTGCACG TTCAAGTAAT	180
	AATTCAGCTA CTTTAACATG GTGTTCTGGT GGTTCGTCAA ACGTTGAATG AACGACTTCA	240
30	GCAGCTTCTA CTGAGCGTTC TAAATCTGTT ACCTCTTCAG GACGCTCGCC AACTAACAAA	300
	ATAAATAGCT TTGCATCTGG TTTGTTCGTA CTGATTGCAT TCGCTATTTC TTTTAATAAC	360
	GATGTTTTAC CTGCTTTAGG TGGCGCCACT ATTAAACCAC GTTGACCTAA ACCAATCGGT	420
35	GTTACTAAAT CCATGATGCG CGTTGAATAA TTTTGTATTT CTGTCTCTAA TTTAATACGC	480
	TCATCTGGAT AAAGTGGTGT CAAAGCTTGG AAATGCGGAC GTTTCTTCAC TTCTTCTGCG	540
	TTATGGTCAT GACAAAGTCA ACTTGTAATA AGCCATAATA TTTTTCGTTA TCTTTAGGTT	600
40	TTCTAACTTT CCCAGTTACT	620
	(2) INFORMATION FOR SEQ ID NO: 812:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1094 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 812:	
	CCGGCTGAAA TTAAGTTCTT GTTATATTTC GCAAAAATGA CAAAGAAAGA TAAAAATAAA	60

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	TGAACTATTT	GCAATTAGAG	aattgttaga	GAAAGGTTTG	ATTGGTGATT	GTATTCAACC	180
	TATAATTGAA	CCAATTAAAT	ATACAACCAC	TAAAAATTTA	ACTTTGCAAT	ACTGTGGTGA	240
5	AAAAGCATTC	TCTATAAATT	TAGTAGTAAA	TTCAAAGTTA	ACTGAAGAAG	AGATTAGTAA	300
	CGAAaCTGTt	GCACATTTAA	CTGAAATAAT	AACAAAAAAC	AAAAGTGTTA	TTCAAAAAGC	360
10	TTACTTGGGT	CCTTCTGATG	AAGGCAATGA	TAGGTTGAAA	CAGCAATTTT	CAAGTAATAG	420
	TTTAGCTATT	TTAACAAGTG	TAGATGATTG	GGAAATGTTT	GGAGATAAAA	ATAAACTTGA	480
	AATGGTTTTT	GTACCAGATG	ATAGACACAT	TAAACGTAAA	TTGCGTAATA	TTCCAAACAA	540
15	AGGCATSATT	ATGGATCCTT	TTAATAAACT	AAGTCGTAAT	GTTGATTATT	TAGATAATGA	600
	TGACGAGTTT	TATAGCGACG	ATCACCTTTA	TTATAAGGAA	GATGGATACG	TAGCATTTTC	660
	AGACTATTCT	GTTATAGGTG	GAGAATATGT	AGACGGTGGC	TTTTCGCCAT	TAGCLATTGC	720
20	Grtacatatt	GTCTATTTTG	ATGAGGCTAA	TGAGCTAAGA	GTTAAGCATT	TtGTCTCTGa	780
	TTCTAATAAT	GATAGATCAA	ATCCAGGTAA	AAnGTTTTTT	GAGGCTGTAG	ATAAATTAGT	840
05	AACATGGTCA	AAAAACTTAG	ATATTAAAAA	TAGATCTTAT	GCGCTTGGAC	AATTTGAAGA	900
25	ATTAAATGAA	AATAATAAGT	ATCCAGGATT	AGGTTTAATT	AAAnGTTATC	TATCAGCATC	960
	ACCTAGAAAT	TATGAATAGA	TACTGGGTCT	CAAAGAAATA	GGAAAAGTTT	ATATCGAACT	1020
30	GAACTGCAAG	AATGCATTGA	CATGGATGAA	. CACACGGGTA	AAATGATCGC	AGCTGAAATG	1080
	ACTATGGTAT	TAGC					1094

(2) INFORMATION FOR SEQ ID NO: 813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 813:

	CITAAAGATG GACATCACTT CAAAGAATTT TCAACGAATA TTATGCCACC GAAATTCCGA	480
5	AAAGATTTTC ATGATCTACT TGAAAAAATG AGTGTTCAAG TTGGTTCATA CATTCAAGGA	540
	CAAATTATCG TITCATTCTG TATCGGTATA CTGTTGTTTA TCGGTTATTC GGTTATCGGG	600
	TTGAAATATA GCTTAGTATT AGCTAGTATT GCGGCAGTTA CAAGTGTTGT ACCATATTTA	660
10	GGGCCTACTA TAGCGATTTC TCCAGCTATT GTAATNGCTG CTATAACAYC GCCGTGGATG	720
	CTCTTAAAAT TAGCAGTAGT ATGGACTTTA GTACAATTTG TTGAAGGGCA CTTCATTTCA	780
	CCAAATATCA TGGGTAAAAC ACTTAAGATT CATCCACTTA CAATCATTTT CATTTTACTG	840
15	TGTGCAGGCA AATTGCTTGG TATTGTAGGC GTTATTTTAG GTATTCCGGG ATATGCTATT	900
	TTAAAAGTAT TtAGTTACTC ATTTATTCCA	930
	(2) INFORMATION FOR SEQ ID NO: 814:	
20 25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 461 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 814:	
30	GTATGATTGC TGTTTTAATA CCAGATGATG GCAGTGGCAA ATCTTATGAC TATATGCTTG	60
	TGAACCCAAA AATTGTAAGT CATAGCGTTC AAGAAGCTTA TTTACCAACT GGTGAAGGTT	120
05	GCCTTAGTGT CGATGATAAT GTTGCTGGTC TAGTTCACCG TCATAATAGA ATTACAATTA	180
35	AAGCCAAAGA CATCGAAGGT AATGATATAC AATTACGACT AAMAGGATAT CCAGCAATTG	240
	TTTTCCAACA TGAAATTGAC CATTTAAATG GTGTAATGTT CTATGATCAC ATTGACAAAG	300
40	ATCACCCATT ACAACCACAT ACAGATGCAG TAGAAGTTAA AACACATTTT CTAATTATCA	360
	AAGCTTAGGA TAALATGATG LCCTAAGCTT TCCTTTACAA CTTTTCGGAT AACCAACAGT	420
	TAATATATCA CCTTCTAACC AAACTTTTAA TCCCTCATTA A	461
45	(2) INFORMATION FOR SEQ ID NO: 815:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 815:

AACGATATAA	TAGAATTGAA	TAAAGTGGGT	GATAATGTGA	CTAAAAATGA	GATTAGAAAA	120
TACATTTTAC	ATAAAATGAA	GAATTTTAAT	AAAGCTGAAA	AGCGAAAAGC	AGACACATGG	180
TTAAGAAATC	AATTTTTTGC	AACTGAAGAA	TACAAAGAAG	CAAACGCAAT	TGCGCTAGTT	240
CITTCTITTA	ATCATGAAGT	AGATACTTTT	TCTATTATTG	AACAAGCCTT	AATGGATCAT	300
AAACGTATTT	TTGTACCGAA	AATGGATTAT	TTAAATCATC	AAATGACTTT	TAAAGAGATA	360
TTTAATCTCA	AAGATATTGA	TGTCGATAAT	AAGGGGATTT	ACTATCCAAC	TTCAAAAGGT	420
GAAACAACGA	ATAACCTAGA	TTTAATTGTT	GTTCCTGGTG	TTGGATTTCA	AGACGATGGA	480
TATAGAATTG	GGTATGGTGG	TGGCTATTAC	GACAGGTTTT	TAGCTAATTA	TCAGACAAAG	540
ACAATAAGCT	TATTATACGA	TTTTCAAATA	ACA			573

(2) INFORMATION FOR SEQ ID NO: 816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3989 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 816:

TAGTTTAACA ATGTCTATTC TCATAGAATT TGTCCAACTA AATGTAGACG ATTCACTAAA 60 CTTCTAAAAA AATAAACCCC AAATTATAAT AGTCTCAATA TTAATATATT ACAATTTATT 120 CATAGGATTT TTATCATTTC AATTAATAGG TTGTTATCAG GGTTAAATAA ACATTTTTTG 180 TAATAGTCCT TTTTTACGTT CTTTTAATAA CTCAATTCTA TTCATTTGAT TATTCATTTT 240 300 ATTGTCTATA GATTTTAACA ATGCACTTAC TTTATCYTGT TCAGTGAGAC AAGGTATTTT AAGATTTATA TTGCATAAGT TCGCATGAGT TAATTTAGCT GGTGCATTAC CTGTGACAAA 360 TGCTCGTAGT TCTTTAAAAT TTAAATAATA ATTCATAAAA AACAAATTAT GATCATTACT 420 TTTAACTACA TGCGCATGAT TATTTACCCA GTATTGCCCA TTAGCAATAA AGCTACTCGT 480 CTCAAACTGC CCCCATTTTG CACCATCTTC TCCTATTAGT AATCGTTCTT CATTATTGAA 540 TAAATAATCT TTTACGTAAT CAATAATTCC AGTTGCACCA TAGTAAGGGT ATAACCCCTT 600 TTCTCTTAAT GAAGAAGTAA TTGGTTTTCT TCTATTATTT TCAAAGATAA AGATGTCTTT 660 TATGAATTTG TTTTCCCACT CTGGATATTC TTCACCATTC TCATCTTTGA ATCGCAATTC 720 TTGTGTGAAG ATTTTCTGCA TATAGCCTTT TTTCTGTTGT TGAAGCAATT CAAGTTTTTG 780 TTCTTCTAAT TCAATTTGTC GGTCGAGTTT GCTGAAGAAC TTGCCTATTT TTTGCTGTTC 840

	TCGACTACCT	CCACTTTGTG	CAAGGAAAAT	TTTCCTTTTA	CCTTTTCTTG	ATAATAGATA	960
	CTGTCCAAAA	AAATTATAAT	AATACTCTTT	TTTCAATCTA	ATAATACATA	CATGTTGATT	1020
5	TAAATTAGCA	TGCGTTTCAA	CTATCGAATT	AATGGCTGTT	CTACCTATTG	ATGCTCCTGT	1080
	AATATTTAAA	AGAACATCAC	CATAGTACGT	TCTACTATTT	TTCATCTCAT	CATCTATATC	1140
10	TTTACTAATA	TAAACTAAGT	CATTAAGATT	TAATTTACCA	TTTCTAATAT	TTTGACTCCT	1200
,,,	TAAAAATGGT	ATGCCTTTGT	TTGTATAGTT	TTCACTTCCA	CCTTTGGGAG	TCTTTCCACT	1260
	ACCTATTTTG	GTAGTAAGAT	TCCCTAACTT	CTTCTCTTCC	CATTCGCCTT	CAAATCCTGG	1320
15	GAATCTCAAC	TCTGGCACAT	TTTTCGTTTG	TGTATTACTC	ATCTTTCAAC	ACCCCAAGTT	1380
	CTTTCAGGTA	TGCATTGATT	TCTTGTTCAA	TTTCTGCGAT	TTCTTTGTCG	ATATTTTTCA	1440
	AATCTTGTTG	GACTTGATCT	AAATCAATTG	GTGCTTCTTC	TTCGAATGTA	TCAACATATC	1500
20	GCGGTATGTT	TAAGTTGTAA	TCGTTATCGG	CGATCTCTTG	TAATGTCGCG	CTGTAGCTAT	1560
	ATTTATCAAT	CGTTGCTTTA	CGCTTATATG	TGTCTATAAT	ACGTTCGACT	TGGGCATCGC	1620
	TTAAATGGTT	TTGATTTTTT	CCTTTTTCAA	AATCATTGGA	TGCATCGATA	AATAGTACGT	1680
25	TGTCGTCTTG	TTGGCGACAT	TTTTTAAATA	CTAAAATACA	TGTTGGAATA	CTTGTCCCAT	1740
	AGAAAATATT	GGCTGGTAAC	CCAATCACGG	CTTCTAAGTA	GTTCTTTTCT	TCTATTAAAT	1800
30	AGCGACGAAT	CACACCTTCT	GCGGCACCAC	GGAATAATAC	ACCATGTGGG	aGTACGACTG	1860
	CCATGGTACC	TTCATCGTCT	AGGTAATGTA	CCATGTGTTG	AATAAAGGCA	AAGTCTGCTT	1920
	TGGaTTTTGG	CGCAAgCTTG	CCGTAACCAC	TGAATCGTTC	ATCATTTTCA	AATTTTGAAT	1980
3 5	CTGCTGTCCA	TTTCGCACTG	TATGGTGGGT	TCGCAATAAC	CGCATCAAAT	GTATTGCCTA	2040
	AAAAGGCTGG	ATTTTCCAAT	GTGTCATCAT	TACGGATCTC	GAAGTTCTCA	TAACGCACAT	2100
	CATGTAATAA	CATATTCATG	CGTGCTAAGT	TGTATGTAGT	ATTGTTACGT	TCTTGTCCGA	2160
40	AATAACGATA	CACTTGCGTT	TCTTTACCAA	CACGTAACAA	CAATGAACCG	GAACCACATG	2220
	TTGGGTCGTA	CACGTGACGT	AATTTATCTŢ	TACCGTCTGT	GACAATCTTC	GCCAGTATCT	2280
	TAGATACTTG	TTGTGGTGTA	TAGAACTCGC	CTGCTTTTTT	ACCCGCTGTC	GCCGCAAAGC	2340
45	GCCCGATTAG	GAATTCATAT	GCATCACCTA	ACATATCAAT	TTCCATGTCA	CTGTGAACGA	2400
	ATGGTAAGTC	GTCAAGATTA	ACCATGACTT	TAGAGATTAA	AGCAGTACGT	TCTTTGACAT	2460
50	TGTTACCTAG	TCGCGTTGAA	CTCAAATCCA	TATCGCTGAA	CAGCCCGATA	AAGTCATTTT	2520
	CACTTTCTTC	ACCTAATGTA	GATGTTTCAA	CTTTGCGAAT	CGCCGTCGCT	AGATGTTCTA	2580
	TATCGAAATC	TTGCGTTTCA	ATTTCACGAA	TCATCGCACT	GAATAAATCT	TGTGGCTCAA	2640

	CCCATGCTTC	TTGATACGTG	ATGTCTTCAC	CTGACAAGGC	ATCTGCATAT	TCTTGTTCGG	2760
	CTTTTTCAGA	TAAGAAGCGA	TAGAAAATCA	AGCCTAAAAT	GTAATTACGG	AATTCACTCG	2820
	CATCCATGTT	CCCTCTTAAA	TCATTCGCAA	TCGACCATAA	TTTTTTATGT	AATTCAGCTT	2880
	GTTGCTGACG	TTGTTTTTCA	GTAATAGACA	TGTGATTCCT	CCGCCTTTGC	ATAAGTAATT	2940
	TATCTCTTTG	TGTAATAGAT	TTATTATAAC	ATTTGGTTAT	GTTGCGATGT	TGATAATTTG	3000
o.	GATGTTGGTG	GTGGAAATTT	TGAGTTTTAG	TGGCGCAATT	GTTATTGAAA	AATTTTATAG	3060
	AAATGTTGTA	GCTTTCAAAT	GCTTTCAAAA	TCATTTATAT	TCTTAATGAT	GTCAAAAAGT	3120
ς.	TGTTCATTCA	TACATAAATA	AAACCAATCA	ACAATTGAGT	TGGTGAAAAT	CAATCGTTGA	3180
,	TTGGCTTTGA	TGCATATTAA	ATAATGCAAT	ATATATTAAT	AAATGTTAGT	TATAGTATAT	3240
	TTTGTCAGGA	TTGGGTGAAT	GTCTAAGTTT	TAATTATTTA	TCTAAATTAT	CTGCAATGAA	3300
o	TTTCTTAATT	TCAGGAGAGA	AATAAACAGC	AAATCCTCTT	GTGCTTTCAC	CTGATGGCTT	3360
	ATTACCGGCA	TAGATTACAC	CAATAGCTTC	GTGTTTACTA	TTTAATATAG	GTGAACCAGA	3420
	GCTACCAGGC	TGAATAATTG	CATCCGATGA	CACTATATTC	CCATTCACTG	ATAATACTTT	3480
5	ACCAGTTGAT	TCATACATTT	GTAGTTTATT	TCCATTAGGA	TTTGGATAAC	CAATGACTGA	3540
	TATAGGTTCA	TTTTCTTTAG	CTTCTGATGC	TATATTAAAT	TTACTAGTGA	AATCTTTGAA	3600
	TTTTCTACCT	TTTGGTTGTG	TTGATTTTTC	TTCAACTTGT	ACAACCGCAA	TATCTTCTTT	3660
80	ACCAGGATAA	TCTACAATCT	TAGTAACTTT	ATAAAGTCCA	CCACCGTTAT	TATAAAAACC	3720
	ATTAGGATGT	GCTTTGATTT	CATCACCGAC	TTTCATGTGA	TAGGTAACAT	GTTTATTGGT	3780
35	AATGATTGTA	TGATTTCCAA	CTACAAATCC	TGTTCCAGCG	CCCATCCATG	TAACACCACT	3840
	GTATGGTGCA	ACATTTGTAT	TTGTAATTTG	TTTAACAGTA	TTTTCGGCTT	TGGCTGTTTG	3900
	TTGAATACCT	TCAACCATTG	TTGTGCCGAC	CACCAGTTATT	GATGTTAAAA	A TCGTCAATGC	3960
40	TGCAATACTT	TTGATGATTA	TATTTTTAT				3989

(2) INFORMATION FOR SEQ ID NO: 817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 817:

CGTTGAGCAC AGTTTTAGAT AATAGATAAT CTTGCLCTAG TTGTTGCAAT GTCTGCGATT

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						AATTGATATC ~	180
	CTTTAGATTT	AATACTTACG	ATGATATCAT	CCATAAAATT	GCTATTGATA	ACATGGATAT	240
5	CATTGCGAAC	TGTGCGGTTT	GAAACATTGA	CATGTTTAGC	AATTTCATTA	GAACTAATGT	300
	GCTTTGATGG	ATTTTTAATA	AAAAACTGGA	GTAGTTTTAA	GTGTCTATCA	AGCATTTAAC	360
	ATGTACCTCC	TTTCTAAATT	TTTCGTGTAA	GCGTTTTTAA	GGGTGTATTA	ATATTATTAA	420
10	ACATGAGAGC	TTATACATAC	GTCAATGACA	TTAAAGCGAA	CTTTTATATG	ATTTTAACAG	480
	AGTGCGAATT	ATGCAAATAA	AGAACAGCAG	TAAGATATTT	CAAATAGAAA	AATATCTCAC	540
15	TGCTGTTTTT	CTGAATTTAT	GCATCTGGTA	CTTGTGGACG	TATCAGGCAA	ATGATTAATT	600
,,,	TTTAGGTGAT						660
	AGCAGGTGGT						720
20	ACCGTGAGTA						
	TGGTACTGTT						780
	AACGTTATTG					COMP COMP	840
25	ATTT		,		GCACIAICAT	CITGTTGATC	900
	(0)	_					904

(2) INFORMATION FOR SEQ ID NO: 818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 818:

TTTAACAtGa	TAATAAAAA	TCTTTTGTTA	TATCATTAGG	AATATTTGAT	GAACTTGATA	60
TTAAGGTTAC	ATTTTGAGAA	ATGGACTTAG	GGATATTTCC	ACTATTATTT	AGTAAGAAAT	120
CTTTAGCTAA	TAAAGATTTT	CCTACACCAT	TTTTACCAAC	AATGTGATTG	ATCTGACCAA	180
GATAGAAATT	TAAATCACAA	TTGTCAACTA	GTTGTTTGTT	TTTAACTTTT	AAAGAATAGT	240
TATTTAGTTT	CATGTATACA	ACTCCTATGT	ATAAAGGGAT	TTATTACACC	GATATTTAAT	300
TGTATTTTTA	AAAATTCtTT	CACATTATGT	ATAGAWGTTA	TAAATTAGTA	TATCACACTA	360
TATTTEGKCT	AAATGATAAA	TATATCGTTA	TATTTTTACA	ATATTCTGAA	ATTTATGTTC	420
GCCTCTGAAT	GCTATATCCA	GTGTAATGTG	TTTTGCATAT	ATGAAAGCAA	TTTCAAAATG	480
TGAATATAGG	TTCATTGTGG	TATGACAAAC	TTCATTGCTT	GTCATGAGAT	GGATATAATG	540

GACGGGACGT	TTTTAGATTC	AAAAAAGACA	TATGATAAAC	TTAGATTTGA	AGCGATTITI	660
ACTGAACTTA	GAAATAGAGA	TATTACATTT	ATTGCTGCGA	GTGGCAATCA	ATATGCGAAG	720
TTGAAGTCTA	TTTTCGGGGA	TAGAGATATG	TATTTTATTT	CTGAAAATGG	TGCAGTTATT	780
TATAATGGCA	ATGAGTTATA	AAATATAAA	AGCTTTAATC	GTCAGGTGTT	TCAACAGGTT	840
GTCGATTACT	TAAATATGAA	GCAAAGTATT	GATCAACTCG	TCATCTGTGG	TTTGAAAAGC	900
GCGTATATTT	TAAAACATAC	TTCTGAAGCG	TTTAAAGAAG	ATACGAGATT	TTATTATCAT	960
CAGTTAAAAG	AAATTGACAG	TCTACAGCAA	TTACCTGAGG	ATGATTATGT	CAAAATAGCA	1020
TTTAATATTA	ATCGTGAGAC	GCATCCGAAT	GTTGACGAAG	AAGTAGCAAC	GCAATTCAGC	1080
AATGATATTA	AACTTGTCTC	AAGT				1104

(2) INFORMATION FOR SEQ ID NO: 819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 819:

CCCnTTTTAC GGATTAANGG CTTTTTCCTA TTTAAAACCT ACGGCATTTT CTTTTCAACC 60 ACGGCGCTC CCATATGGAT GGTATnGGGA TTGGGGTTTA TAAAATGGGG ATTGGAAATG 120 GTCCATCCTA AATACTCAGT TTAGTGCTTA TTTCCTTTAG TGCTGACGAA TAAATATGAT 180 CTAACTCTAC GAAACCTAAT AACGTATCAA ATGCTTCATC ACCATTTTCA AATTTACTTA 240 AACTATTTT AAAATCATGT CGCAAATCCT CTAAATATAG TGATGGTTTT CGATCTACAT 300 ACATITTAT ACTAACCTCC GATATATAAT CATCTTTATT GTACCTAACA TTTTATTAAG 360 ATAATACTAA TACACTATCG AACTTTGGGC TGATACTGAA ACAGCACAAA GAAACTCAAA 420 CAATTCGAAT TATGTATCAA AACCTTCAAT, TACAGGAAGT GATTTTAAAA TGATTTAACG 480 CAAAAAAACA CCTGTTACCG TTATATAGGT ACAAGTGCTT AATTGATAGA GATGTTATAC 540 GTCTTTAAAT GATTCCACAA CTTTTGGATG TGGACCATCC ATAAGCGGTT CTCTTTGTCG 600 AACGCCACCA CTTTGGTTGC CAATTGATTC GCTATCAAAG TACGATTTAT CTTGATTTGA 660 720 TTGTTCTTGA ATATGTTCTT CATTATCAGT TGTTGCATAT TCACTATCCA CCTCTGTTTT TTCCATTGTT GCTGTATGGA ATTGTACGAA GTTCTCTTCT TCTAATGCTT TGATTTCTTC 780 TITCGATAAC GCTCGATACC AATCITTCGC TITTTTCGCC GCAaTAGGAa CAaCAtCTTT 840

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	TACTTCAAAT TCTTTCCATT TTTCGGGGTA ACCTTTCATT GTAAAGGGCA TTCCCTTAAC	960
	CTCCAATATG TTATAATTCA TGTTATATAC CACCATAATT ATAAAATGAA-ACATATTAAA	1020
5	CACAATTTT TAGACTCCCG TCATAATAAC TTCAGACAAA CGTTAGTCTG ACCTGATAAA	1080
	TATTTAATTT TAAACGTTCT TGTCTCTCTC ACGAAAACCA TTGTGTTGAA TATTCATCAT	1140
10	TGCTGATTGA ATATAATTAT ACTGTGGTAA ATCTGGTAAT ATCTTTATTT CTAATTCTGT	1200
	ATTTAATTCG AAATGCTTAG CGATGTTTTC AAATATTGCT AAATACTCGC CCATTAATTG	1260
	TTCATTTATT GTAAGTCTAT CTTCATTAGC CATGGCTCTA TTTAACATAA AGCTAATTTC	1320
15	TTCTAATGCG AATAAGCTAG GATAATAATT TTGAATCAAT GTCTTATCAC TAAATAATTC	1380
	ACCATTAGCT GCATTATAAA CTTGCGTGCA TGTTATTTAA TTTGC	1425
	(2) INFORMATION FOR SEQ ID NO: 820:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1165 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 820:	
30	NCGNCCTTAT ATATGTTTTT CATGTCCTAC AAAAAACGAA ATATTCCAAT TGCCTATATA	60
	CAGATATTCA TTAATGACAC ACTCAATAGC AACCATNACA ATATTATGTT ACCTATTTAA	120

nconcer IMI	AIAIGIIIII	CATGICCIAC	AMAMAACGAA	ATATTCCAAT	TGCCTATATA	60
CAGATATTCA	TTAATGACAC	ACTCAATAGC	AACCATnACA	ATATTATGTT	ACCTATTTAA	120
ATGAAATAGT	TCTTTTAAAG	AAATACATTT	TTCACATATT	AATCTATAAT	CAAAATCAAC	180
TGACCGATAT	TCTATAATTT	ATGATTAAAA	TAAGTTATAA	TATAATAGTA	AAGATAAAGA	240
TAGAGGTGGC	TATAATGTGT	GGACTTAGAA	GTATAACATT	AGGTACAACA	AATATAGAAC	300
AGACaAAACa	TTTCATGGTT	GACATATTAG	GATTAAATTA	TGAAGAACTT	CTTGAAAACT	360
CAATTCGTTT	CGGCGATGCA	GATATAAGCC	CAGGAACAAG	ACTTCAATTT	ATACAAGTTC	420
CAAGTGAGCA	ATTAGAAGAA	TCTCACTTTG	TGGGTATTGG	ATTACGTACA	CCAACTGACT	480
CAGGTTTAGA	GGAGTATGCG	GAAATATTAT	CGAATAAGGA	TATTCCATTT	ACAACAGTTA	540
AAGAATTAAA	TGGCAATAAA	TATTTCAGTC	TCGAAGATAA	CAATGGTCAT	ATTTTCTCAA	600
TATATTCAAA	CGAGAATAAT	TATGGCGTTG	GTTTAGGTAT	GCCTTCTTYT	GAGAGTGCGG	660
TCAATCCGTT	ACATCAAGTG	CAAGGTTTAG	GACCAGTGAT	TCTTAAAGTG	AATCATGTAG	720
ATATTACAGG	TCAAATTTTA	ACAAATATAT	TCGGACTTGA	AGTATTTGCA	GAATACCAAC	780
CCTTCGACAA	TGCTGACTAT	CATGTCCAAG	TATTCAAAGT	TGGAACGGGT	GGTCTAGGTG	840

	ATCAAGTIGA GTTTGAAACG AAAGATGCAG ATTTCTTTAA TCAAGCGAAA TCGCGCTTAG	960
	ATGAAGTGGA AATACCATAT CAAACGCTTG AGCAAGATGA TATTGAATCA ATTAGAATTA	1020
5	CTGAAAACAG TGGATTATCG TTTATATTCA CTTTACAAAA ATAATTTTTT TACGATAGCG	1080
	AGGACAAAAT TTATGTTACA TGAAACTTGG AAAGAACGTA CACCAATCAA GAAAGTAGAA	1140
	GTCATTAATA CAGATGCAAA GAAAT	1165
0	(2) INFORMATION FOR SEQ ID NO: 821:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 821:	
	TCGCCCAATT ATTATGAAAT ATTCAATACA GTTTATTGAT CAAAAAACAA AAATCCATTA	60
	TGAACCTTGT CATCACGAAT ATTAACTGAC GTTAGATGGA CCTCTTTAAT GATAGAACAA	120
25	TTAATAAATA ATGCACTTAA GTATGCGAGA GGTAAAGATA TATGGATTGA ATTTGATGAG	180
	CAATCCAATC AATTACACGT AAAAGATAAT GGTATCGGTA TTAGTGAAGG NACTTGCCTA	240
	AAATATTTGA TAAGGGCTAT TCAGGTTATA ATGGCCAGCG CCAAAGTAAC TCAAGTGGGA	300
30	TTGGTTTATT TATCGTAAAA CCAATTTTCA ACACACAA ACCATCCGTT TCCGTCGTAT	360
	CTAAACAAAT GAGGGTACAA CCNTTACGAN TNCCATTTCC	400
35	(2) INFORMATION FOR SEQ ID NO: 822:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 760 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double 	
40	(D) TOPOLOGY: linear	
	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 822:	
45	TGATATAATA CTTTTGTAAA GAAAAGCATG TGTGGGAGGT ATGACCTGTA TGTCGAACGA	60
	AATACTTATC GTAGATGATG AGGATAGAAT CAGAAGATTA CTTAAAATGT ATTTAGAAAG	120
50	AGAATCTTTT GAAATCCATG AAGCAAGTAA TGGCCAAGAG GCTTATGAAC TTGCAATGGA	180
	GAATAATTAT GCTTGCATAC TACTAGATTT AATGTTGCCT GAAATGGATG GTATCCAGGT	240
	GGCAACTAAA TTGCGTGAAC ATAAACAAAC ACCGATTATT ATGTTGACTG CTAAAGGTGA	300

	TTCACCAAGA GAAGTAGTCT TAAGAGTTAA AGCACTTCTA AGAAGAACGC AATCTACAAC	420
	TGTAGAACAA AGCGAACCTC ACGCACGTGA TGTGATTGAA TTTAAACATT TAGAAATAGA	480
5	TAATGATGCA CATCGCGTAC TTGCTGATAA TCAAGAGTT AATTTGACTC CTAAAGAGTA	540
	CGAATTATTA ATATATTTAG CTAAAACACC AAATAAAGTA TTTGACCGTG AACAATTATT	600
	AAAAGAAGTT TGGCATTATG AATTCTATGG TGATTTAAGA ACAGTTGATA CTCATGTTAA	660
10	ACGCTTAGAG AAAAGTTAAA TCGTGTGTCT AGTGAAGCTG CGCATATGAT TCAAACAGTC	720
	TGGGGCGTTG GGTATAAATT TGAGGTTAAA TCTAATGATG	760
15	(2) INFORMATION FOR SEQ ID NO: 823:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 465 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 823:	
25	CAAAGGAAAT TGCACAATTA GAAGACCGAT TACGTTCACG CTTTGAATGG GGGCTAATTG	60
	TTGATATTAC GCCACCAGAT TATGAAACTC GAATGGCAAT TTTGCAGAAG AAAATTGAAG	120
	AAGAAAAATT AGATATTCCA CCAGAAGCTT TAAATTATAT AGCAAATCAA ATTCAATCTA	180
30	ATATTCGTGA ATTAGAAGGT GCATTAACAC GTTTACTTGC ATATTCACAA TTATTAGGAA	240
	AACCAATTAC AACTGAATTA ACTGCTGAAG CTTTAAAAGA TATCATTCAA GCACCAAAAT	300
35	CTAAAAAGAT TACCATCCAA GATATCCAAA AAATTGTAGG CCAGTACTAT AATGTTAGAA	360
	TTGAAGATTT CAGTGCAAAA MAACGTACAA AGTCAATTGC ATATCCGCGT CAAATAGCTA	420
	TGTCTTGTCY AGAGAGCTTA CAGATTTCTC ATTACCTAAA AATTG	465
40	(2) INFORMATION FOR SEQ ID NO: 824:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 355 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 824:	
	CACCGCGGTG GCGGACGCTC TAGAACTAGT GGATCCCCCG GGCTGCAGGA ATTCGGCACG	60
	AGGTAAGGAG GTCTCTGTAC CATGGCTCGT ACAAAGCAGA CTGCCCGCAA ATCGACCGGT	120
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GGAGGGGTGA	AGAAACCTCA	TCGTTACAGG	CCTGGTACTG	TGGCGCTCCG	TGAAATTAGA	240
CGTTATCAGA	AGTCCACTGA	ACTTCTGATT	CGCAAACTTC	CCTTCCArCG	TCTnGTGCGA	300
GAAATTGCTC	AgGACTTTaa	AACAGATCTG	CGCTTCCAnA	GCGCACTATC	GGTGG	355

(2) INFORMATION FOR SEQ ID NO: 825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 825:

TTCACTTGGC	TTGTTGACTG	ACTTGTALAT	GATGATGTGC	TTTGTGAATC	GGATTCGCTC	60
GTGCTTGTAC	TTGTTGAGTT	TGAGGCACTT	TGGCTTGCTG	AGTTTGAGTC	TACTCCGCTT	120
TGATTCATTG	AGGCACTTAG	TGACAATGAT	GTACTCGTTG	AGTCAGACAA	ACTTGTACTC	180
GTTGACGTAC	TTGTACTTCC	TGATGTTGAT	TGAGACATAC	TTATGCTCAT	TGATGTTGAA	240
TCGGATTTAC	TTTCACTTGA	TGATGTTGAG	TCGGATTCAC	TTTCACTTGT	AGAACCACTT	300
AATGATGTGG	ATGTACTAAT	GGAATCAGAT	TTACTTGTAC	TGATTGAATC	ACTTGTCGAC	360
ATTGATGTAC	TTAATGAATC	AGACTTACTA	TCACTTGTGG	AATCACTTAA	TGATGTTGAC	420
AAACTTGTAG	AGTCAGACAA	ACTTGTACTC	GTTGACATAC	TCAGTGATGT	TGAAACACTC	480
TCGCTCTTAA	ACGTTGACGT	TGATTCACTG	ATACTTGTCG	ATGTTGAAAT	GGACGTACTA	540
CCACTTGTTG	AATTACTTAA	TGATGTTGAT	GTGCTACCAG	ATTCTGATGT	ACTGTCTGAT	600
AATGACGTAC	TCTCACTTGT	CGAACTACTC	ACTGACTCTG	ATGTTGATTC	AGACGTACTT	660
TCACTTAATG	ATTCACTTAA	AAAGGCAGAT	GCACTTTGTG	ATTCTGAATC	GCTAGTACTA	720
TTTGATTCAC	TTAATGATAT	AAACGTGCTC	TCTGAAGCAG	ATATTGCTTC	ACTTATAGAG	780
TCGCTCGTTG	ACGTTGATTC	ACTTATTGAA	TCAGACTCTG	ATGTACTTAA	GCTTGTGGAA	840
TCACTCaTAG	ATGTTGaTGT	ACGTTCTGAA	TTACTTGTAC	TTAACGATGT	CGAAGTACTT	900
ACCGAACCAG	ATGTGCTCGT	AGAAGCACTT	TgTGATATTG	ATTCACTTGA	TGCAGTTGAT	960
GCTGATTTGC	TATCACTCGT	TGÀATCACTA	AACGACGTTG	ATATGCTCAt	TGAATCGGAT	1020
TGACTTGCAC	TCAnTGAACC	AGACGTACTT	TGTGATTCCG	AAGTACGTAC	TGAAGCACTT	1080
GTCGACGTTG	ATGTACTTG					1099

(2) INFORMATION FOR SEQ ID NO: 826:

5	(A) LENGTH: 338 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	-
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 826:	
10	TATGCGTATC CTGATAGTCA CTTTGATTTT GATATGGAAT TAGCGAAAGA GCAATCTCAA	60
	GACAATCCAG TTTACTATGC TCAATATGCA CATGCGCGTA TTTGTTCAAT TTTAAAACAA	120
	GCGAAAGAGC AAGGTATTGA AGTGACTGCT GCGAATGATT TTACAACGAT TACTAATGAA	180
15	AAAGCGATTG ANTTGTTGAA AAAAGTAGCT GATTCGGANC CTACAATTGA AAGTGCTGCT	240
	GAGCATAGAT CGGCACATAG AATTACTAAT TATATCCAAG ATTTAGCCTT CTCATTCCAT	300
20	AAATTCNATA ATGCTGAAAA GTGTACCAGT TGGTATTG	338
20	(2) INFORMATION FOR SEQ ID NO: 827:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 838 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 827:	
	GTATTTCTT TCGCGAATGA TTTTATTACT TGAATACCAC GAATAACCTC CAATACCTTT	60
	TCCACTAATT GGTTTTGTAC ATTATGATAC GCTGGCGCAT TTTGTCGACT CTTTCTTTCT	120
35	AATAATTGAA TCGCAAAAAA TGATAGTAAT ACGCCAATGC ATGCTAATAA TGATACTTGC	180
	CACGAAACTA CAAGTAGAGA CAATATGAGT ACTGTAATTA ATATGTATCC ATTAACAACA	240
40	ACGTCCACCA TTTTCATAGC AAAGTTTTCT AAAAAGGTTA AATCTGTTGT TACTATTGTT	300
	GTTAACTCAT TTGAATGATG CGAATTAAAA TAACCTAACC	360
	CCTATATCTA AACGTTCTTT CGCACTCATT TCATAAGCGA TGCTCTCATG GCTTTTGCTT	420
45	TTGAAATATG CTGTAATAAA TCGTCCAATC ACTAATAAAA CCATGATAAT TACAACATTC	480
	AATATATCTT TCATATAAAT AGGTTTATGA GATAGCACAT TATTAAATAT TTTTGCAGCT	540
	AAAAAGATAG GTAACGCAAT AAAAATAGCA TTTAAAAATG ACATGCTAAA TCCTAAAATC	600
50	ATTCTTGCTT TATATGGTCT TATCCAGTTT AAAATTTTAA ATGTAATTTG AAACATATTT	660
	GACCTCCTTT TCTCATTAGT TTAATTATGT CCAGTATTGA TTCCCCAATC TTTTGTATGC	720
55	ATGTGCGTAT CCCACATTTT CTTATAATTA CCGTTTAATT TTAGCAATAA GTGATGTGAC	780

(2) INFORMATION FOR SEQ ID NO: 828:

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 898 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 828:	
	TCCnAAAGAA GAAATAaCAT TATCATaAAA TCCATTGAAT ATAAATTCAG TCATCCCCTC	60
15	TGAACTECTC CATAAATATA ATGGTGAATA AGTATTTGTA ATGCAATTAG TAGTTGTTTG	120
	ACTTATTAAA TAAGCTTTTA TAATTAAATT TTTAAATCCA TCAGTCTTAT AACCATTTAA	180
	TCGAACTCTA TCTCTAATTA TTTCCATATT GTAATCACTA GGCAACTTAA CATGATATTG	240
20	CATTGCATGC ATTTAGCATA CCCCCTTTTA TAAAAAGGAT AGCAATAATA AGTAAAATCT	300
	CATATTATCC ÅÅTTGTGATA TAGTTATCAT AAAAAGTGAT AGGTGATTAA ATTGAACTTT	360
	AATGATTTGG AAATTTTTAT AACTGTATGT GAAGAAGCAT CTATCAATAA AGCTGCAATT	420
25	AAACTTAGAT ATGCACAATC TAATATATCT CAAAGAATTA GCAAGCTTGA AAATGAATTA	480
	GGTGTAGTTT TGCTTTTTAG AAATCAAAAA GGTGCTAAGG CAACTAAAGC AGGCGAAGAA	540
30	TTCTTAGCGT ATAGCAAAAA AGTATTAAGA GATACAGAGA CTATAAAAAA TAAAATGAAA	600
	AATAATACTA TGTCTATTTT ATGCTCAGAA CTGTTATTTA ATTATTTATC TGAGAGCGAA	660
	GAAATTATGA TGTCGAATAA CTCAATTAAT TTTATTTCTA GTGGAAATAT TAGAAAAGCT	720
35	ATAGAAAAA ATAATTATGA TAAGGTTATT TCATTCATAA AAATTAACGA CTCAAATTAT	780
	AGACTTAGTA ATGTTGATAC TATGAAAGTA ACGCTTTACA GTAATGGAAG TAATTATGAT	840
	AAAGAGGCTT TACTAATAAA TAAAGATGAG TTTGGTCCTT TAAGGNAAAT AACTTTAG	898
40	(2) INFORMATION FOR SEQ ID NO: 829:	
4 5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 798 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 829:	
J U	AGTAGGAGTC ATAAAATCGn ATTTCAAAAG CAATTAATGC AAAATACTGA GTCTACAGTG	6
	CTATTTGCGA AAGCGTCCAT ACGAAGTTGA GCAATGCTAA TAATAATGGT CTATCAAAAA	12
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	AATATGTTGA TAGTTACACT GATTCTCTTA CTGGAGTAAC AACTTCTGCT TTTTTAAATA	240
	AAGATACAGG CAAAGTAACT CTCGGGATGA CTGGGACTAA TTTACAAGAC GAAGCCTTTA	300
5	AAAAGTTAAA AGAAGGTGAA TTTTCAAGAC AAAATGTTAC CAATGCTTTG GAAACAGTTA	360
	AAGATGGATA TGCAGATCTT AAAATATTAT ATTCTCCTGC ATCTGATCAA AACTATAGAT	420
10	ATGCGAATAC ACAAGAATTT ATAAATAAAA TAAAAAGTAA GTATGACATT GATTTTATTA	480
10	CTGGACATTC ACTAGGTGGA AGAGATGCGG TAGTTCTAGG AATGAGTAAT GGTATTCCGA	540
	ACATTGTGGT TTATAATCCA GCTCCTATTT CTATAACTAG TTTGAATCCT AATTCCCCAG	600
15	ATGGAAAACG TTTATTAGAA TTATATAAAA ATTATAAAGG TAATATTACT AGGTTTGTTG	660
	CAGAAAATGA TGCATTGACA GAAAATCTGA AGAAATATAA GCATTATGTT TTTTTCGGTA	720
	ATGATAAAGT CTTTAAAAAT GGTAAAGGTC ATGAAATGKA AGGCTTTCTG ACCGAAGAAG	780
20	AACAAAAGC tataaaan	798
	(2) INFORMATION FOR SEQ ID NO: 830:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 830:	
	AATATCAATC TCTTCATAAG CTGAATTATT TTCATGCACT TCTTGATGTG ATGATTTGTC	60
35	ACGAACHGCT ACAACTAACA TTTTATCGTC TAAAATAAGT TGTTTATATT TTTCTAATTC	120
	ATCAGGCGCT AAGTTGTAGC GTGATAAAAC TGCATGTTCA CCATCTTCTC CTGTTAACAG	180
	TITAGTCATT CTATCACTAA ATGTTCCACT TGTTGAGATA AGGGGAGATT TCAGAGTCGT	240
40 -	GTAAGTCATT AGGTGTAATT TACTTTTACT AATAATTGTT AGCCTGATCT AAATAACTTC	300
	AGATTCTTTG ATTGATANGT GNATAATCGC AGTGCATTAC ACAGAATACT GCCAAGTGCG	360
45	CCCTTAAAAT TGTTATTAnC TTACCTCTAT ATAAGAACCC	400
45	(2) INFORMATION FOR SEQ ID NO: 831:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 475 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

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AAGTCTGCAT	GACTTTTATT	TGCAAGTTCG	ACTGCTTGAT	CAAAAGCGCG	ATGATCTTCA	60	
GGATLAGCAC	TTTGAACTGA	GCTGAAATTC	GGATCAGGTT	TACATTGTGC	TTCTACAAGA	120	
TTAAATTGAT	TGAAATTCAA	AGATTGTAAT	AACTCAGGTA	CAATCGGAAC	ACTTGTACCA	180	
TGCAAACTAG	TGAACACAAC	TTGTAAATCA	GATTTAGGAA	TATAGCCAAT	CATATTTTGA	240	
ATGTGTTTCA	TATAGTCATC	AGTTACAGAT	TTCGGAAAAG	GCTTGaTATA	AGATGTATTT	300	
TGTTTAGAAA	tAGGTATATC	AATCTGTAAT	GGATCGCCAA	CTTCTTCGAT	ATAACGACTT	360	
GCAAGCTCAG	ATGCATCAGT	CGATAATTGC	GCACCATCAG	AACCATATAC	TTTGATGCCG	420	
TTATAGTCTT	TCGGATTATG	ACTTGCtGTA	ATCATAATGC	CAGCAGTAGT	AATTAA	475	
(2) INFORMATION FOR SEQ ID NO: 832:							

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 832:

CTTGAATTGA	AGGATACGCA	AATGATGCAT	AATCAGCTTC	TGTATAAAGC	TGTAATGTAA	60
TGTCATCAAG	GTCACCTTTT	CTAACAAGCA	CCTTATTAAT	AGAAGTATGA	TTCGCTTGCC	120
AAGTACCTTG	ATTATTTTGT	TCTAAATGAA	TGACTTCGCC	TAACGATTTC	AACGTAATAT	180
CTGCACGCTC	GTCTTCGCTA	ATAGTATATG	TCTTACCATC	TCGCAAATTG	AGCATCTTCA	240
ATTGTTTGTT	ATATTTTATA	ATCAATTTAT	GCATTGTCTT	TGCCTCAGTC	CTATACTATT	300
TTTTTCTTTC	AGCTTCTTGG	CGTTTTTCTT	TATCTTTTTG	TGCTTGTTCT	TTTTGTTTCT	360
TTTCGTTCTC	TTCTTGTTGC	TTTAATTTCT	CATCTTTCGC	TTTTGCTTTC	TCTTCTTCAG	420
ATTTCGCTTT	TTCATCTTTA	ACTTGTTTTT	CTTTGTCTAA	AATATCTTGC	AATTTATCGT	480
TATACTTTTT	CGTTTCTTCA	GAACGTTTAT	CATTCGATAA	ATCTCCGTTA	TTTTTAATCT	540
CATTTAATTT	ATTAATCAAC	GCTAACTTTG	TAATATCGTT	ATCATCTAAA	TAAGTGGCAA	600
TATTAATCGC	TTCATCAAGA	TGTCCTTGTC	CTAATTCCAT	CCAATATAAT	AAGTAGTCTT	660
TGTTTGAATT	TGGTGTCACA	TTATTAAGTA	AATTTTCTTT	CGTATCTGTn	TCTAAACCnT	72
GTTn						72

- (2) INFORMATION FOR SEQ ID NO: 833:
 - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 994 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 833:	
	AGCAGTTTGG CTCGTAGAAA TCTCCCGTCT CTATTCTATG TATTAACTTT TATTATATTT	60
10	GTTATGATAC TATCGATATG AAAGCGTTGT CAATGGTTTT TGTAAAAATT TTGTCAAATT	120
	TAATTTTCA AGTCTTTATA AAAGTAGTTT AATTTGAAAA CTAGAAATAC CAATCCTAAC	180
	TAATTTATTT ATGACGCTCT TTTGTTTAAT TGACATTCTT CAGCCATATT TTTTATGACT	240
15	AGTTGCATTT TTTACTAATA AACACCTCTA AAACTTTAAT GATTTTAATC GTTTTAGAGG	300
	TGCTAATTAT TTTATTTGAT TATTTTTTGT TTGATACCTA CTGCATATCC CATATGAAAA	360
	CGGCTTTTTT ATTATGTTAT ATGACTAAAT CTCGTGAAAA ATGAAATTTT TGCAGACTTA	420
20	TGATTTACCA AAGTTTATCA TAACTAGTAG TTACATATTT CGCTCCATTT TTAACAGCTT	480
	CATTGACTTC ATCTATTGTA TTAATTAGGC CACCTGCAAT GACTTGTGTG TTTGTTTCTT	540
25	TCTGAATATG ATGAATCGCT TTACTCGCAA CACCTGGAAG TACTTCAACA AAATCAGGTT	600
	CAACTTTTTT TATCAAATCT ATACTGCGTT TCAATGCTTG ACTATCAATA ATAAATACTC	660
	TAAAAATCGT TAAAGTATTT AATGATTTAG CTTTTTTTAT TACTTTAGAT TTAGTCGATA	720
30	CGATACCTTT TGGCTTGTAT TGCTGAATAA TAAATTCACT TGCAAATTCA TCGTGGCTTA	780
	AACCTTTTAT CAAATCTATA TGAATAAAAC ACTCTATATG ATTTTGCTTC AGCAATTCCA	840
	TAATACTTTT TATATGTCCT ATATGCATAT CTAGAAGCAC ACACATTTTA TAGTCTGTnT	900
35	TAATCCAGTT TCTCTAAATC nTTAATGTTT CCTATAAGCA GGCAATATGT TGTTAATTCA	960
	CTMGATCCAT CCTCTCTACA TCACACGCTT AAAT	994
40	(2) INFORMATION FOR SEQ ID NO: 834:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 783 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
45	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 834:	
50	TCNACAAAGT CGGTATTAGG CTATGGGCCA TTTNACTATT ATAACTAATC GGAAATATAC	60
	CACATAACAT CATTATTGAG TTGATTCTAT CATTTGGCTT ATTAGGGTTT TTTATCATAA	120
	TGATTTGCAT TTTGCTACTA GTTTATAAAA TGATTAGGAA CTATGATCCA AACACTATAG	180
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ATTTAGTTGT	AAGTGAATIT	TGGTTTGTGT	TGTTCTATTT	TATTACAAAA	GGACGGCGTC	300
ATCATGGCTA	AGAAAGTTTT	TATTATGGAT	AGCGTAAAGA	CAATAATTGG	TACGTTGCTT	360
ATAGCTTTAG	GATTACAATT	TTTAGCTTAT	CCAATTATTA	ATCAACGAGT	AGGTAATGAA	420
GCGTTCGGTT	CTATTTTAAC	GATTTATACA	ATAATAACAA	TCACGAGTGT	TGTATTAGGC	480
AATACGCTTA	ACAATATACG	mTTGATTAAT	ATGAATCTAT	ACAAATCCAA	TCATTACTAC	540
TGGAAATTTC	CATCGATACT	TTTAATCTCA	ATTCTGATTG	AGAGTATAGC	TTTAATTATT	600
GTATTTCTTT	ACTTTTTAA	TTTGAACATC	ATCGATATTA	TCTTTTTAAT	TCTACTTAAT	660
ATTTTAATGT	GTTTAAGGAT	TTATCTGAAT	GTATTTTTTA	GGATGACTTT	TAATATAAA	720
CAGATTTTGT	ATATTGCTCT	TATTCAATTT	TTAGGTTTGC	TGATAGGACT	ATTTCTATAT	780
nAT						783

(2) INFORMATION FOR SEQ ID NO: 835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 835:

TTACCTAATT TTTCAAtCaT AAGATTCCCC CTATTGTTTA AACATAAAA TATTATACGA 60 TTAAGCACGA GMCACTTCAA TATATTTTTC AGAATATTCT TATAAATATT AATATGATCA 120 TITCACTATT TAAACACGTT TAATATTAAA ATAAGTTATT CATATAAACT GGTGCTGTTT 180 GATCCAATTG CAGACTTACG AGTCATTGAA AAGTCTCACA AACTATTGMA AGTAAALATC 240 TTAAAATAGA AAGTGAATGG TTAATTTAAG TATATTTMAA AAATATTAAC CTTTTTAAGC 300 ACTGCTATTT AGGATATACT AAATAATAAC TAAGTTTAGA AAAATAGGAG GAACATCGTT 360 TATGTTAAAC AAGGTTTGGT TCCGAACTGG CATCGCTCTG ATTATGCTGT TCATTCTCAT 420 CAAACTATTT ATGGAAGTGC ACGAAGTATT TACTCCAATA GCTACAATCA TCGGTTCTGT 480 ATTTCTTCCA TTTTTAATTA GTGGTTTTTT ATTTTATATC TGTCTACCTT TTCAAAACTT 540 ACTTGAAAAA GTCGGTTTTC CAAGATGGGC TAGTATAACA ACAATCATGT TAGCTTTGTT 600 TGCTATTATC GGCTTAATTG TTGCGTTTGT TGCACCAATC ATCATTTCAA ATATCAACAA 660 TTTAATTAGT CAGACACCTG GCCCTACAAA AAGGAAGCAG AGCAAATTAT TAAATTCGCA 720 CTGGCTCAAA TGGNTAAATT ACCTGGAGGA TGTAACCANG TGGATTACCA ATATGGTAAA 780

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(2) INFORMATION FOR SEQ ID NO: 836:

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 836:	
	TGTTTATACT GTGCCTGAAT TAGAAGAGGT TTTAACACCT ATGAGACAAG ATGGAACTCG	60
15	TGATATTTAT GTTAATTTAG AAAATGTGAG TLATATGGAT TCGACAGGTT TAGGTTTATT	120
	CGTAGGTACA TTAAAAGCAT TAAACCAAAA TGATAAAGAA CTATACATTT TAGGTGTGTC	180
	AGATCGTATC GGTAGACTAT TTGAAATTAC TGGTCTTAAG GATTTAATGC ATGTTAATGA	240
20	AGGAACGGAG GTCGAATAAC ATGCAATCTA AAGAAGATTT TATCGAAATG CGCGTGCCaG	300
	CATCGGCAGA GTATGTAAGT TLAATTCSTT TAACACTTTC tGGCGTTTTT TCGAGACTGG	360
	TGCCACATAT GATGATATTG AAGATGCCAA GATTGCAGnT	400
25	(2) INFORMATION FOR SEQ ID NO: 837:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 433 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 837:	
	ATTGATCCAT TTTGCGGTTC GGGTACAATA GCTATAGAAG CTTGTTTAAT TGCTCAAAAT	60
	ATCGCACCTG GTTTTAATCG CGAGTTCGTA TCAGAGCAAT GGAACATCAT GCCAGCAAAT	120
40	ATTTATGATG ATTACCGTGA TGAAGCGGAT AAGATGGCTG ATTATGATAA AGAAATCGAA	180
	GTATATGCTT CTGATATCGA TCCAGAAATG GTAGAGATTG CTAAGCGTAA CGCTGAAGAA	240
45	GTTGGGTTGT CTGATATTAT TAAATTTAGT GTAAAAGATG TCAATACATT AACAATTGAT	300
45	ACAGAAGAAC CGGTGGCGTT AATTGGAAAT CCTCCATATG GTGAACGTAT TGGTGATCGT	360
	GAAGAAGTEG AAGAAATGTA CCGTTATATT GGTAAACTAA TGAAACAACA TCCATTTTTA	420
50	TCTACATACA TTT	433
	(2) INFORMATION FOR SEQ ID NO: 838:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 926 base pairs	

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 838:	
	ATTGGGCCAA CTAATCCTGT ATATCCAAAT CCAGCAGACA ATGGTGTTCC TTTAACCTGA	60
10	AGAACGTAAG CAATGATTCC AGTAATTATT CCATTTATAG TCAATGGTAT CGAAATAATT	120
	AAATTTTCA AGTAAACTGG GATCATCATT TTTGCAGCTC CTATGAGTAA AACTGCATTT	180
	ACACCAATAG AATTGACACG CAATGAGCCA AATAAGAAAG TAACACAGGC AGCCACTATA	240
15	CCTAGGTTTG CTGCTCCACT TCCTAGTCCG TTTAAACTAA TCGCAGTTGC AATCGCTACT	300
	AACGATATTG GTGTTACCAT TAATAATGAA AATGCCACAC TAATAAGTAT AGACATTAAC	360
	AACGGATTTA AGTCTGTAAA AGAATGAATT ACATTTCCAA TTGCTTGAGT AATTTTTCGA	420
20	ATGTAAGGTA ATGTGATTAG ACCGATACCC CCACTAACGA TAGGTACTAA AACTGGTAAT	480
	ATAATTAATT CAAAAGATCC AAGTTTGTTT TGTAATACCA TATATATAAG ACATGCAATA	540
25	ATAACAACCA AACTCGTATT TATAATGtCa CCTATACCTT TTAACATAAA ACTATTATTG	600
	CTATATACAA CAGCACCTGA ACCAATCATA GCTGATGTAC CTACTATAGC AGCACCTGCA	660
	CCATTAAATT TAAATTGATG AGCAGCTAAA ACCCCAATAA TAAATGCCAT AAATGATTGA	720
30	ATTAGTATCA CTAACTGATA CGTTAATTCT AAAATTTCAT TACCACTTTT AAATATTTTt	780
	AATACTTCAC CTAATAAAGC ATTCGGAACA AGTGCAATAA CAACACCAGC ACCAATAGAA	840
	TITAAAATCT TACTGAAAAA CTGTTTATTA TCAGCATTAT TTGCGTTACT CATAAACGAC	900
35	CTCCAATTTG AACATTANAC TCATCA	926
	(2) INFORMATION FOR SEQ ID NO: 839:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 839:	
	CTTCGAAACG TACTTGGTCA TTCCCTTTAC CAGTACAACC ATGTGCAATA CCTACTGAAT	60
50	TTGTTTTCTC AGCAATCTCT ACTAATTTTT TAGCGATTAA TGGTCTTGAT AAAGCTGAAA	120
	CTAATGGATA TGCATTTCA TACATTAAAT TTCCTTTGAT TGCATAACTT ACATACTCAT	180
	CACTAAATTC TTTTGTTGCA TCAATAATAT GACATTCAAC TGCTCCCATA TCTAAAGCTT	240
55		

	CGTATCCLTT GTCGATAAGC CATTGAACGG CCACACTTGT ATCTAGLCCL CCKGAATATG	- 360
	CTAAAACAAT TTTCTCTTTC ATAAAATTCA CCTCATTGTA	400
5	(2) INFORMATION FOR SEQ ID NO: 840:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1043 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 840:	
	GGATCGCGGT GTTGTGCTTG ATATACTTTG TAGCGATAAC GTTTACCTAC ACAATCATAA	60
	CGACAATGAA AATCGTCATC GACTGTAACT ACATTGTTGA CATAAATATC ATCAGGTAAC	120
20	GTTCGGTTCA TTGCATATTG CCATTGTGAC ATAGGTATAT TCAGCTCTGT GTCGAAATGA	180
	AAGTATTGCT GTATCGCATG TACACCTCTA TCAGTCCTAC TTGAAGGATG GATTCTCACA	240
	TGTCTTTTAT GCATGCGTTG TAATAGCTTT TCAAATTGTT GCTGTACCGT TCGACCATTT	300
25	TGTTGAATTT GAAAACCTAG AAAATTATTT CCTTGATACG CAATTTCTAC TAATATACGC	360
	ATGAATTTAC ACTCCTGAAT ATTTTAATAC GAATAAAATA ATTGCAATTG GGATAATCAT	420
30	GGTTAAAGAT ATCGTATCTC TCAATTGCCA TTTAAGCTGT CTGTAGCTCG TTCTCTTAAC	480
	ATTGGCATCA TAACCCCTAA CTTCCATTGC GACCGCTAAT TCTTCGGCGC GTTGGAAAGC	540
	TGAGATGAAT AGTGGCACTA GTAATGGAAT AAATGATTTA ATACGTGTTG CAATGTTCCC	600
35	TGAACTTATT TCAGAACCAC GCGACTTTTG CGCCAAAATG ATTTTATCTA ACTCATCCAT	660
	TAACGTCGGG ATGAATCGTA ACGCAATGGA CATTATCATA CTTAATTGAT GAACTGGTAA	720
	TTTAAACATC tTTAGTGGTG CAAGTAATCT TTCAAACGCA TCTGTTAAAT CAATTGGACT	780
40	TGTAGATAGT GTCATAATTG TTGCAATCAT TACAATCCCA ATTAAACGCA GTGTTATATA	840
	TAGCCCTTCT AAAATACCAT TAGTTTCAAT CGTGATGCCA TGCCATTCAA CTAATACATA	900
	TCCACCTTTA GTTAAAAATA TATGCATCAT TAATGTGAAG ATTAAAAAGA AAAATATTGG	960
45	TGTTAAACCT TTGATTAGGA ACCATAATTG AATTTTTGCT AATCTCATAA TGAANANGAT	1020
	AAGTGCAAAC ACCCAAAGAT ATG	1043
50	(2) INFORMATION FOR SEQ ID NO: 841:	
55	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 343 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double 	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 841:	
5	TCGAAATCAA ATTATAATAG ACAATTTTAG GAGGTGGACT TTCGATGACC AAAGGAATCT	60
	TAGGAAGAAA AATTGGGATG ACACAAGTAT TCGGAGAAAA CGGTGAATTA ATCCCTGTAA	120
	CAGTAGTAGA AGCTAAAGAA AATGTTGTAT TACAAAAGAA AACTGTAGAA GTTGATGGAT	180
10	ACAACGCAAT CCAAGTTGGA TTTGAAGACA AAAAAGCATA CAAAAAAGAT GCAAAATCTA	240
	ATAAATATGC TAATAAACCA GCTGAAGGTC ACGCTAAAAA AGCTGACGCn GCACTGAGAG	300
15	nTCCCCTCAT AATTTCCCCA AnCGTAACCA TGTGTGAATA AAT	343
,,,	(2) INFORMATION FOR SEQ ID NO: 842:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 430 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 842:	
	ATGAGTATTT TAATGATGCG CTACGAGCGT ATGGTCTTAC TGTGANAACA GGTGAATTTG	60
	GAACACACAT GAATGTTAGC ATAAATAATG wtGGwCagTC TCTGGTAGTT TAGAATTAGA	120
30	AGAATTAAAG CAATTTAGAC AATGGGGTTC TAAAACACCA GGTCATCCTG AATACAGACA	180
	TACAGATGGT GTAGAAGTTA CTACCGGACC ACTTGGACAA GGTTTTGCTA TGTCmGTAGG	240
35	ATTMGCTTTA GCAGrAGATC ACCTAGCAGG GAAATTTAAT AAAGAAGGAT ATAATGTTGT	300
	AGATCATTAC ACATATGTAT TAGCTTCTGA CGGTGATTTA ATGGAAGGTA TATCGCATGA	360
	AGCAGCTTCA TTTGCTGGAC ATAATAAATT AAGTAAATTA GTTGTTTTAT ACGATTCAAA	420
40	TGGATATTTC	430
	(2) INFORMATION FOR SEQ ID NO: 843:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 329 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 843:	
	GGACTGCCCG ATGATTTGAC AAATGAATTG CTGATTTGAT TTATATATA TCTGNAATTA	60

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	TCATCTATCC AACAATATGT CTTATCAATG GTATAGTCTT TGCACACCAA TGGAGGNAAA	180
	TAAATCTCAA CCTTACTATA TTAATATATA ATCAAATCTT AGATTAACTA GTGTAATGAT	240
5	ACAGATGGAT AATTGAGTAC AAATTTAAAA CCCTGAGATT TTCGCTTTAA TTTGAAAAACC	300
	TCAGGGnTTA TITGATTTT ATATAATGA	329
10	(2) INFORMATION FOR SEQ ID NO: 844:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844:	
20	AGATGAAGAA AGTGTTTCAT CGATTATCTT AACAGTTGTT GCTTTATATA CTACAnTTCT	60
	TCCTAGATCT TGTACCGTTG AAAAGAGACC TGGTTGTAAA ATCTTAATTG ACATTTTCAA	120
25	TCACCACCCA GTCATCAACA TTAAAGTTGC CATCTGATAT ATCTCTTTCG ATTTGTATAA	180
23	ATTTCTGTTC ATCTATTGCA TAAAATTGTA TCCATTCTCC TGCTTCGTAC ATTGACATTG	240
	GTTCACGCTC GCTGCTAAAT ACTTTTAACG GTGTGCGTCC AATAATTTGC CATCCGCCAG	300
30	GGAAATCTGA TGGGATATAG TCCTGTTTGA TTATTCGCAA TACCTACAGA ACCTGGCATG	360
	AATTTTTTAA CCTTGGGCNG ATTACGTCTA NGGNGTATGT	400
	(2) INFORMATION FOR SEQ ID NO: 845:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 535 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845:	
45	CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT	60
	TATTTCTTAA CTGATTAATG TTTCCCCAAC TCTCGGATCC AAACACTTGA ATATGACTAT	120
	ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTGC CATAACCATT	180
50	TTCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT	240
	CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA	300
	GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA	360
55		

	ACCGATTCGG AATTAAATAA AAGCTAAAAC TATGTTAAAT AAACTTAAAC AGTTAGTAGT	480
	GTTATTTAAG CAAAACTTAT CATTTTTAAG TTGGACAGAA CAGATCAATA AGAGC	5 35
5	(2) INFORMATION FOR SEQ ID NO: 846:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 509 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 846:	
	TCAATCGATC AAATGGTGAT TGACCTTTTA AATTTGTATG ATCAAAATAA TGATTGTTGG	60
	CCATATCTTT ACTATGCTTA CGTGCAGTTT CAGAATTCTG TTTAGAATAC TTCAATGTAG	120
20	ATAATTGATG TTGTTTTCTT TCAGCATTAA CTAAATCAAA ATTTTGTAGT TCAAAACTAT	180
	CTGCAAGCGA TTTCGATGGT GCTCCATATT GTTCTTTTAA TCTATTTTCC ATAGCATCAC	240
	TTACTTGTAA AACAGCTGTT ACATTATTAC GTCGATGCTT ATCATAAAAT ACCGTCGTAT	300
25	AAATGTGATT TTTATGGAAA ACATCATATT CTTTATTATT TTGTTCGTAA CGCACTCTAC	360
	CTITAACAAT CTCTGTTTCT GGTTCGCCTA ATCTTTGCCT TACAACCGAT TTAGGTGTAT	420
	TGTATTTAAT TTTTGATTTT GAAGTGATTA TATTTTGATT TGTATATAAC GCATTAACTT	480
30	TATCTTTCAT GTAACTTATC ATTATAAAA	509
	(2) INFORMATION FOR SEQ ID NO: 847:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 847:	
	CGTATTGATC TATAAATAGT GTTTAGATGC TATAGTCGGA TGCTTAAGTA ATTTAAAGAA	60
45	AGTATCTTTA ACATCGATGT GTGTATAATC ATTTTTAGAA GTATTATAAT CTTTTTCTTC	120
	TCCCTTCTAA AATATATACA GGTGCTTCAT CAGCTAGTGG TTCAACTGGA ATGTCAGCAT	180
50	AAACTTCGCA TCATATGTTA AACAAAAACG ATTGTATCTG TACTTCACCT ATAACAGCAC	240
30	TATCCAATTC GTGCTTATCA AATAAACTAA GATTTTTGTC AGTACCTTTT CACAACTAGT	300
	ACATACGTCT TGAGTTCTGA AGCATCATTT CATAAGGAGA ATACTGGCCA CGTGTGGACT	360
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(2) INFORMATION FOR SEQ ID NO: 848:

5	(A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 848:	
	TACCACTTGA ATACATTGCA TATAAAATAC GACGTTGTAC TGGTTTTAAA CCATCACGAA	60
15	CATCTGGCAA TGCACGCTCT TGAATAATAT ATTTACTATA TCTTCCAAAG CGATCACCTA	120
	AAACATCTTC AAGTGATAAA TCTTGAATTA TTTCACTCAC TAGATTTCCT CCTCATCAAA	180
	TTGATCATTT TCAAGCACTT GTACTTCAGA ATTATCTAAA ATACTTTGGT CCTCTTGCAT	24(
20	ACCANACTCA ACATGCTTTT CAATCCATTC ACGTCTAGGT TGTACTTTGT GCACCCATTG	300
	AATGTTGTTA CACGTTTAGA TGGAACGCAC TTGCATCTTG CAACTTGTGA CACGNATTGA	360
	AAGTTnCGTG TTTGCGGGGG TTnCAGCGTC GTTTGCCCAT	400
25	(2) INFORMATION FOR SEQ ID NO: 849:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 849:	
	TTTATATGAT TTATTTGAGG AGTTAAGAGA TTTATTTA	60
	GACATCATGC GAATTTGATT TTACAAGAGA AGGTGAATTA AAAGTTTCAT TTGATTATAT	120
40	TGATTGGATA AATTCAGAAT TTGGTCAAAT AGGTCGACAA AATTACTATA AGTATAGAAA	18
	ATTTGGAATT TTACCAGAAA CGGAATATGA AATTAATAAA GTTAAAGAAA TCGAGCAATA	24
	TATTAAAGAG CTAGAAGAAT AAACTATCTT AATGTAAGAC TAAACAATAA AGCTTTGTTT	300
45	AGTCTTTTTA GCGTTTAAGT AAAAAGCAAT AGATACCGTA AAGTTGATGC TCATCAAATA	360
	ATAATATAAA GATAATTTTA GGTTTTTAAA CTTTTAATCG	400
50	(2) INFORMATION FOR SEQ ID NO: 850:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 923 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 850:	
5	CAGGCCATAC TTACAATTTT GGCCATCGTC CGGATGTATT nGGAATCGTT GGATAATAAG	60
	CATCAAGGTC GTGACTATTT CGTAAAATTC CAACTGTCCC AGAATTTACA TCATTATGTC	120
	CAATTACTGG GCAACCAGAT TTTGCCAACT ATCTATATLT CATATATTCC AAATGTTAAA	180
10	ATGGTTGAAT CAAAATCTTT GAAATTATAC TTATTTAGTT TCAGAAATCa CGGTGATTTT	240
	CACGAAGATT GTATGAATAT TATTATGAAT GATTTGATAG AGCTTATGGA CCCACATTAT	300
15	ATTGAAGTCT GGGGCAAGTT CACACACGTG GTGGAATTTC TATTGATCCT TATACAAACT	360
	ATGGACGTCC AAATTCTAAA TATGAAAAAA TGGCTGAGCA TCGTTTGATG AATCATGATT	420
	TATATCCCGA AAAAATAGAT AATCGTTAAA TGTATCATTT AATAAACACA CCAATAAGTT	480
20	GATTTTCCTA ACTTATTGGT GTGTTTTTCA TTTAGCATAC ATAATAGGTT ACATTAAAAT	540
	AACATITTAT ACCAAAGTAC ACCAAAAGAA TATTAGTACA CGAATTAAAC AACATITTTA	600
	TAGAAACCTA TTGCACTTTA ACGTCAATAA GTATATTTTT ATATTATCTC TAATTAATTG	660
25	TGCGCGCTTA ATAACAGAAT ATTCTCAATA TTTTTATTTT TTTGTGATTT GTTGGAATAT	720
	TTAGTTGATA AGGCACAATC AAATTTACTT AAACTATTGT ATTAGGGGAA GAAAGGATGG	780
	GATGTATACA TGACACAACA AAACTCCCAT GGAAATCAAA TTCAAGACAT ACCTCAAACA	840
30	GGATTTTTCG GGCATCCTCG AGGACTAGGC GTACTCTTCT TTGtAGAGTT CTGGGrAAGG	900
	KTTAGTTATT ATGGGCATGC GTG	923
35	(2) INFORMATION FOR SEQ ID NO: 851:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1004 base pairs (B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 851:	
45	TTANTTGCAT CTATTTCAGT TGGTGTAAAG AAAGCGGAAT TTGATTTAT TGAAAAGTTA	60
	GCLCAAGAAA AATTAATCCC CGAATATATT ACAATAGATA TTGCGCATGG TcACTcAGAT	120
	TCaGTGATAA ACATGATTAA ACATATAAAA ACCCATATAC CTGATAGTTT TGTTATTGCT	180
50	GGTAATGTTG GTACGCCAGA AGGTGTTAGA GAATTAGAAA ATGCTGGTGC TGATGCTACC	240
	AAAGTCGGTA TAGGTCCTGG TAGAGTTTGT ATTACAAAGA TTAAAACAGG TTTTGGTACT	300

	GCCGATGGTG GTATAAGAAC GCATGGCGAC ATTGCTAAAT CAATTAGATT TGGTGCATCA	420
	ATGGTCATGA TTGGTTCATE WTTTGCGGCA CACGAAGAAT CACCTGGTGA AACTGTAGAA	480
5	CTTGATGGTA AACAGTATAA AGAATATTTT GGTAGTGCAT CTGAATTTCA AAAAGGCGAA	540
	CATAAAAATG TAGAAGGTAA AAAAATGTTT GTAGAACATA AGGGTTCATT AATGGATACC	600
10	TTAAAAGAAA TGCAACAAGA TTTACAAAGC TCAATTTCAT ATGCCGGTGG AAAAGACTTG	660
70	AAATCATTAC GTACTGTAGA TTATGTTATT GTTAGAAACT CTATTTTCAA CGGTGATAGA	720
	GATTAATATT TATAGTAGGT GAKGTAAATT AAAAAATTCA TAGTAACTGT TGTTGCGTTT	780
15	TTATCAATTA TTATCATTGC GCCAnTAACA GAATTTAAAC CATTCATTCA TTTACAAAAT	840
	GAAGTAAGAC AATATATTGA CATTCACATC AATAAAGAAA CAATTTCTGC GGAAAATAAA	900
	TTGGATACAC CGAAGAAACA ACAATTTGCC TTTAATAATA TACAAATGAA CATGTCGAAA	960
20	TCAGATGTTG AGAAAACATT AAATAAACCA AAAAGAGTGA CATn	1004
	(2) INFORMATION FOR SEQ ID NO: 852:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 852:	
	GTTCGCTCCA ATGTACGCAG TTGTATATGC ATAGACACCA AAATCGAACC ATTCCATTGC	60
35	ATTACCGATA CCGGTTGCAA CAACGGTTTT TTTAGCTTTC TTTGCATCCA CCATGTTAAT	120
	ATTCTCTTTA TTAAAATCCA TGAATTCATA CACTCCCTCT TGTATGTTTC ATAATTATAC	180
	GGAGTTAATT AGTTTTGTCA AATTTATAAG AATTTAAACT TTTATATAAA TACCAAAGTA	240
40	TGTTTGTTCA AAAATTTCGC TTTATCGnAT TAAATTCATG GTTTTATACC TCATACATTG	300
	ATTAGACATA ATAATCTAAA CACGACGTTA CTTTGGATAT ACTNAATGGT NNCACACTCA	360
	GTAGGAAGCA CGCATTCGCT CGATAATGTA ACCATACTCA	400
45	(2) INFORMATION FOR SEQ.ID NO: 853:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 361 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	GGTGAAATTG TAACTATATA ATCGATATTA CCTTCAGTGT TCAAAACTGG AAAATAATAA	60
	TTACCATCAC TCTTTTGTT GAATTTATAA ATTTTAAAAG GTTCACCAAG TGTATACGAG	120
5	GCTTTCTCTT TATTATAGAT TTTATCAAGT GAAGTAACAT AAGAAAGATA GTCTTTTTGC	180
	GCTAAATTAC GTACGTCAGT AGGAACACTC TTGTCCTCGA CATTAACTTG CACATGCTTC	240
	TTATCTTTTG CTTTGATATT TGAATTGCTC TCAGCGTTTG CAATAGGGGT AACACTTAAA	300
10	GAAAATATTA AACTTAAAGC TATTAATTTT GGAAAGTTTC TTTTCATATA AAAACTCCTT	360
	т	361
15	(2) INFORMATION FOR SEQ ID NO: 854:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 605 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 854:	
25	ACNTTATACT AGANAAAGNT ATTAAAGTAT ATCTGCTTTA CACCATTAAA AAGCGGCAAA	60
	TGCTATAGAT AATCTAAAGC ATCTGCCGTA TGAGNATTTA TTTATTTTTG ATTGTCATAA	120
	TCGTGTGGTT TTAAATTAAT TGTTTCTAGC TTTACAAATT TTGTTTTGTG AATGATTTTA	180
30	TGAATAAAGT AAATCAACGC TAGAATGATT AAAGGTAAAA AGTTTTTAAA AGCATTTAAC	240
	CATTGATCTT TTAAAATATA TTCAACTGAG CCACCAAATA GCAAGAATAA TAGTGTAGTG	300
35	ATGACAATGA TTGGTCCTAA TGGATAAAAA GGTGCTTTAT ATGGTAGGAC CTTATTAGGG	360
	TCTTGACCTT GTTTTTTAAT AGCTTGTCGC AATCGTATTT GTGACCAAAT GCTTGATCCC	420
	CAAACAACTA TAATCATTGA ACCAATAATT TCAAGTAAAT TAAAAACGGC ATTTGAATTA	480
40	AAGTTTGCAT AAATAATAAC AATAACAACG ACTGCATAAG TAGTTAATAA TGCTCTTAAA	540
	GGTAACTTAG TIGTCTTGTT TAATTTACTT AAAAATTGGG GTGCTTTTTT GTCTGAACTT	600
	AAGGA	605
45	(2) INFORMATION FOR SEQ ID NO: 855:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 515 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

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	TTGAACAAGC	ATTTTTAAAT	AGTCAACAAC	ATCAMGCAAT	TAGTGAAGAG	GCACAACTTT	- 60
	TAAATAATCC	AGATGAATTA	ATGGCATTTT	TAAAGAATAA	GCGTAAAAAT	ATTTTAGAAA	120
	ATGCATACAT	TATGCCGCAT	AATATGAGAG	AAATGTTACG	AAGTTATTTG	GAAAGTATGT	180
	CTCAAGACTT	TAATGTTGGC	GGATTTTTTA	ATAAAAAGAA	GAAAAAACTA	CAAATTCAAC	240
	AACAGCGATT	ATTAACAGCG	ACAGATGCGT	TACAAGAACA	TGTTAATCAA	CAAATTCGTC	300
	AACCAATGCG	AGAAGATATG	TCATTTGTTA	CGCGTTTTAT	СААТААААА	GmAGCTTCAG	360
	aTAmAGTATT	AAATCAGCAT	TATGACGTTA	AGCCAGAAAT	GATTGAAGGT	TTATATCAAC	420
	CACAAACATC	AATCAGCAAT	ACTTATGTAC	TTACATTTTC	AGACGAAGTG	GTTAAAGCCA	480
	TTAAGAAATA	TGTTGAACAA	CAATCAACAC	CAATT			515
	(2) INFORMA	TION FOR SE	Q ID NO: 85	56:			
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1607 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear							

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 856:

GICATITITA	AAATTICGCA	TTCGCGTTTA	ATTTTTCTC	TITTTTTTTT	TTCTTCTAGT	60
GACATACTTT	CTTTAGGTGT	TTCAACCAAT	TCAGATGTAT	CTACATCATC	AATTTTAGTG	120
ATTTTGTCTA	CATCTTTCTT	TAAATCTTCT	GGGACGTTCT	CGAAACGCTT	ATATTGCTCT	180
TTAGAGATAC	TAGCAGCTAT	TTCATTAGCT	CCTAAAATTT	CATCTATCAA	GCCGAAAGAC	240
AAGGCTTCTT	CTGCAGTAAG	CCAAGTTTCT	GCATCTAACA	TCTGTTTTAA	GTGTTCTTGA	300
TCTAAATCTT	TTGCTTTATC	TAAATAAGCT	GAATTACTAA	CAGCATCTGT	TTTTTCAAGT	360
AAATCCGCTG	TCTTTCTTAA	TTCTTCTGCA	TTACCTACAG	TCATAACCCA	TGAATTATGA	420
ATCATTAAAA	AACTATTTTT	GTGCATAAAA	ATAGTGTCAC	CACTCATAGC	GATAACACTA	480
GCAATTGATG	CCGCTAAGGC	ATCGACATAG	ATATTAATTT	TTGCAGGATG	CATTTTTAGC	540
ATATTGTATA	TTGCATGTCC	TTCAAATACA	CTGCCTCCAG	ATGAATTTAT	ATGAACATCT	600
ATTTCACTGA	TGTCTCCTAG	TTCATCTAGT	TTATTTTTGA	AATCTGTAGC	AGTTACATCA	660
CTTTCAAACC	ATTTATCACT	TACAATATCA	CCATAAATGa	ATATTTCACC	TTTACTTTTT	720
GATTTTCTTT	TCATTTGAAA	ATACTTAGCT	TTCATTGACA	TTTTTATCAC	CACCTTTCaA	780
AGATTTTCTT	AATTCAAGTG	GCGTGTCAAT	TGGGTATAAA	TCACCGCTTA	ATTAGCGGCT	840

AACCACTACG	AACTGCTTTA	AAGTACACTT	CTGCTTGTGT	TGCACTATCA	GCCCTTAAAT	960
AAGATTTAAC	GTTAAATTTA	AAATACCTAT	TTTTTTCTCT	GTCTGTTTTA	GTAAGTAGTT	1020
TCCGATTAAn	TTCTTCTTCA	TACTGTTTGA	CGATTGGCAA	TAAGGTATGC	TGCAAGTAAA	1080
ATCTGTTTAA	CTCTTCATTT	TTCGCGAAAT	TTGTATTTGA	TCTTGCATTT	AAGAATATTG	1140
AGGGCAATTG	AAAAACGTTA	GCTACTCTTT	CTCTTGTTAA	ATTCTCGCTT	GCCACTATAT	1200
CTTCAGAGAC	ATATTTTTTA	GGTAAAGGTT	CGATTTCAAC	ACCAGGCTCT	TGGAATAATA	1260
TTCCACCGTT	TTCTTCATAG	TACTGTTTGA	AATCTTCTAA	CACTTGTTGC	CTTTTTTCTG	1320
TACTTACATT	GGAACCATAT	TTAAGCATAA	AAGAATCTGG	TTTTTGCATT	TCTGTAAGAT	1380
TAAAGGTTCT	TACTGCATTG	TCAAAATCAG	TTGTATTCTT	CAACACATCA	ATCGGACTAA	1440
TACCTTGAAC	CATATTAGAT	GCCACGATGT	GTTTAAAATG	CAACATGTCC	aTATTATGAA	1500
CAATCAATTT	ATTTCCAGTT	GCAGCATGAA	TGGAATAATA	AAGTTCACcG	TGATTGGTTT	1560
TCAATTAACA	TTTCAACAAC	ATCTGGATTT	AATAAGAAAA	GCTTTGA		1607
(2) INFORM	ATION FOR S	EQ ID NO: 8	57:			

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 857:

ATGCGCATTT	AACCGCATTT	AGAGATGCTG	AAGATCAGTA	TAAAGCTTTG	TTAGAAATTA	60
CAACATTACC	AGAAGGTAGA	ATTTATGTTG	CTCGCCAAGA	TCAACTCATT	GTGGGTTATG	120
TCACTTTCCA	CTATCCTGAT	GAAATTGAGC	GCTGGTCTAC	AGGTAAGCTT	CCATATTTAA	180
TCGAATTGGG	GGCAATTGAA	GTCAGCATCA	ATTTTAGGCA	ATTACAACTT	GCAGAAAAGC	240
TGATACAACT	TAGCCTTCTA	CACCAGAATT	CGAGAATTAT	ATCGGnATAA	CTACAGGATA	300
TTACCGGCAT	TGGGGGTTTA	AAAAATTCCC	AGTnAGAGGT	ATTnCC		346

45 (2) INFORMATION FOR SEQ ID NO: 858:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1176 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

	ATTACTATAA	TGAATCTTGC	GAGATATTTA	GAAGTAATGA	TACAAnataa	TGGACTTTAG	60
_	AATTTmAATT	TACAATAAAT	AGTTCTATGA	TTAAATGTCA	GTTTTATGAC	ATTTATTTAT	120
5	TGAAAATACG	AACGAATGaG	CGATaTGATA	ATATAGATAA	GAATGATTTT	AATTTAGGAG	180
	GCCTTTATGG	TGCATAATAA	AAACAATACA	АТТТТААААА	TGATCAAAGG	TGAAGAAACA	240
10	TCACATACAC	CTGTTTGGTT	TATGCGACAA	GCTGGCCGTT	CGCAACCAGA	ATATCGAAAA	300
						CGCTTATGTA	360
	ACACATTTAC						420
15	ACACCATTAA						480
	CATAATCCAA						540
	GATGTACCAT	*					600
20	CTAATAGGAT						
	TCGAAAAATT						660
	TTAATGAATC						720
25	GCCGAATTGA						780
	CGTTACATTA I						840
	CCGGTAATTT :						900
30	ATTGATGTAT						960
							1020
35	ACTAAAACAT 1						1080
33	GAAGAGAGAT 1				ACGGTAAACA	CATCTTTAAT	1140
	TTAGGACACG (1176
40	(2) INFORMAT						
	(<i>)</i> (E (C	A) LENGTH: 3) TYPE: nu	NESS: doubl	irs			

- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 859:

ATTTGGTGCA	TTGGTAnAAT	TGACCTGAAA	Gnaaaaagtg	GTTTAGTTGC	ACATTGAGTG	60
nAAGTGCGCA	GATGAATTAT	GTTGAAAACG	TGAGGAAGAG	CACCTTTGCT	GTTGGTGATG	120
AAGTAGACGT	AAAAGTATTA	TCTATTGCTG	ATGATGGAAA	AATTAGTCTT	TcAATTAAGA	100

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	AAAAAGCCGA AGATTTTGAA AAGAAATTAA GCAATTTCTT AAAAGATAGT GAAGATAAAT	300
	TAACTTCAAT CAAACGTCAA ACAGAATCTA GACGCGGTGG CAAAGGTTCA AGACGTTAAT	360
5	TAAAATAAAT AAAGACTGTT TCGATAAGGA ATATATTTAG AATGATGCGT ATCGAATAAT	420
	CGATTGCAGC GTTAGACAAT CTAAGACTGT TTCTTAAATA AGGAGCAGTC TCTTTTATTT	480
	GTAATGATAT AACTAAGACT TATACCATTT TTGAAAATTG TAAAAGTGAG GTGATGTTAT	540
10	GCAGTTAAAT AGTAATGGTT GGCATGTTGA TGACCATATT GTTGTCGCTG TTTCTACAGG	600
	TATTGATAGT ATGTGTTTnn T	621
15	(2) INFORMATION FOR SEQ ID NO: 860:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 544 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 860:	
25	TATATTAGGT ACTTGTGTTG GTATTGTGCC AGCTTTGCTG TCTACTATAA TTTCTAAAAG	60
	GTTTGAACAT ATAAAAGGGA AAGTGCTAGG TGTATTTAAT TTTGTGAGAT ATATTGGAAT	120
	GACTGTCGGT GCATTATTAA TTGGTATCAT TTCTCAGCCG TTGGTAGCCT TTTACTTCAC	180
30	AACTATAACT ATCATGTTAA TAGTAATATT TCTTTATATA AAGATAGTTG ACTTTCAGCT	240
	AAAGTATGCC AAATAAACTT AAAAAAGCAG TGAATCATTT CAATAGATGG AATGATTCAC	300
35	TGCTTTTTGT TTATAGAAAT TTAAAATTCA TGCCTTTATG CTAACAACAA TATTATTTTA	360
	CTCTCTTACG TTTGCCAATG TAACCGTATA GCAAAGTAAA TGACTGCGAT AATGATGACA	420
	ACATACATAL ACGTGAATAG GAAGGAAGAC CAGTCATCAA CATACCAAAG CTATCGCTCA	480
40	AAGTGCGnCT GGTAAATTAA ACCGAATTCC ANGATTGTAG GAACCCDATT AATGGAAATA	540
	ACGG	544
45 50	(2) INFORMATION FOR SEQ ID NO: 861: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 651 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 861:

	AATTTAAAAT ACATTTATGC TTTACCCATT CGAAAATACC TTAATCATTT TCATTTATAG	120
	CATTGTTTGA TTGAAGGATA AAAAGTTGTT GTTTACAATA AAAATAATGA GTATCTGAAA	180
5	TGAGGGATTC ANTATGACAC ATGTGGAAGT AGTAGCGACT ATCGCGCCAC AATTATCTAT	240
	CGAAGAAACT TTAATTCANA ANATTAATCA TCGTATTGAT GCAATAGACG TATTAGAATT	300
10	ACGAATTGAT CAAATTGAAA ATGTCACAGT TGATCAAGTG GCAGAAMTGA TTACAAAGCT	360
	GAAGGTTATG CAAGATTCAT TCAAATTATT AGTTACGTAT CGTACAAAGT TACAAGGTGG	420
	CTATGGGCAA TTTACAAATG ACTCGTATCT TAATTTAATA TCAGACTTAG CAAATATCAA	480
15	TGGCATAGAT ATGATTGATA TAGAATGGCA AGCAGATATT GACATTGAAA AACATCAACG	540
	AATCATTACA CATTTGCAAC AGTATAATAA AGAGGTGGTT ATATCACATC ATAATTTCGA	600
	AAGTACGCCT CCATTAGATG AATTGCAATT TATATTTTTn nAAATGCAAA A	651
20	(2) INFORMATION FOR SEQ ID NO: 862:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 401 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(0) 20102011 2211002	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862:	
30		60
<i>30</i>	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862:	60 120
30 35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862: TGTGAGTGGT AATGACACAC AAGCAGATTT AATAGGTTAT AGTTTTAAGT TTGACGGTGC	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862: TGTGAGTGGT AATGACACAC AAGCAGATTT AATAGGTTAT AGTTTTAAGT TTGACGGTGC GATTTCAAGG CAAGAGGCTT CTAAAGATGT ACATGCAGTT ATATTATCGA ATAAAACACT	120
<i>35</i>	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862: TGTGAGTGGT AATGACACAC AAGCAGATTT AATAGGTTAT AGTTTTAAGT TTGACGGTGC GATTTCAAGG CAAGAGGCTT CTAAAGATGT ACATGCAGTT ATATTATCGA ATAAAACACT ATATTTATTA GATGTATTAC AAAAATTACC GATAGATAAA ATGAATTCAT TGAATATCCA	120 180
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862: TGTGAGTGGT AATGACACAC AAGCAGATTT AATAGGTTAT AGTTTTAAGT TTGACGGTGC GATTTCAAGG CAAGAGGCTT CTAAAGATGT ACATGCAGTT ATATTATCGA ATAAAACACT ATATTTATTA GATGTATTAC AAAAATTACC GATAGATAAA ATGAATTCAT TGAATATCCA TCAAGAAATT ATTGATGAAA TGTCAGATAT CATTTTAATG TTATATCGTG AATATGCAGG	120 180 240
<i>35</i>	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862: TGTGAGTGGT AATGACACAC AAGCAGATTT AATAGGTTAT AGTTTTAAGT TTGACGGTGC GATTTCAAGG CAAGAGGCTT CTAAAGATGT ACATGCAGTT ATATTATCGA ATAAAACACT ATATTTATTA GATGTATTAC AAAAATTACC GATAGATAAA ATGAATTCAT TGAATATCCA TCAAGAAATT ATTGATGAAA TGTCAGATAT CATTTTAATG TTATATCGTG AATATGCAGG TATGTTTTTT AAAAGTCAGA AACTAATCAA CCAATTAAAA AGATTGGAMC AATAACATAA	120 180 240 300
35 40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862: TGTGAGTGGT AATGACACAC AAGCAGATTT AATAGGTTAT AGTTTTAAGT TTGACGGTGC GATTTCAAGG CAAGAGGCTT CTAAAGATGT ACATGCAGTT ATATTATCGA ATAAAACACT ATATTTATTA GATGTATTAC AAAAATTACC GATAGATAAA ATGAATTCAT TGAATATCCA TCAAGAAATT ATTGATGAAA TGTCAGATAT CATTTTAATG TTATATCGTG AATATGCAGG TATGTTTTTT AAAAGTCAGA AACTAATCAA CCAATTAAAA AGATTGGAMC AATAACATAA AATAATAAAA GGTATTCAAG TAGCCACATA GATGTGTTTA TTTGAATACC TTTTKGAATA	120 180 240 300 360
<i>35</i>	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862: TGTGAGTGGT AATGACACAC AAGCAGATTT AATAGGTTAT AGTTTTAAGT TTGACGGTGC GATTTCAAGG CAAGAGGCTT CTAAAGATGT ACATGCAGTT ATATTATCGA ATAAAACACT ATATTTATTA GATGTATTAC AAAAATTACC GATAGATAAA ATGAATTCAT TGAATATCCA TCAAGAAATT ATTGATGAAA TGTCAGATAT CATTTTAATG TTATATCGTG AATATGCAGG TATGTTTTTT AAAAGTCAGA AACTAATCAA CCAATTAAAA AGATTGGAMC AATAACATAA AATAATAAAA GGTATTCAAG TAGCCACATA GATGTGTTTA TTTGAATACC TTTTKGAATA GAAAAGAGAT ACTGGCAATT TTACTAACCA GTATCTCTTT T	120 180 240 300 360

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 863:

ACAAAGTAAT	CAATATGTAA	TATAAAATAC	ACTGGTACTC	TAATATAAA	GATGATAAAA	120
TTAATTTTAA	TTAGATAGAG	TTGCTTTGTG	TTTTTAACGC	nGATGCTACT	ACTTATCTTA	180
ACAGTTGATT	AAGTAAATCA	TTTAACAGCG	AGATTATnCA	ACCAGGGGGA	TGACTTAATG	240
AATTTATTCA	GACACCAAAA	TTTAGTATCA	GAAATTTAAT	GTCGGTATTT	TTTCAGCTTT	300
AATGCCAC						308

(2) INFORMATION FOR SEQ ID NO: 864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1827 base pairs
- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 864:

TTCTACATCT	TAAACGATGA	CCTAACTATG	ACGTTAATCT	GGAAAGATGG	GGAGTTGCTA	60
GTATGATGTT	GAAATTTAAA	GCTTGGGATA	AAGATAAAAA	AGTTATGAGT	ATTATTGACG	120
AAATCGATTT	TAATAGTGGG	TACATTTTGA	TTTCAACAGG	TTATAAAAGT	TTCAATGAAG	180
TAAAACTATT	ACAATACACA	GGATTTAAAG	ATGTGCACGG	TGTGGAGATT	TATGAAGGGG	240
ATATTGTTCA	AGATTGTTAT	TCGAGAGAAG	TAAGTTTTAT	CGAGTTTAAA	GAAGGAGCCT	300
TTTATATAAC	TTTTAGCAAT	GTAACTGAAT	TACTAAGTGA	AAATGACGAT	ATTATTGAAA	360
TTGTTGGAAA	TATTTTTGAA	AATGAGATGC	TATTGGAGGT	TATGAGATGA	CGTTCACCTT	420 .
ATCAGATGAA	CAATATAAAA	ATCTTTGTAC	TAACTCTAAC	AAGTTATTAG	ATAAACTTCA	480.
CAAAGCATTA	AAAGATCGTG	AAGAGTACAA	GAAGCAACGA	GATGAGCTTA	TTGGGGATAT	540
AGCGAAGTTA	CGAGATTGTA	ACAAAGAACT	GGAGAAGAAA	GCAAGCGCAT	GGGATAGGTA	600
TTGCAAGAGC	GTTGAAAAAG	ATTTAATAAA	CGAATTCGGT	AACGATGATG	AAAGAGTTAA	660
ATTCGGAATG	GAATTAAACA	ATAAAATTTT	TATGGAGGAT	GACACAAATG	AATAATCGCG	720
AAAAAATCGA	ACAGTCCGTT	ATTAGTGCTA	GTGCGTATAA	CGGTAATGAC	ACAGAGGGGT	780
TGCTAAAAGA	GATTGAGGAC	GTGTATAAGA	AAGCGCAAgC	GTTTGATGAA	ATACTTGAGG	840
GAATGACAAA	TGCTATTCAA	CATTCAGTTA	AAGAAGGTAT	TGAACTTGAT	GAAGCAGTAG	900
GGATTATGGC	AGGTCAAGTT	GTCTATAAAT	ATGAGGAGGA	ATAGGAAAAT	GACTAACACA	960
TTACAAGTAA	AACTATTATO	aAAAAATGCT	AGAATGCCCG	AACGAAATCA	TAAGACGGAT	1020
GCAGGTTATO	ACATATTCTC	AGCTGAAACT	GTCGTACTCG	AACCACAAGA	AAAAGCAGTG	1080

AGTGGTGTAA	GTAGTAAAAC	GTATTTAGTG	ATTGAAACAG	GCAAGATAGA	CGCGGGATAT	1200
CATGGCAATT	TAGGGATTAA	TATCAAGAAT	GATGAAGAAC	GTGATGGAAT	ACCCTTTTTA	1260
TATGATGATA	TAGACGCTGA	ATTAGAAGAT	GGATTAATAA	GCATTTTAGA	TATAAAAGGT	1320
AACTATGTAC	AAGATGGAAG	AGGCATAAGA	AGAGTTTACC	AAATCAACAA	AGGCGATAAA	1380
CTAGCTCAAT	TGGTTATCGT	GCCTATATGG	ACACCGGAAC	TAAAGCAAGT	GGAGGAATTC	1440
GAAAGTGTTT	CAGAACGTGG	AGCAAAAGGC	TTCGGAAGTA	GCGGAGTGTA	AAGACATCTT	1500
AGATCGAGTT	AAGGAGGTTT	TGGGGAAGTG	ACGCAATACT	TAGTCACAAC	ATTCAAAGAT	1560
TCAACAGGAC	GACCACATGA	ACATATTACT	GTGGCTAGAG	ATAATCAGAC	GTTTACAGTT	1620
ATTGAGGCAG	AGAGTAAAGA	AGAAGCTGAG	CGCAAATACG	AGGCACAAGT	TAAGATAAGG	1680
AGAGATGGAG	ATGCCAAAGA	AAACGGTAAC	GATTGATGTA	GATGAAAACT	TATTAGTAGT	1740
AGCTAGTAAT	GAAATATCAG	AACTATTATA	TGAaTATGAC	AGTGAGTtAA	TGTCAGCTGG	1800
ATGGAAGATG	GCGATAATAG	GGATATC				1827

(2) INFORMATION FOR SEQ ID NO: 865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 865:

TCAATTGCAT	CATCATATGA	AATTCTAGGG	AATGGTGTCG	CAACTTTTTC	AAGTTTTGAT	60
GTATCACGCT	CTAAAATTTT	CAACTCTAGT	TTACAATTTT	CTAAAACTGA	TTTTACAACA	120
TGTGTTACAT	ATTGTTCTTG	AATTTCTAAA	CTTTCAGCAT	GATTTGTGAA	AGCCATTTCT	180
CCTTCAATCA	TCCAGAACTC	GATCAAGTGT	CTACGTGTTT	YTGATTTTTC	AGCTCTGAAA	240
GTTGGACCAA	ATGAAAATAC	TTTTCCGTGT	GCCATTGCTG	CAGCTTCTAA	GTATAACTGA	300
CCACTTTGAG	ATAAAAACGC	ATCTTGATCA	AAGTATTTAG	TATGGAATAA	TTCACTTGTA	360
CCTTCTGGCG	CACTTGCTGT	CAAAATTGGT	GGATCAACCT	TTGTAAATCC	ATCTTTGTTG	420
AAAAATTCAT	ACGTTGCACG	AATAACTTCA	TTTCTAATTT	TCATTACAGC	ATGTTGTTTT	480
TTAGAACGTA	ACCATAAATG	ACGGTGATCC	ATTAAGAATT	CTGTACCATG	ATTTTTAGGT	540
GTAATCGGAT	AGTCATGCGC	TTCTGAAATA	ACTTCAATTG	ATTTCACTTG	CATTTCGTAT	600
CCTAAGTCAG	AACGATTATC	TTCTGTAATT	GTGCCTGTAA	CGTATAGAGA	TGATTCTTGA	660

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TGCATAAAGC	CTGTTCCATC	ACGTAATTGT	AAAAAGGCGA	TTTTACCACT	TGAACGTTTA	780
TTTGTTAACC	AAGCACCAAT	TGTAACGTCT	TGGTTTAAAT	GATCTTTCGC	TIGTTTAATC	840
GTTGTTTTCA	TAACCATTCT	CCTATTTATT	TTTTCGkTAT	ACAATACTCA	TTCATTTTAA	900
CAAAATCCGC	TTTCAAGTTC	TAGAACTAGA	CTAAAAGATA	ACGEGTAAAT	GGTAATGATT	960
TACGCACAGA	TTTGAACATT	TTATATTTAA	AAGACAATAC	AATCATCAĠT	TTCAGACAAA	1020
ATATATAATA	AAGCCTCAAT	ATTATTAGTA	TGAAGGTCGT	TTTTTGTnCT	AACATTCAAG	1080
TTTAATTATA	AAACTCAAAT	TTTGACGACC	AAACAAAAAT	TCTTGTAACA	GAACATAGCA	1140
CATGTCATGT	CACAAGAATT	TTACTTTGTA	TTTCACTTTT	TCTTTTTTTG	AATTTGTCTT	1200
AATAATTTTC	CAAACTGTTG	AATGTCGCCT	TTTTTCTGAC	GATAATTTTC	AAGTGTTTGT	1260
TCAAAAAAGT	TTTTATAATT	ACTGTTTATG	AGTCGATCAT	CAAATGAAAC	TATTATGCCG	1320
CGATCATTTT	CATTTCTAAT	TAATCTTCCA	AGTCCTTnGT	CTAnAACGTG	TAACTGCAT	1379
(2) INFORM	ATION FOR SI	EQ ID NO: 8	66:			

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 450 base pairs

(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 866:

Anggttntaa	TTGGATATTG	AGTACGTTGT				450
aACCATA ATC	TACTTTALCL	TTCGAAAACA	CTCCLTATCA	GTTATTAAAT	CAATTTTATG	420
CAATTCGCTT	ACTTGGACCA	GGTGGATGCG	CTTTTAAAAA	AGTTTGAACA	AGAACATCTG	360
GATGTGGTGA	TACTTTAGCA	ATCATCAAAC	CAATTGGTCC	GTAACCACAA	CCAACATCGG	300
TTTTGTTTTT	TTCAACTAAG	GCTAGCGCTC	TGTGATTAAC	ATCTAGCATT	GTAATTGAAT	240
CTTCCACAGC	AGACAAAGCA	TCACTTTCCT	TTACGATCAC	ATTATCAATA	CCATTTAATT	180
GCACGGTTTC	TTTCCCTGCT	CTTATTGGTG	GATTGGTTAA	AATAAAATCA	AAACTTTTGT	120
TTACAACGAA	TAGTTCACCG	TTCGAGTCTA	ATCTATGTAA	TGCTTGCTCG	AATATACGAT	60

(2) INFORMATION FOR SEQ ID NO: 867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 867:	
5	AATGTTAACA ATATAGCACC AATTAACCCC GACATGATAA TAACGTGTAA TGTTTTATTT	60
	CCTATTAATT GTCTCGCAAT ATGAGGTGCA ATTAATCCTA AAAAGCTAAT ACCACCGACA	120
	ACTGAAATTG CGGATCCTGC TAATATTACT GCTAAAATTA ACAATAGCAT TTTAATAGTT	180
10	TTAACTTTTA AACCGAGTGC GGTTGCAACA GCATCACCTA GATTCAATAC ATCTAATTGA	240
	TAACTCCATA AAATGATGAT GGATCGTTAT TAAAACCAGG GAATATAGAT AATATCCGCA	300
	TATCAGGCCA TATAGCTACC TGTCACCAAC AGGTTTnTGC TCCAnGGTTC TnTAATAAGA	360
15	CGCACACGCG ACAATGCGCT TGCTACCATT AGGCAGCTTG	400
	(2) INFORMATION FOR SEQ ID NO: 868:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1132 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 868:	
	AATCCHTHAA GTGCCATAAC ATCATCTCCT AACATCTTTA TTATACATCA ACATTTTATA	60
30	AAAATAACnT CTTATGATAA AAATGAAAAT ACTAATTTTA ATGAGAGCGT CTTAAGCCGC	120
	AATTGATAAA ACATATGCTA CAATATTTTT AAACACTATA CAGGAGGTAC TCTATGACAA	180
	AATATACATT TAAACCTAAA GATTTCAAAG CGTTCAACGT AGAAGGCTTA GACGCACGAA	240
35	TGGAAGCTTT AAACGAATAC ATACGACCAC AACTCCGTGA ATTAGGAGAA TATTTTAGTG	300
	ACTICITIAC AAGTCAAACT GGTGAAACAT TITATCCTCA CGTAGCAAAG CATGCTAGAA	360
40	GAAGTGTGAA TCCTCCTAAA GATACATGGG TTGCTTTTGC AACAAACAAA AGAGGCTATA	420
	AAATGTTACC TCATTTCCAA ATTGGTATGT TTGAAGATCA ACTGTTTGTT ATGTTTGGAA	480
	TCATGCATGA AGCAAAAGAT AAAGCAACaC GTGCAAAAGT TTTTGAAAGA AAATTTAAAG	540
45	CTATTCAACA ATTACCTGAT GATTATCGTG TTTGCTTAGA TCATATGAAA CCTGATAAAC	600
	CATTTATTAA AGATTTAACG GATGATGATT TAATAGAAGC GATACAAAGA GCCATCAATG	660
	TGAAAAAGG TGAATTCTTT ATAGCGCGTG CAATCACACC ACAAGATAAA AGATTAAAAA	720
50	GTGACAAAGC ATTTATTGCA TTTTTAGAAG AAACCTTCGA TCAGTTCTTA CCATTTTATT	780
	CTGCATAAAT AACTTTGTTT AAATAATAGA GCACTTAATC ACATCCATGA TTTCGTGCtC	840

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TTETTTCTTA ATATTAAATC GAACGTECAA CATAATAATT CATACTTTTA AAAAAATTAA

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GGTGAGTCAA AATGAATAAT AAACGACATT CAACAAATGA ACAATTAAGT TTAGACGAAA	1020
TARACARTAC ARTTARATTC GATCATCGCA GTTCARATAR ACAGARATTT TTATCATTTC	1080
TTGGACCTGG GTTATTAGTC GCTGTTGGTT ACATGGATCC CGGAAACTGG AT	1132
(2) INFORMATION FOR SEQ ID NO: 869:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 418 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 869:	
CTCAATGTAT TGACTGTGAT TTGGAGTGTA TAATGCTACT GTTTTGTCTA TAGCCATCGC	60
ATCAAATATT ATATTTGAGT AATCAGTGAT AACGACATCA GACATTAGAA TTAAGTCTTG	120
AGCACTAAGA TACTTTGGTG CAACAAGCGC CTCTTCTGGT AAGATCGCTT CATCAACACC	180
CTGAACCACA ACATGATAGG CTTTGAATAA AGCATCTGAT AGTGGTAATT GTTGCGCACT	240
CACTAATCCA ATAGGTGCGT ATAATAAAAC TGGTTTTTGA TCATTTATTT TAAACGATTT	300
CTTATACTGT TGTTGAGTAG TACTTTCGTT ACTCTTTTGT AGTAAATATT GGTGTTTAGG	360
ATTACCATAA GCCAATACAT TGCTTGGTGA CTAGGAAAAG nCGTTTGATA AAAGGGCT	418
(2) INFORMATION FOR SEQ ID NO: 870:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 587 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 870:	
GAGTNIGITA CAGIAATIGA TITTATIGGI AATINIAAGA CAAATIATII AATICCGATI	60
GCGCTTTCTG GGGATCAATC GCAANATAAA GATAATTATA AGAAGTTTTT AACGAATAAC	120
GATTCGATTA ATGGAGTATC TACAATTAAT TTTGAAGAAG TTGCTAAAAA ACAGATTTAC	180
AATTCATTGG ATGCAGTATC ATTAAATCAA AATAAATTAA TATTAAAAGC TTATGAAGAA	240
GTTGAAAATA GATTGGGACA CATGCCGTTA CTAATGGATT TCATACAACA ACATTCTATA	300
GATCCAAGCG TTATATTTTC TAAATTTAGT AATTATTACG AGTTCTTAGT GAGATATAAA	36
AAAATAGATA CATTATTGAC GGAAAATGAA TCTAAAAATC TGGTTTTCTT TTCAAGGCAA	42

	TTAACATATG ATGAATTAAA AAATAAAATG TTGAACGAAG TTAAGGATAT AACAGAAGAT	540
	GATATAGATA CTTCATTAAG AATTTTAGAT TTTTCATTTT ACAACGC	587
5	(2) INFORMATION FOR SEQ ID NO: 871:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 971 base pairs (B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 871:	
	CTACTAAACC AGGTAATCGG TAGAATCCAA GCAGGAATAA ATAAATTAAT GCNACACCAA	60
	TAAACGATGC AAACACAGTn TTATCTAATG CATCTTGACC AAATTGGGCA CCTACTGAGT	120
20	TTGAATAAAT TTCTTTCAAG TCAACTGGTA AAGAACCTGC ATTTAACAAT kCGGCGATTT	180
	GTTTTGCTTT TTTAACGCCT TCTTGTCCTT TAAATCCACC CGAGATTTCT ACGCTATCAG	240
	AATTGATTGG TTGATCAACA CTTGCTGCAG AAATAAATTT AGGGTTTTTC TTTTGTGCTT	300
25	CTTTTTTATA GCTGTCACCT TTTTTGAAAT CTAACCAAAC AACCATGACA TTATCACGTT	360
	TCTTAGAGAT TTCTTCCGTT ACTTTTTAA ATTTGTTTTT GTCTTTTACT TTAAAAGTAA	420
	CTGTAGGCTG GTTTGTTTCC tGtTTAAATT CTTGtTTGGC AGATCCCTGT TTAATATCAG	480
30	AACCGCTTAA TTTLACTTTA TCTTCTGCAT CGCGAATTGT TAAATTAGCT TGAGAAGATA	540
	AAATTTTACG TGCTTCATTC TGGTCTGTTA CACCAGCAAG TTGTACTCTA ATTCTATTAG	600
35	GTTCTTCAAC TTGAATTTTA GGTTCCGAAA CACCTAAAAC GTTAACACGA TTTTCTAATG	660
	TTTGCGCTGT TGATTGTAAG GCTTTTTTAT CTATTTTGTC GCCTTTATTT AAAGGATCGA	720
	CTTGATAAAG CACCTCAAAT CCACCTTGCA AATCAAGTCC TAAATTGmCA TTCTTTATAA	780
40	CACTTTTATA AGTTGCAGCC ATTCCGGCAA ACAACAATAC GACTAAAAGC AAGAACGCAA	840
	TTATTCTACT ACTTTTCTTC ACATGAACAC CTCATTATTT ACGTATGTAT TTAGAATACT	900
	TGAATACTAT TTTATAACGC AAGTGAAATC TTTCTTACAA AATTTATTAG CCTTATACAT	960
45	ATTAACATAC T	971
	(2) INFORMATION FOR SEQ ID NO: 872:	
	(i) SEQUENCE CHARACTERISTICS:	
50	(A) LENGTH: 636 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
<i>55</i>		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 872:	
	CTGGTTAACA ACATCTGGTT CGGCATCTCC TTAGCTTCCA CTAAATCTTG GATGTCTTGG	60
5	NNATCTTGCG CAAGTNGTGC TTTGGCTTGT TCAATTECTY CTTTAGTCAT CGCATTGTTA	120
	ATGCCGTTAT GACCTTGTTG AAGTATTTGA TTAATACGAT CTTTAAGTGC TTGTTTTTCC	180
10	TTATCTGTTA GATTTGGATT TCGATCAATT TCGTCAATTA ATGCTTGAAC TTGCTTATCA	240
10	ACGTCTTTAT TGGCATCAAT TTTTGCTTTT GGTATTTCAT TGGCATGCAC TTGTTCAATC	300
	GCGTGGTTGC CTGCTGTTTG AACTTGAGAT ACAGCCTGAT TACTTGTTGC TTTATTAATG	360
15	TTGTTGATGA TGCTGTTTGC CAATTCTTCT GCTTTATTTT TCGCAATAAG CTTGTCTTGA	420
	TCCGTCGCAT TTGAAGCTTC GATTTCTTTT AGCTTATTAG CTAAAGCTTG ATTAATAGAT	480
	TGAATTGCCT TGTCTTTAGC ATCTTGTAGT CGTTGATCAC CATTAAGATT ATGGATTGCA	540
20	TCATTGACEG CTTGGATTGC GCCATTGATA TCATTCACAT ETGTGTATCA CTATTTAGCA	600
	ATGTATTTGC TAGACGTTGG CATCATCGAA GTTTGT	636
	(2) INFORMATION FOR SEQ ID NO: 873:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 659 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 873:	
35	CTCTGAATGC ATTCATTAAA CGCTGGGTCT CTTTATATGA AACGTATTTG TCATTTTTAG	60
00	AACTCAATCC GTAAAAATTG TCAACTTTCT TTTTAATATT ATCGTAATCA ATGGTTACAT	120
	TACTTAAATC AATATCTAAA TCTATATTTT CTGCATCTTC TTTAAAGCCC GCTATACTGA	180
40	AAAAGCCTTC AATCGGCTGA TCAATCATTT CAATATATTT TAAAGCTGTG ATTGAACCTA	240
	AACCATGTGT TACAAAATAT GTATCCTTTT TGCGTACATT AATTTGTTTC GTCATAGCTT	300
	CAATCCACTG ATCCACTGTC TTCGCTtCAG GGGATTCAAA ATTAAATAAT GTTACGTCAT	360
45	ATCCTTCTAA AGTTAAGTTA TGCTCCAACC ACTGATACCA ATGATTTCTA CTATTTCCAT	420
	GCATAGAATG TACAATALTA CATCTGTCAT CTCATTCTCT CCTTTCAACT TACTACTTCT	480
	TTTCTATTTT TAAAAAAATG ACTGATTACC TATAATTGTA AAATAAAAAC ACCTTAATTA	540
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GAAATGTTAT ATCGCAAAGT GACATTTCTA ATTAAAGTGT ATTGTCATCA TTTCAATATC

ATTCAAAAAC AGCTAAACCT TTGTCTCTGC TTCAATTTCA CAAAAATAAT TCCCGCTGA

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659

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 base pairs

5	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 874:	
	AAAATAAAAT CCATTTTAGT ATTCGTAGAA AATGAGAGCC CCCTTTACCA CAATATGTAA	60
	ATGTATATTG TGAAAAGGGG GCTTTTATTT ATGACATAGT TGTTCAACTC ATACATTCAG	120
15	TTGATAATGC AGTGCGTTAT GCAGCTATCC ACTTCATATG TATGGCGCAT ACTTGATATA	180
	TGAATATCAT CAAGATTTTA AAAGTATCGC TAATTTTAAA GTCTTAAAAC GCAGATTAAT	240
	GGTCATGATG TGTTAnTGCG TTTTGGTTTT TAGAGCCACG TAATTCCCAn GGACATATAG	300
20	GAGGAACCAT TCCAC	315
	(2) INFORMATION FOR SEQ ID NO: 875:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 482 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 875:	
	TACACGACCT TGTAACTCAG CTGCTTTATA AGCTAGGGCG ATGTTATCAA AGTTGGATGT	60
35	ACTTTGAGCT TGGCATTTCG TTAATACTTT TAACGAAGGA TTTAATATAT GTCTGATACG	120
	TATATATTGA TTATATTCAA TTCTTAATTL GGATAAGATT GCTGATAATT TGAAGCAATC	180
	GGAGCTAAAT GGATCGAAAA ATGAATAAAT TTCGATTTTA CTTACAGGTG ATAGATTGAT	240
40	ATCTTCACGA CTCTTATTTT CCATTAWTCG TAATTCTCCA GCCATGTTTA TTCACCTACA	300
	ATTAATTITA GGAATTCACC ATATGATTAG CAGTTAATCT TAAGCGCTCA AATAAATAAT	360
45	CTCCAACACC TTGTGGAAAC caGCgCGaTT AATTGCTGTC TGCATATTTT CTAGCCATGC	420
	ATCTCTTTCA AATTCAGTGA TTGTAAAATC TATATGTCTT TTTCTTAGCA TAGGATGTCC	48
	GT	48
50	(2) INFORMATION FOR SEQ ID NO: 876:	
55	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 670 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double 	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 876:	
5	ATGCAATTGA ATTCTTAAAA GCAGAAGGCT TTGATGATAT TGAATGGGGC GAAGATTTTG	60
	GTGCGCCACA TGAAACAGCC ATTGCTAATC ATTATGATTT ACCGGTGTTT ATTACTAATT	120
10	ATCCAACTAA AATTAAGCCT TTCTATATGC AACCAAATCC TGAAAATGAA GAAACTGTAT	180
,,	TATGTGCAGA CTTAATTGCA CCTGAAGGAT ACGGTGAAAT TATTGGTGGA TCTGAACGTG	240
	TGGATGACTT AGAATTGTTA GAACAACGCG TTAAAGAACA TGGATTAGAC GAAGAAGCAT	300
15	ATAGTTACTA CTTAGACTTA CGTCGTTATG GTAGTGTGCC ACACTGTGGA TTTGGTTTAG	360
	GTTTAGAGCG TACAGTAGCA TGGATTTCTG GTGTTGAACA CGTTCGTGAA ACAGCGCCAT	420
	TCCCAAGATT ATTAAACCGT TTATATCCAT AAGTTTTAGG GTCGTTACTT AAAATATATA	480
20	TTATGATAAT AAAAAGAATC GTCCAGCCTA TATTAATAGC TGGGCGATTT ATTCTTGGAA	540
	AATGAAGATT GATAACGGCT TATATTAATC ATGAACAAAC TTTTGTTTAG TAACTATATT	600
	TGGAAAATAA ATAGTTCATC TGATTATCCA TAAAGTTCAT TGTTAAAATC TAGTGTTAAA	660
25	AAATACTGTT	670
	(2) INFORMATION FOR SEQ ID NO: 877:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1258 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	\cdot	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 877:	
	TGCAAAGTAA ACTGGATGGC TnTCTTGCCG CCAAGGATCT GATGGCGCAG GGGATCAAGA	60
40	TCTGATCAAG AGACAGATCC TAACCTCTCA TTTCCGATAA GTTTAGTATG TATTATAGGT	120
	GATGATTnTC TTGTTTTCAA CCTTATACAC AATATTTTTG ANATTTATAT TATATTCATA	180
	TAAGGAAGGC GATTAATTAC GATTCATCAT TATATCTCTA CGTGTTAATT TATTAACCLA	240
45	TACTATATTT ATCAACACAA CAGTTTTTCC TTTCATTTTC AAACATAACA GAAAAAGCCT	300
	GAGACATACT TAGTCCCAGA CTGTTCTATA ATTAATTAAA GATATAACAA GGTTAATCAT	360
50	TCARAGCTAA CATCACATTT ATTCACTGTA ATTTTTCATA AAGAATAATA ATGACTGTAA	420
	TTCTATACCT AAGTCAATTT GATGTACTTG CACATCTGAA GGCGTATTAA TTCTACCAGG	480
	AGTGAAGTTT AAAATACCTT TCACACCAGC TTGGACGAGT TCATCTGCAA CTTTCTGTGC	540

TAATTCATCG	TTATCTTTAA	CAATAACGTT	CCCTATTTTC	TGGCCAATAA	CATCTTCTTT	660
TACGTCAAAC	GCTTCTGTAA	TCGTCATATC	GTCATGTATT	GAAAAGTTAT	ATGTGAGCAA	720
AGCTTTCCCT	AGGTTCCCAA	CTCCGACAAT	TGCGATTTTG	ATCATGTCAC	TCTCGCTTAG	780
TTCAGATTTA	AAGAAATCCA	ATAAACTATC	TATATTATAT	CCGTaCCCTT	TTTLACCTAA	840
TTCGCCAAAA	TATGAAAAGT	CACGACGAAT	TGTtGCCGAG	TCAATTTGTa	ACGCATCGCT	900
AATCGCTTTT	GAATTTACAC	GATCTATACC	TTTAGATTTT	AATGAACTGA	CAAATCTATA	960
ATATAACGGC	AAACGTTTTA	AAGTTGCTCG	AGGAATTTTA	ACTTGGTCAC	TCATTCGCTA	1020
TTTCCTCCTT	CGTGTTTGAA	TGAATTATAT	CTATGTATTC	AAACGAGTTA	GAGCGTAATT	1080
GTTAGATTAT	TAAAArACAA	ATAATTGaTT	ACAATGAATA	CCTAAATATT	ATACATTAWT	1140
GAATTTTAAA	AATAAATATC	TTAGTTTCAA	GACGGCGTTT	TATACTGTAA	AATGGTTATT	1200
AATGTAATAA	TTACGCTTGT	TTCATAAGTT	AATAAAATTT	GAGAAGACGA	AGGTGAAG	1258
(2) INFORM	ATION FOR SI	EQ ID NO: 8	78:			

im old in tok bbg ib no. 070

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 878:

AAACAATCCC	Cnccaaagta	ATTCCACCAC	TAATTGTAAA	TAACTTTGGA	AAGGATGTTG	60
TTTGTnATTC	CCATGGACAC	ATGCCATCTn	ATTTAAGTTT	TATACTCTAT	TTTTCTGATG	120
TCTTGATTAA	TTGCAAGCGG	TCTTGCGAGC	CTTGTTCAAG	CTCATATTCT	TTATCTACTT	180
GCTTACCGTT	TTCryTTATT	AATCTTACGG	TTGCGGTAAT	CTTATCACCA	TGTTTTTCAG	240
CATCTATAAT	TTGTGGTGAA	CTAATCATCA	TTAAACTTCC	TTTAGATACA	CGCTTCTTTA	300
CATCATCATA	AAAAGATGAT	CCTTTTTTTA	TATATGATGA	TACAAAATCA	AAATCCGACT	360
GATTAAACGC	AGCATTATTC	GCTAAAGAAT	ATCCAGCAAA	GAATTCTATC	AATTTGTTCT	420
TCAAGCTGTT	TTCTTCTTTT	TCTTTCTTTT	CAACATAGTC	TTCGATATCT	TCACTGTCAA	480
AATTCAAAGT	TATCTCTGTA	TTGTATTTTA	AATCGCTAAG	CTTTAATCGT	CTTCGTCTGT	540
GATGTA						546

(2) INFORMATION FOR SEQ ID NO: 879:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 870 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 879:	
	TTTATGAATT TTTTATGTAA CATTAAATAT TCTTCTGGCA ATCTTCCLAC TATKTCTKTT	60
10	ATATATCCTT CTTCTCCTTC TTTAAATACT AAACCTGTGG GAGTTAGTGT GTTATACCTA	120
	ATTTCTATCT CATTCAAATG ATCATTCAAA AGGTCAAAAA ATTCTCTATT AAAATAACCC	180
	CATTTCCCAT TTTGTAATAA ATATTTCTTT CCATCTTCCA TTTCAACTTC TGCATGTAGT	240
15	ATCGTTTTTA GTaGCATATT ATTTGAATGC CCCAAATTAT CKATCACKTC AATTCTGACA	300
	TCATTTATAG AATTAACGTC ATATTTTAAT AAGTAATCTC CTATTTCAGT GATGTAATCA	360
	ACTTCAGGAT CAGTCGCATC AAATGTCTCT AATGTATTAT TTTTAAAAGA ATTTATATAT	420
20	ATATTGACGT CGAGCATATC ATCTAACAAG AGTATCATAT TACTTAGTTC TAAAAATCTT	480
	GATATATCTA TAGATATATI TTCTGTAGTT GAAGAATTCG ATAGTTTTTT TAGCAATAAA	540
	GTATCTAATA CTTCTATTTT ATTCAAGTCT TTTAAAGTTA CTATTCTAGG AAATTCACTA	600
25	ATTITITGAG GAAGATTAAT AATAGCGTIT ATTICTITGA TTATCACACT AATTITATCT	660
	ATGAATTGCT GCTTTCTATT CGGLACACGC AATGAAATAC TTGTACCACA AGTCCATTGL	720
30	TTTTCCaAAA ATTTGAGGaT TCTGTGGATG tCCTTGGACT GGATATATAA GATTCTGAAG	780
	GTCTAACGTA ATCTACACTA TTCCTTCTAT AATTAACAAT CTCTTTAAGC CTGTTTTGTT	840
	GAAAAAATT AACATTTTA nTAACTAnGG	870
<i>35</i>	(2) INFORMATION FOR SEQ ID NO: 880:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 880:	
45	GGTTTACATC TTTATCAACT GTAATTTCAT TGACATCTTC ATTCATATTT AAAACACCAT	60
	TAAATGTCCC TGAATATTCA CTTGTTTGTT TAACTGTGGC AGTGACTTGT CGTTACCATA	120
	TGTCATCATA TATTGTGCAA ATGTTAAAGT CCCCATTGAG TTGACCGACA AAGTTGAATT	180
50	TATCGAATTG TATTCAGATT GTAAACTTAG CAGACATTTT TAACCACGAG CATTCTTATC	240
	CARATAGRICC TIGICTGTTA TITTCAAGTC AATTITCACA ATAGGATCAC TGCATCTTTT	300
	CUMUTABILE TIGICIGITA TITICARATE ARTITICACA ATTICACA ATTICACA	

	ACCCTCTTT TCTGCTnCTC ACATAACTTT CAGATGGACT	400
	(2) INFORMATION FOR SEQ ID NO: 881:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 881:	
15	AAGATATTGC GAAAAGAAGT GACAGTAACA GAGGAATTTC AAAATTTATT CAACCATATA	60
.5	TTGAAAATTG ATGAAATGGT GCATGCAAAT GAAGCGCGTA TTGCGTATGA AGCAGACATG	120
	CGAAAACCTT TATATAGTAA ACGCATTTAT CAAAATTTAA CATTAGACTC TATTGTTTTT	180
20	AGAAATACAT TGAGATATAC AGCGATTATG ATGATAGCGG ATATTTATTG CGTTAATGTT	240
	TGATTTTGAA AAAGCATCCT GGATCCCGTT ATCTGCACAT CCAnTATTCC TAGGGCCATC	300
	Ancetatace atgreaters agagaggtat ggn	333
25	(2) INFORMATION FOR SEQ ID NO: 882:	•
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 617 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 882:	
	ATTGAAAGAA AAACTGACGT ACTTATCCGA TGATAAAATG AAAGAAGTAG ATAATGCACT	60
	AATGATTAGT TTAGGGCTGA ATGCAGTAGC TCACCAGAAA AATTAGGCGT CTATTATATG	120
40	TATTTTCAG AGATAAATAA AATATTGATA TAAAAGACAA TAACTTTATA ATAATTATAA	180
	CTATTTCTAA ATTCTGTACG AAGAATTTTC TTATAAACAA AGATTTTAGC AAATACCAGT	240
	TATGATATTC ATATTTTTA TTATAAAAGG ATGTCTTAAG TTTTTTAGGC TTTAGGTATT	300
45	CCATCCTAAA GTTTTTTTAG CTTAAAAGTA TCATCTACAG CAAAATTGCA AACGACAAAA	360
	TTGATAAGTG CAATTAAATA AATGTTAGTA AGTGAATCAT AATTATCCTT GCTTAAGCAT	420
50	TTGCTTTGTA AGGGAAGTGA GGAGGCAACT AATCGTGGAA GAATTTAAGC AACATTATAA	480
	GGGTTTAATT GATGAAAGTT TAACGTGCCA AGATAAAGTA GAATTGATAA AAAAGTGTGA	540
	GAAATACACT GACGAAGTGA TTCGTAAGGA CGTCTTGCCT GAAGACATTG TCGATATTCA	600

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(2) INFORMATION FOR SEQ ID NO: 883:

5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 583 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 883:	
	GTTGTATTAA AATTTTCAA TTTAACAACG AAACAATACG AAGAAAAACA TATTACTGAG	60
15	CCACTGGAAT TGACGAGCTT ATTAGGTAnT ATTTCTCGTC TAGACAATGG TCATTTTGCA	120
	CATTTGCATG CTACTTTCGG TACTCAATCA TATGAAACTT TTAGCGGACA TCTCGCTAAA	180
	GCAATTGTTT CTGCAACTGC TGAAATCATT CTTACTGTAA CTGATTTGGA CATTCAACGT	240
20	TCATTCAAAG ATGCAGTCGG TTTAAATTTA CTTGATCCTC AATAGCACTT TACTTTTTAG	300
	TTGAATCAAA TTTTATTACA AGTTATCATA AGTGCTTAAT CATAAATGCA TTCTCGTTTA	360
25	TTAATATACT TCAACGAGTT AAATTAAATT TTTAATTAGG AATTGAATGC GTTTATAACT	420
23	ATCACATTTG AATGAATAAC TTTTTCATTA GAAAGTAGTG TKTATTATTG ATGCAATCTC	480
	GATACATCGC TAGAATTTAC TTTtaATTTT ATTTATCGTC TCCCTTnTTG AGACTAAAAT	540
30	TTTTCAATTT ATGACTTTAA ATTTGTTTTT AGCATATATA CCT	583
	(2) INFORMATION FOR SEQ ID NO: 884:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 524 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 884:	
	GCAGAGGGCT TACGATAAAA AGAAAAATCT CGCTCGCCCG CTTCAGTCAA ACTCACAAAA	60
45	GCTAACGCAL GWYTGCTYCA TTCGTGCGAT ACACTTTTGA TACATCTACA CCAATACTTG	120
45	ATATCGTTTC AATAATGCTA TCTCCAAATG CATCATTACC TAATTGTGTA ATCATALACG	180
	CTTGTTGTCC LAACTTTTGA ACTGTACAAG CTACATTGCA TGGCGCGCCA CCAATTTGCT	240
50	TCGTAAATGT TTGAACATCT TTTAAATTCG CATTTGTAAC ATTTGGAATA AAATCAATTA	300
	ACGCTTCTCC TATTGAAAAT AGACGTCTCA TTTATGTTCA TCCTTTAAAT CATATTTAGT	360
	AAATTGTAAA TATACTTGCC CTGATTCTGT TGATGTTTTA ATACCTAGTG CGTCTTCTGT	420
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	TGTATCAACA AAAATTTGTA ATTGCTTTAA TGGCGTGTCT AATA	524
	(2) INFORMATION FOR SEQ ID NO: 885:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(b) Topologi: Timear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 885:	
15	TTAATGATTT CTTCGTATGA TTCACCAACA ATTTGCGCTA AAATATCATG CGCAAGTACT	60
	TCACCTTCAA CCATAAATTC TATTTGCTCT ACTAAAAATT TTACGTCATT CATGCTATTC	120
	ATTTTTGGAA TTAACAAAGC ATATAAGTTT GTAAATTCTT TTAAATACGC AGCATCAGCT	180
20	TTTAAGTAAT GGCGTAATGC GTCACTCCTA TATCTCCGGA TAACATCTTC TGAATAAAGT	240
	CATCCTCATA AATATCATAA TGATGGCTTG CAGCTGGGTA CAATTTTGTG AAATTCCATG	300
	TAAAAATCCT CCCTAAATAA AAAACTACTT CCAACATGAA GAGTTGAGGC ATGTGCAAAC	360
25	TAGCCCATCA CTCATAACAC TTCCACGTGG GACTACCAAC	400
	(2) INFORMATION FOR SEQ ID NO: 886:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 857 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 886:	
	AAGAATTTAA ACAAAATGAT ATTTGGAAAC ATTTTAAAGC TGTGAAAAAT AATCATGTTT	60
40	ATGACTTAGA GGAAGTGCCA TTCGGTATTA CAGCAAATGT TGATGCTGAT AAGGCAATGA	120
	CTCAATTATA TGATTTATTT TATAAGGATA AAAAATAGTG AGTTGATATG ATGATAAAAA	180
	ATAAAAAGAA ACTACTATTT TTATGTTTGT TAGTCATTTT AATCGCAACT GCTTATATTT	240
45	CGTTTGTAAC CGGTACAATT AAATTGTCAT TTAATGACCT ATTTACAAAA TTTACAACTG	300
	GTAGCAATGA AGCAGTGGAT TCAATCATTG ATTTGCGATT GCCACGTATA TTAATTGCAT	360
50	TGATGGTTGG CGCAATGTTA GCAGTTTCTG GAGCATTATT ACAAGCAGCA CTACAAAATC	420
-	CTTTGGCAGG GCGAATATCA TTGGCGTTTC CTCAGGTGCA CTTATAATGA GAGCCTTTGt	480
	ATGTTGTTLA TTCCACAATT GTACTTTAC TTACCATTAT TAAGTTTTAT TGGAGGTTTA	540
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	ATATTAGTAG GTGTTGCGTT ATTCGTATTA TTAAATGGTG TTTTAGAAAT TTTAACTCAA	660
	AACCCTTTAA TGAAAATTCC TCAAGGCTTA ACAATGAAAA TATGGAGCGA CGTATACATA	720
5	TTAGCAGTAT CAGCATTATT GGGATTAATA TTAACATTAC TATTGTCCCC TAAATTGAAT	780
	TTACTAAATT TAGACGACAT ACAAGCGCGA ALATCGGTTT TAATATTGAT CGTTACAGAT	840
	GGTTAACAGG GTTATTA	857
10	(2) INFORMATION FOR SEQ ID NO: 887:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 675 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 887:	
	GATTTATTTT AATATTATTG TTAGAAGGAA TTTTTACAAA TTCAGCGAGT GCAATCGAAT	60
	ATTCAGACTT ACATCATAAA AGTAAGTTTG ATTCAAAGCG TCTAAGTAAT GCTAAGATGT	120
25	CATTCATCAA TCCAACTCAG CTTGAAAATA AAAACACAAA CGATAGACTG TTGAAGCATG	180
	ATTTGTTATT TCATGACATG TTCGTAAATG ATGATTGGAA AAAGGATTTT AAAGTTGAAT	240
<i>30</i>	TTGAAAATGA GGCACTTTCA AAGAAATTTA TAAATAAGGA TATCGATATA TTTGCTGGAA	300
	ATTATGGATA CGGATGTCAT GGGGGAGCAA CCAATAAAAC GCAATGTAGT TATGGTGGTG	360
	TTACTTTAAG TGACAATAAT AAATACGATG ATTATAAGAA TATACCTTGT AATTTATGGA	420
3 5	TTGACGGACA TCAAACAGAA ATAGAACTAA CTGCAGTAAA AACGAAAAAG AAAATTGTTA	480
	CTATTCAAGA ATTAGAGGTT CAATTAAGAA ATTATTTGAA TGAGAAGTAT AAGTTGTACG	540
	AACAAGGTGG CGACATTGTT AAAGGGTATG TTAAATATTA TAATGATGAT GAACAAAATG	600
40	TAGAATATGA TTTTTATAAT TTAAATGGTG AGTATGGTCG TGAGGTATTA AAAATGTATG	660
	CnGATAATnA AACnA	675
45	(2) INFORMATION FOR SEQ ID NO: 888:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 851 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEO ID NO: 888:	

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	AATTCCTAAT TAACAATGCC TTCATTTAAA AACCTTCTTC CATCAATTTG ATGTTTTCAT	120
_	GATATTTAGG TTTTCTCTTT TCAAGATAAA CCATTAAGTY CTCAATAGAA GGTGTAGTGA	180
5	TATTCACTTT AKGACCTAAA ATTTCTTTAA ATACTTGCGC ATGTTCTGTT AATCCTATAA	240
	ATCCCGTACG CTTATGTTCT TCATAAATAA GTAGAGATGC TAATTCATCA TCAAGGTCCT	300
10	CAATAGCACC ACTCACAACT TGATATCTTT GTAACAGTTG TTCTTTTGAA CCATTTAAGA	360
	TAACTTCACC GTCACTTAAG TGAATGATAT AATCAGCTAT TTTTTCTAAA TCTGAGATAA	420
	TGTGTGTCGA CATGAATATT GTTTTATTTT CATCAATTAA TTCTTGCTGA ATTATCTCCA	480
15	ATAGCTCATT TCTAGCTAAG GGATCGAGAC CTGAAGTAGG CTCATCAAAA ATATACAATT	540
	CAGCATGATG TGAAAATGCA ACTGCTAGTG ATAATTTCAT TTTCATCCCA GTCGAAAATG	600
	TTTTTATTGA TTTATTGATT GGTAAATCGA ACTTTTCAAG ATAAAATTCA AATACTTGAT	660
20	GGTCCCATTT ACGATAAAAA GGGGCAATCA TTTTTTCAAG TTGCTTCGTA GTCCATCTCT	720
	CATTAAAATA ATTTTCAGAG TAAACNAACC CAATTCTATT CTTTAACTCT ATCGGATTGA	780
	GAGCCATATC CTCTTCTAAT ACTCTAATAA CACCAGTTTG TGGGTGATAC AAATCCATAA	840
25	TTAACCTAAT n	851
	(2) INFORMATION FOR SEQ ID NO: 889:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 362 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
3 5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 889:	
	AATCACCTTC ACGCCAATAT TGATTTTCAT GCGTAAATAC TTGTGCCGTT TCATGATACT	60
40	TTGTCAATCG TGCGTGTTGC TGGGGGGAAT ATTTTTCAGT AGCCCAATTG GCTGCATGAC	120
	CTTCAATGGC TAGTTCAATT GCAGGATTAA TTAAATCTTC CAATGACAAT TTAGCATAAC	180
45	GCTTGTGAAT ATAATCAAAC AGCTTTGGAA TTGCTGGCAC ACGACAGTTT TACCATGTGT	240
45	AGTCATATCA AAAAATGATT TATATTCGCC TGAATCANCT AGATAAAATT GGTTGGCTAC	300
	ATGGTCAGGG TGCTGGCTCA CGGTGCATCA AACGCNGNTA ATACTGCCCA GTACCTTTGC	360
50	·rc	362
	(2) INFORMATION FOR SEQ ID NO: 890:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 747 base pairs	

(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 890:	
	TTGGTTTATT CCCAAAAAGT ACGCGAAAAT TAGTAGAGAA GAATTTGAAA GTTTAAATAT	60
10	TGTCAAACCC GCTAAAAATA ATACTTTCTG GCCTGTTGCA GGATTTGCAG TGTTATTAAC	120
	AACCTTAACA AGAAAATATA TCTATTTGCT TAACATCCAT TTAGAAAAAG AAATAGTTAT	180
	ATTAACATGC TGTATGATAC TTCTAGGTGT TTTCGCATTG TTTATATATA TAAATACAAA	240
15	ATTGAAGTTA CATATTTTTG ATAAAAATAA AAGTAATAAC GAAAAGATCA TATTAATACC	300
	TACATITAAA AATATIIGIT TATCCITATI TGCTTATATA TTATTIGGIG GATIGICAAC	360
	AATGGCTCTG AGTATGTTAG TAACTTCATC CCCTCAAAAT ATAATAGAAT TTCTTGCTTT	420
20	AATTGGCATG ACTGCATGCT TCTTTCTACT GAATATGTCA TCGGTTCTAG ATAAAAAAAT	480
	TCATGTTATT TTAAAAACAA ATAAGTAGTA AAATTGATTA ACTTAGGTAG TATCGGATAC	540
25	TTAAATGTTG GTTCATAAAA AGCAATGATT TTAAATCGAG GAGCTATCTT AGAACAGGGA	600
25	AATAAAACAG CCAAAGTTAT AAAAAGTGAA TTAATAACTA ATTATATTAT	660
	CTTCAAATAA AANATAATTA GAATAAGGTG GGATTGATAA TCAANGCTAN GCGAATCTAA	720
30	AATCATCAAT AAAAACCCCA AATATAG	747
	(2) INFORMATION FOR SEQ ID NO: 891:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 526 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	٠
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 891:	
	ATTTTGAAAT TTTAGCAGAT ACTGATAATG GTCTCGATGC AATGAAACTT ATTGAAGAAT	60
45	ATAATCCTAA CGTTGTTATT TTAGATATAG AAATGCCAGG CATGACTGGA CTTGAAGTTT	120
45	TAGCGGAAAT TAGAAAAAAG CATTTGAATA TTAAAGTGAT TATTGTAACA ACTTTTAAAA	180
	GACCGGGATA CTTTGAAAAA GCAGTTGTGA ATGALGTGGA TGCATATGTT TTAAAAGAAC	240
60	GTTCTATAGA AGAATTGGTG GAAACCATTA ATAAAGTAAA TAACGGAGAG AAAGAATATA	300

360

420

GCGCCACATT GATGACTTCA TTTTTTGTAG ATAAAAACCC ATTAACGCCC AAAGAACAAA

TIGTATTAAG GGAAATTGGC AATGGTTTAA GTAGTAAAGA AATAAGTGAA AAATTATTTT

	ATCGTTTTGA TGCTTGGGAA AAGGCAAATG AAAAAGGCTG GACCTA	526
	(2) INFORMATION FOR SEQ ID NO: 892:	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 751 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 892:	
15	TATTTGATGT AAAAGCGAAn GAACCATACA ATGTAACAAT TACTAGTGAT AAATACATCC	60
	CTAATACTGA TTTGAAACGT GGGCAAGCTG ATTTATTTGT AGCGGAAGGT TCTATCAAAG	120
	ATTTAGTGAA ACATAAGAAG CATGGTAAGG CAATTATAGG AACGAAAAAA CATCATGTTA	180
20	ATATTAAGTT ACGTAAAGAT ATTAATAAAA TCTATTTTAT GACAGATGTT GATTTAGGTG	240
	GACCAACGTT TGTCTTAAAT GACAAAGACT ATCAAGAAAT AAGAAAGTAT ACAAAGGCAA	300
	AGCATATCGT CTCTCAATTT GGATTCGATT TGAAACATAA AAAAGATGCT TTAGCATTAG	360
25	AAAAAGCGAA AAATAAAGTT GATAAATCTA TTGAAACAAG AAGTGAAGCG ATAAGCTCAA	420
	TATCAAGTTT AACCGGAATA TTATTATTTG TAACATCATT TTTAGGTATT ACATTCTTGA	480
30	TTGCTGTATG TTGCATTATA TACATAAAGC AAATAGATGA AACCGAAGAT GAGTTAGAGA	540
00	ATTATAGTAT TTTGAGAAAG CTTGGATTTA CACAAAAAGA TATGGCAAGG GGACTAAAGT	600
	TTAAAATTAT GTTTAATTTT GGGTTACCTT TAGTTATTGC ACTATCACAT GCATATTTTA	660
<i>35</i>	CATCATTAGC ATATATGAAA TTAATGGGTA CAACGAATCA AATACCGGTT TTCATAGTAA	720
	TGGGATTATA CATTTGTATG TATGCTGTTT T	751
	(2) INFORMATION FOR SEQ ID NO: 893:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 357 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 893:	
50	GGATGTTGTA CATTATTCAG ATTACTTTGA AGGGGCACAA AAATATTTGA GCTATTTAAA	60
50	ATCAACAGTA GATGTTAACT TTGAAGGTTT GAAAATTGCT TTAGATGGTG CAAATGGTTC	120
	AACATCATCA CTAGCGCCAT TCTTATTTGG TGACTTAGAA GCAGATACTG AAACAATTGG	180

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	TAGCTGAAAA AGTAGTTGAA ACTGAAATGA TTTTGGGGTT AGCATTTGGA CGGCGATGGG	300
	AGACAGANCC ATAGCAGTAA GATGGAGANG GNCCAATCCG TTGACGGTGG ACCCAAT	357
5	(2) INFORMATION FOR SEQ ID NO: 894:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 464 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 894:	
	GCTAACCTGC AAAATTCGAT AAGCGATTCA ATaCTGACGC CTGCATTTCG CAAATTTTTC	60
	ACTAAATAAA TCCAATTTAA ATCACTATCA TTATATATTC TATATCCATT TTCATCTCGA	120
20	TTAACTGGTG GAATCACACC AACCTTTTCA TAATATCTTA AAGTGTCTTG AGATATATTC	180
	ATGAGCGCTA CGACTTCTTT AGTTTTCATT GCGACTATCC TTTCAGTTAT GTTTGGTCGT	240
	CTAAAGTAAT GTTGCTTTAT ATATTGTCAT CTTCGTTTGA ATACTTCTTA TTTTATTACT	300
25	CAÁTTTAAA TTTGTCTCTT TTTTAACATT TTACATTTCA TCGTTTTTAA TTACTTTAAA	360
	AATTGTATAA CTKAAATATT TAAAATGATA TAAWCACTAA GATTGATAAT AtTTAATTnT	420
30	TTGGAAAATT ATnTTAAGTT GCCAATTTTG GGGGGATGCG GAAA	464
	(2) INFORMATION FOR SEQ ID NO: 895:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 599 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 895:	
	ANAATGAAAG AGTTACAGGA CTTTATTGCT CGTTTCTCAG TAACGCTTCT AAATCTAAAC	60
,	AAGCAACAAG TCGTAAAAAA CAACTCGAGA AAATTGAATT AGATGATATT CAACCATCAT	120
45	CAAGAAGATA TCCTTTCGTT AAATTCACAC CTGAGCGCGA AATCGGTAAT GACTTACTAA	180
	TCGTTCAAAA TCTATCTAAA ACGATTGACG GTGAAAAAGT ATTAGATAAT ATTTCATTCA	240
50	CAATGAATCC AAATGATAAA GCAATTTTAA TTGGGGATAG TGAAATTGCG AAAACCACAT	300
	TGCTTAAAAT ATTAGCCGGT GAAATGGAAC CAGACGAAGG TTCATATAAA TGGGGTGTAA	360
	CAACGTCATT AAGTTACTTC CCTAAAGATA ACTCAGAATT CTTTGAGGGC GTTAATATGA	420
55		

	GCGGCTTCTT AGGCCGTATG CTATTTAGTG GAGAAGAAGT TAAGAAAAAA GCTAGTGTAC	540
	TTTCAGGTGG AGAAAAAGTA CGTTGTATGC TAAGTAAAAT GATGTTATCA AGTGCAAAC	599
5	(2) INFORMATION FOR SEQ ID NO: 896:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1057 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 896:	
	TCATTAGTAG AAATCGTTAA AGATGCATCT TGCAATTTAA AATCCGAATC TTTGTATTGT	60
	TTGTTCACAC TATCTACGTT TAACAATGTT GTCATATCCA TGCTCCTCTT TGTTTAATTT	120
20	TAATAAAAAC GTCTTCTCTT CAATAAATAA CTAAAGGCGT TATATATGAA AATAGCAATG	180
	ATAAGTAGCA AACTAAAGCT TTGATTAATT CCAGTAGTAA TTGAATAAAG CCCAATTACT	240
	ACAATGGCTA GTATCAATAT TGATAAGTTG ATCGCATATG TTTTAAATAA TGCAATTAAT	300
25	TCTATATGGC GTTCACCTTC ATCCAATATT TCCAATCGCT TTTCAGTGTA ATTCTTATCT	360
	GCAATTTTTG GTATTCTGTC ATCAAACCTT CTATTAAACA GTGTAAATTG TGTATTGAAA	420
30	ATAGCACTAG CAAAAAATGG TATTAAAAAG AATAGTATTG CATTTGCTGC AGCGTGCCCT	480
	ACCACAAAA TAAGCAATAC TAAAAAAGCA ATAACTGTCT GCAGAATACT TAATATACTT	540
	CCATTTAAAA CATAACGATT CGCAAGCAAC TCATATTGAT CTGTTGCATC GATATCTACC	600
35	TCTTTATCTA CAAGTTGCTT ATACTTCAAT GCACGTCTTT GATTCATCAA AACAATGGCT	660
	TCTACCAATA TGATAATAAT CGTCGCAACA ATCGATATTA CAACGACATT GTTATATGTC	720
	GCAAACGTCA AGTTCTCAAT ACCAAATCCA TCAAAATTAC CTAAAATTCC ACCTATGATA	780
40	CCCCCTACAA GTCCACCCAG TAAAAGATAT CCGATATATC TTAGTATTTT CATGCCTCAT	840
	CCTCCTCAAT AATAAAAACA GTTYCCACCG TTTCATTGAA AATGCGAGCA ATTTTTATTG	900
	CCGTTAATAC TGATGGCATA AAATTGTTTC GCTCAATTAG CGATATGGTT TGTCTTGAAA	960
45	CGCCCGCTTG TTTAGCAAGT TGCGTTTGGT TTAAGCCATC TCGTGCTCGT AATTCTTTCA	1020
	ATCGATTACG CACATCGCAT CAACTCCTA ATTACAC	1057
50	(2) INFORMATION FOR SEQ ID NO: 897:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 336 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 897:	
5	AAATTATTGA GTTAACAAAT CATTACGGAG CACATAATTA TTTACCATTG nCAATTGTCA	60
	TTTCAGAAGC CGANGGGGTA TGGGTTAAAG ATCCTGAAGG CAATAAATAT ATGGATATGT	120
	GANCTGCATA TTCCGCTGTT AACCAAGGTC ATAGACATCC GAAAGGTATT CAAGCATTAA	180
10	AAGATCAAGC TGATAAAGTG ACTTTACTCT CACGTGCTTT TCATAGTGAT AACTTAGGTG	. 240
	AATGGTACGA AAAAATTTGT AAACTGGCAG GTAAAGATAA AGCTTTACCA ATGTAATACA	300
	GGTGCTGTAA GCAGTAGAAA CAGCTTTGAA AGCAGC	336
15	(2) INFORMATION FOR SEQ ID NO: 898:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 302 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 898:	
	TGNTGNTTTC TTATTGTTGA CCAATTATTT TGCATACCAA ATCCAAATCA TGTATTTATC	60
	AATCACATCC TAATGCTAAA TCCAATGTAT TACATTGTTT AATGGTATAG CACAATCTAT	120
30	CATATTTGGT ATATCAAGTA TGGAAAACAT TCCATATCAT TTTTACTTTA TTTTATTCTT	180
	ATGTTTAATA GCTGCAGTAA ATTTCGTATT AGCAGGTATA CGACACACGG CAATTTATAA	240
	TAAAACATCT AAAGTGACAC AAACTGATAA TCAACAGGGA GTTTCAAAGA TAGTCAGACG	300
35	GG .	302
	(2) INFORMATION FOR SEQ ID NO: 899:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 469 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 899:	
	CCACTAGCTG ATACAGTAGG TATACCAAGA TTCGTCATCG TTACGACATA TCAATTTGGT	60
50	CAATATGCGA TGTTATTCTT AGCGCCGACT GGACTTGTTA TGGCCACACT ACAAATGTTA	120
	AACATGCGAT ATTCACATTG GTTCCGATTT GTATGGCCGG TAGTTGCTTT TGTATTGATT	180

	TATAAAAAT ACTAATGGGG TTTTATGCAT CTCGTAGGTT TGTAGAAATA CTAAACTAAG	300
	CGAGGTGCAT TATTATTTTT GATTAAGAAA ATAATGACGG TAATGATAAC ACTAGTAAGT	360
5	AATTGATACA ATGCTCTATT TAATAATGAT ATTTTTAAAA TTTGTTTTTA ATGTAATGTT	420
	AGATCTATGG TATATTATAT TTAACGTGGT AAATATGTAT TTGCTGTAA	469
	(2) INFORMATION FOR SEQ ID NO: 900:	
10 15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 821 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 900:	
20	CTTTATTGGT AACTCTCTAT aATATLTTAA CATTTTTACG CTATCGTGCA AACGCAACCa	60
	CTTTGAATTY TCTGATATTT TTAGCATATA ATTTACACCC TGCACGATGA ATTGTTAATC	120
	CAGTTGTATA AATATCGTCA ACGAGTAATA TTTCCTTACC ATTTAAATCT AATTCCGTAT	180
25	CAATAATAAA TGGATTTTCA TCTGCCAGAC GCTCTTTCTT AGTTAAATGA GACTGTTTTG	240
	GTCTATTTGA CATCTTTAAA ATCTTATCAA AGCGAATCCC TTTAGCTTTT AGTACTGCTT	300
	CTACCGGGTT AAATGTTCTA GATAAATCAT GTGCCGGCGA AGAAGGAATT GGCACAATAT	360
30	AGTCATAAGA TGTTTGTGGT ATTTCAATCA AATGTGCCAA TAATTCACAT AAATAATAGT	420
	CTTTCAAAAA TTTATACTGA TGTATCATCT CTTTCATTAA ACCGTCATAT TGAAATTGAC	480
35	AATATAATTG TTCCATTAAA TTAAAGTGTG CCGATAGAAA CTTGCAGTCT AAACAATACG	540
33	CTTCATCTTG ATTTAAGTGT TTTAAGCACC TTGAACATCG CCTTGCTTTA ATATCAAGTT	600
	TAATATTGTC CCAATTCTCT TTGCATCTGT CACATAATCT ATTAGGTTTC TTGAACAAAT	660
40	TATAAATGGT TATATTTTCA TATAACTTAG CACCACAACT CAAACAATTA TTCATCAATC	720
	CAACCTCTTT TTAATGCTAA TTTGTTCATC CTTTGAATCT CTTTTTTAGC TTGAATCATA	780
	TTCATACTTA CCCCTTnCAT GAAAAACAA TACTTTTTCC A	821
45	(2) INFORMATION FOR SEQ ID NO: 901:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 349 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

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TGATGCTATT AAAAAGTTAA TTGTGCGGTC TGTTTTGATA ATTTTAATAA TAACTTCAGG	- 60
TAACTAAAAA TCCTAATATT GAAAAAACAA AGCCATTTAA AACATAACCT AGTATATTCC	120
ATGTATGATT GTAACTCATT TGCCAGTTnT GTACTGACTT GCATAATTCT GTCACGTnCG	180
AACCATGTAC AAGCCTGCAA CTACTGCTGA ATGATTCCTG ATGCGTGAAC AATTCAGCAA	240
TTAAATACGT AACAAATGGT GTTACAATTG AATAATTGAA ACATATTAAT GTTTCATATC	300
CTCGACGNCA TCAATGTTAA TCCGGACCTT ACTAATGCAT ACCTATAAG	349
(2) INFORMATION FOR SEQ ID NO: 902:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 390 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
20	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 902:	
CAAGTGGTAT AAATTTACCT GGTGAAATGT AGGTCGTGGT GGCGATGATA CATTATTCGC	60
TAAAATCGAC GGCGTTGTTA AATTCGAACG TAAAGGTCGC GACAAAAAAC AAGTTTCTGT	120
ATATGCAGTT AGCTGAATAA TTTTGTCTAG TTAACACCAG AAAGTGAATC TTCTGGTGTT	180
TTTTACTTTT TATAAAATGT TTTTCATTAT TATTTTCATT ATGnTATTTA AAAATGGGGA	240
TTTTAGACGT TATACTAAAT GTGCACTGTA TAGGGGCCCT AATCACTAAC TATAGGGGGA	300
CAAGGATACA GTGCAGCGTT AAGGATAACT GnCCACATTG GTCTGGGAAT ATAGGATTTA	360
AGCAAGGTTA TAAAGTACTC nTAGGCCCTA	390
(2) INFORMATION FOR SEQ ID NO: 903:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 334 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 903:	
GGAATAGACG TATATGCGCG TTGAATTTAA TCCTAATAAG CTTTCGCATG ATGAAGTGCT	60
TTGGTTAAAA CAAAATATCA TCAGTTATTT GGACGATGTT AGTTTTACGA GATTAGATTT	120
50 GGCTTTTGAT TTTGAATTTG ATTTAAAATG ACTATTATGC ATTGTCAGAT AAGNCGGTAA	180
AAGAAACTAT ATTTTATGGC CGAATGTAAA ACCAGAACAA AATATTTTGG TGTnCGAATA	240

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	GATTCACATT CTATGCGGTG GAATTGATTA AACG	334
	(2) INFORMATION FOR SEQ ID NO: 904:	•
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 334 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 904:	
15	CAAGTTGGGG ACACTGTTTC AAATGAAACA ACAGTGTGTA TTTTAGAGGC AATGAAACTA	60
,,,	TTTAATGAAA TTCAAGCAGA AATTTCAGGT GAAATTGTTG AAATCTTAGT AGAAGACGGA	120
	CAAATGGTAG AGTATGGCCA ACCGTTATTT AAGGTGAAAT AATGAAAAAG GTTTAATTGC	180
20	AAACCGCGGT GAnTCGCAGT TAGGATTATT CGCGCTTGTC GTGATTTAGG CATCCAAACT	240
	GTTGCATCTT TCTGAGGGGA TAAAGATCGC TACATCTCAA ATGCTGATGA GGCATAT71CG	300
	TGGGCCnCTT GTCTAAGGTC ATATTTAATA TCCG	334
25	(2) INFORMATION FOR SEQ ID NO: 905:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 399 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 905:	
35	TTCACCCTGT AATTCTTaAC CGTCAATTGA CCTTTATGCA GATTTAATAT TCCTAAAACG	60
	TATAACTCTT CTAATGATAA TTGACACATA TTTÄAATAAC ACTTTAGATT CCGCAATAAT	120
40	TCTTGTGACG ACAATAAATA CGATACATAG TCACAACTAA AATCAAATGT ATATTGACCA	180
	AAATAACGTT CAATATAGTC ACTAAGCTCA TTATTCATAT ATTCTATTTn ATCTATATGC	240
	ATTTTATTAA TCGAAATAGT CAATTTACGT TGATCCCTTT GATCTCTTCC TTTCAATAGC	300
45	CATTGATGAT TGTnTAAATA ACTTAACATT TGAAGAAGGG CCATCTTAGA TTGGATTTCT	360
	TTCATTnTTA ATAAACTATC TATTGAAGCG CTATTGGAA	399
	(2) INFORMATION FOR SEQ ID NO: 906:	
50	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 1478 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
<i>55</i>		

(xi) S	EOUENCE	DESCRIPTION:	SEO	ID	NO:	906:
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TACATTTTTC	AATTTATGGC	AAAATnCACA	ATTTTCATCG	AAATATTTTG	TANANAATCA	60
TTGCTAGGTG	ATGAGTTATC	TCGGTTAATT	ACAAAACGAT	ATCTAAGTTT	AAATATTAGA	120
TCATAAAAAA	ACTATCTACT	GAATATCCCT	CCATAGCATC	ATTTTTCTAA	GCAAAAGTTA	180
AACTTAGTTA	GATAAAATGC	AAATGAGATT	ATTGTAGATA	GTCTCTTTTT	AATGTTTAAA	240
AATGATTAAT	GCCaTAAACA	TAAATAATTC	CaAAGAATGC	CGCGCCACTA	AGCACTGTTA	300
ATATAAGACT	TAGTAACAAT	GTGCGTTTAT	AATGTTTaAC	AAATGCtATG	AACAAAATGA	360
CTACATTATA	CGCAAAGAAA	AGTCCGAATA	ATGTCATTGT	TATTTTCAAA	TCAGAATAGA	420
AAATATTAA	TAGTAATACA	ATGACTGCAT	ATAATTAAATA	CGGAATAACT	ATAAATTTGC	480
GTTCAAATCT	TAATTGTTCG	AAaCGtTTAT	CTTCGTTTGT	CATGATATGC	TCCTTTATGA	540
TTTAAAAGTA	AATAAGTTTA	CGGAALATCT	TGTCCGaTAA	TAGCGGTGTA	AAtGTCAAAC	600
CACGACTGAT	CATCLAAATT	AAGTKGTAGC	CCtTCGATTG	CTTGATCAAT	ACGCTTTAAC	660
TGACTTGTTC	CAAGTATCCG	GCATGATACG	ATGCGGTATT	TTTACTAACC	ACGCTATCAT	720
CACAGCTGTG	TCACTYACAC	mATATTTGTC	AGCTATTGAT	TGAACAACTT	TCATAATACG	780
TTGCGCTTTA	ATATCTTCCT	TGTCGAAAAT	TTTACCGCCT	GCAAAAGGAC	TCCAAGCCAT	840
GATTTGAACA	TGGTTTTGAT	ACATTGAATC	CATTGTTCCA	TCTTGTAAAC	TATCAACGTG	900
ATATGGCGAT	AATTCTAATT	GATTGATGCT	AATATGTAGT	CTTTCTTTCA	TAATATATTG	960
ATTTAACAAT	TGGTATTGTG	AATGATTAAA	ATTCGACACC	CCGAATGACT	TCAACTTACC	1020
TTGTTTAACA	AGTTTAGTTA	ATGCATCAGC	AACTTGTTCT	GGaTCCATCA	ATGGTGaAgG	1080
ACGATGAATG	AGTAGACTAT	CTAAATAATC	TACATTCAAA	TTGATTAATG	ACTGTTCAAC	1140
AGATTTCACG	ATGTGCTTAC	TACTCAAATC	ATAACGATGT	CCATTTGTAA	AATCAAATTG	1200
CTTAGAAGGC	AAAATGATAC	CACATTTCGT	AACAATTTGA	ATTTTATTTC	TTAATTCGGG	1260
TGATAAATCC	AAAGCATTAC	CAAACAGTGA	TTCACATTGA	TAATCTCCAT	AAATATCAGC	1320
ATGATCCATO	GTTGTAATTC	CACGTTCAAC	TAATTCATTI	TAATAAATA '	TTAACTCTTT	1380
CGCAGTCATC	TTCCATTCAT	TTGCACGCCA	AAAACCTTGT	ACAAGCCTAG	AAAAATGAAC	1440
ATAGTGATTA	ATCATTATTI	GTTCCATATE	TCATCCAC			1478

(2) INFORMATION FOR SEQ ID NO: 907:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 543 base pairs

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AGAAGAACAT TTAGTTCAGA GTTTAAGTTA CAAATGGTTA GATTATATAA AAATGGTAA CTTAAGAATG AAATTATACG AAAGTATGAT TTAAAACCCT CAATTATCTC AAATTCGAT AAACAACACC AAAATACTGG ACCCTTCAAT CATCAAGATA ATTTAAAAAG TGATGAAAA 15 GAGTTAATAA AATTACGCAA AGAAGTTCAA CATTTAAAAA TGGAACATGA TGTTTTAAA CAAATTTTAA AGTTGATTA GAAACTGAAC TTTTTAAAGA TACATTACTT GAAGATTCT AATTTACTGA TTATATAAAG AACCAACTTC CAACGATATG GAGAGACTAA GAAATAGTT GCATTAGGAA TTCGCTTATA ATTAGATGT CAATATATATA AGTAAGTTAG ATTGCTTTT GCATTAGGAA TTCGCTTATA ATTAGATGT CAATATAGAC TTTTTTACAC ATACATGAA TAT (2) INFORMATION FOR SEQ ID NO: 908: (1) SEQUENCE CHARACTERISTICS: (A) LENCTH: 751 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908: TTTTCGGTTG AACATGATTA CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGAATACG TACTGGAGTA TTCAGAATT GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTAC ATTTAGCTAT TAAAGAATTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT AAAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACCAAGGTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGT TTGCAACTGC AACAGAAGA AAAAGTAATG ACCAAATCGT AGAAACATT AAGGATATCA TGCCTTTATC ATTTGGAGAGA AAAAGTAATG ATGAGATTAAT TTAATGATAG GCGGTGACTA TGCAACTCAA ATCAACCAA AAAAGTAATG ACCAAATCGT AGAAACATTT AAAGGATATCA TGCCTTTATC ATTTGGAGAA AAAAGTAATG ATGAGAACTTT ATAAGAACTTA TAGAGATTAC TTACCTTATC ATTTGGAGAACAA AAAAGTAATG ACCAAATCGT AGAAACATTT AAAGGATATCA TGCCTTTATC ATTTGGAGAACAA AAAAGTAATG ACCAAATCGT AGAAACATTT AAAGGATATCA TCCCTTTATC ATTTGGAGAA AAAAGTAATG ACCAAATCGT AGAAACATTT AAAGGATATCA TCCCTTTATC ATTTGGAGAACAAA AAAAGTAATG ACCAAATCGT AGAAACATTT AAAGGATATCA TCCCTTTATC ATTTGGAGAA		(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
TICTATGAGA ATAGATATTG TTAAATTAAG AAAGTAGTCA ATTITATTAT GACAAAAGA AGAAGACACT TTAGTTCAGA GTTTAAGTTA CAAATGGTTA GATTATATAA AAATGGTAA CTTAAGAATG ABATTATACG AAAGTAGAT TTAAAACCCT CAATTATCTC AAATTCGAT AAACAACACC AAAATACTGG ACCCTTCAAT CATCAAGATA ATTTAAAAAG TGATGAAAA GAGTTAATAA AATTACGCAA AGAAGTTCAA CATTTAAAAA TGGAACATGA TGTTTTAAA CAAATTTTAA AGTTGATTTA GAAACTGAAC TTTTTAAAAA TGGAACATGA TGTTTTAAA AAATTATTT AATTTCAATA AAAACTCATA ATAATATTTA AGTAAGTTAG AATGCTTTT GCATTAGGAA TTCGCTTATA ATTAGATGTT CAATATAGAC TTTTTTACAC ATACATGAA TAT (2) INFORMATION FOR SEQ ID NO: 908: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 751 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908: TTTCCGGTAG AACATGATTA TGCGATTGT AAAGATACAG TACTGGAGTA TCCAGAATT GATCTGGAAC TTGCAATCA ATTTAACAT GCTAATATCG GTATTCATCC ATTTAAACT GATCTAGAAC TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATCA ATTTAACAT GATCTAGAAC TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATCA ATTTAACATT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT AAAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT AAAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTTGCAGGT TACAAGTTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGGT TACAAGTTCC TAGAGAAGA AAAAGCAAATGA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGAAGACCAA ATCAACCAA AAAAGTAAGA AGGGATTAAT TTAATGATAG GCGGTGACTA TGAAGACCAA ATCAACCAA AAAAGTAAGA AGGAAACATT TAAAGAACATT AAAGAATCAA AAAAGTAACA AAAAGTAACA AAAAACTAA AAAAGTAACT AAGAACCAA TGAACACCAA ATCAACTAA AAAAGTAAG ACCAAATCGT AGAACCATT AAAGATACA TACACTAAA AAAAGTAAG ACCAAATCGT AGAAACCATT AAAGAATCCA TCCCTTTATC ATTTGGGAA AAAAGTAAG ACCAAATCGT AGAAACCATT AAAGAATCCA TCCCTTTATC ATTTGGGAA AAAAGTAAGA ACCAAATCGT AGAAACCATT AAAGAATCCA TCCCTTTATC ATTTGGGAA AAAAGTAAGA ACCAAATCGT AGAAACATT AAAGAATCA TCCCTTTATC ATTTGGGAACAA AAAAGTAAGA ACCAAATCGT AGAAACATT AAAGAATCCA TCCCTTTATC ATTTGGGAACAAACAAAACA	5		
AGAAGAACAT TTAGTTCAGA GTTTAAGTTA CAAATGGTTA GATTATATAA AAATGGTAA CTTAAGAATG AAATTATACG AAAGTATGAT TTAAAACCCT CAATTATCTC AAATTCGAT AAACAACACC AAAATACTGG ACCCTTCAAT CATCAAGATA ATTTAAAAAG TGATGAAAA 15 GAGTTAATAA AATTACGCAA AGAAGTTCAA CATTTAAAAA TGGAACATGA TGTTTTAAA CAAATTTTAA AGTTGATTA GAAACTGAAC TTTTTAAAGA TACATTACTT GAAGATTCT AATTTACTGA TTATATAAAG AACCAACTTC CAACGATATG GAGAGACTAA GAAATAGTT GCATTAGGAA TTCGCTTATA ATTAGATGT CAATATATATA AGTAAGTTAG ATTGCTTTT GCATTAGGAA TTCGCTTATA ATTAGATGT CAATATAGAC TTTTTTACAC ATACATGAA TAT (2) INFORMATION FOR SEQ ID NO: 908: (1) SEQUENCE CHARACTERISTICS: (A) LENCTH: 751 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908: TTTTCGGTTG AACATGATTA CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGAATACG TACTGGAGTA TTCAGAATT GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTAC ATTTAGCTAT TAAAGAATTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT AAAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACCAAGGTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGT TTGCAACTGC AACAGAAGA AAAAGTAATG ACCAAATCGT AGAAACATT AAGGATATCA TGCCTTTATC ATTTGGAGAGA AAAAGTAATG ATGAGATTAAT TTAATGATAG GCGGTGACTA TGCAACTCAA ATCAACCAA AAAAGTAATG ACCAAATCGT AGAAACATTT AAAGGATATCA TGCCTTTATC ATTTGGAGAA AAAAGTAATG ATGAGAACTTT ATAAGAACTTA TAGAGATTAC TTACCTTATC ATTTGGAGAACAA AAAAGTAATG ACCAAATCGT AGAAACATTT AAAGGATATCA TGCCTTTATC ATTTGGAGAACAA AAAAGTAATG ACCAAATCGT AGAAACATTT AAAGGATATCA TCCCTTTATC ATTTGGAGAA AAAAGTAATG ACCAAATCGT AGAAACATTT AAAGGATATCA TCCCTTTATC ATTTGGAGAACAAA AAAAGTAATG ACCAAATCGT AGAAACATTT AAAGGATATCA TCCCTTTATC ATTTGGAGAA		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 907:	
CTTAAGAATG AAATTATCG AAAGTATGAT TTAAAACCCT CAATTATCTC AAATTCGAT AAACAACACC AAAATACTGG ACCCTTCAAT CATCAAGATA ATTTAAAAAG TGATGAAAA GAGTTAATAA AATTACGCAA AGAAGTTCAA CATTTAAAAA TGGAACATGA TGTTTTAAA CAAATTTTAA AGTTGATTTA GAAACTGAAC TTTTTAAAGA TACATTACTT GAAGATTCT ATTATCTGA TTATATAAAG AACCAACTTC CAACGATATG GAGAGACTAA GAAATAGTT GCATTAGGAA TTCGCTTATA ATTAGATGT CAATATAGAC TTTTTTACAC ATACATGAA TAT (2) INFORMATION FOR SEQ ID NO: 908: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 751 base pairs (B) TYPE: nucleic acid (C) STRANGEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908: TTTTCGGTGG AACATGATTA CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATT GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTAC ATTTAGCTAT TAAAGAATTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACCAAGTTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGT TTGCAACTGC AACAGAAGA TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGCCAA ATCAACTAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TGCCTTTATC ATTTGGAGAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TGCCTTTATC ATTTGGAGAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TGCCTTTATC ATTTGGAGAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGAA		TTCTATGAGA ATAGATATTG TTAAATTAAG AAAGTAGTCA ATTTTATTAT GACAAAAGAA	60
AAACAACACC AAAATACTEG ACCCTTCAAT CATCAAGATA ATTTAAAAAG TGATGAAAA GAGTTAATAA AATTACGCAA AGAAGTTCAA CATTTAAAAA TGGAACATGA TGTTTTAAAA CAAATTTAA AGTTGATTTA GAAACTGAAC TTTTTAAAGA TACATTACTT GAAGATTCT ATTTATCTGA TTATTAAAAG AACCAACTTC CAACGATATG GAGAGACTAA GAAATAGTT GCATTAGGAA TTCGCTTATA ATTAGATGTT CAATATAGAC TTTTTTACAC ATACATGAA TAT (2) INFORMATION FOR SEQ ID NO: 908: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 751 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908: TTTTCGGTTG AACATGATTA CGATATTACT TCTAAAACGA TTCCACCAAA ACCAGGAGA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATTT GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGAAGA TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAA AAAAGTAATG ACCAAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGAGA AAAAGTAATG ACCAAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGAGAA AAAAGTAATG ACCACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGAAGA AAAAGTAATG ACCACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGAAGA AAAAGTAATG ACCACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGAA AAAAGTAATG ACCACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGAA	10	AGAAGAACAT TTAGTTCAGA GTTTAAGTTA CAAATGGTTA GATTATATAA AAATGGTAAG	120
GAGTTAATAA AATTACGCAA AGAAGTTCAA CATTTAAAAA TGGAACATGA TGTTTTAAAA CAAATTTTAA AGTTGATTTA GAAACTGAAC TTTTTAAAGA TACATTACTT GAAGATTCT ATTTATCTGA TTATATAAAG AACCAACTTC CAACGATATG GAGAGACTAA GAAATAGTT GCATTAGGAA TTCGCTTATA ATTAGATGTT CAATATATTA AGTAAGTTAGA ATTACTTT AATTCAATA AAAACTCATA ATAATATTTA AGTAAGTTAGA ATACATGAA TAT (2) INFORMATION FOR SEQ ID NO: 908: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 751 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908: TTTTCGGTTG AACATGATTA CGATATTACT TCTAAAACGA TTCCAACCAAA ACCAGGAGA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATTT GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGAAGA TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAA AAAAGTAATG ACCAAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGAGA AAAAGTAATG ACCAAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGAGA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGAGA AAAAGTAATG ACCACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGAGA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGAGA		CTTAAGAATG AAATTATACG AAAGTATGAT TTAAAACCCT CAATTATCTC AAATTCGATA	180
CAAATTTAA AATTACGCAA AGAAGTTCAA CATTTAAAAA TGGAACATGA TGTTTAAAA CAAATTTTAA AGTTGATTTA GAAACTGAAC TTTTTAAAGA TACATTACTT GAAGATTCT ATTTATCTGA TTATATAAAG AACCAACTTC CAACGATATG GAGAGACTAA GAAATAGTT GCATTAGGAA TTCGCTTATA ATAGATGTT CAATATAGAC TTTTTTACAC ATACATGAA TAT (2) INFORMATION FOR SEQ ID NO: 908: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 751 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908: TTTTCGGTTG AACATGATTT CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATT GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACCTT TACAAGTTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGAAGA TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAA AAAAGTAATG ACCAAATCGT AGAAACCATT AAAGATACA TCCCTTTATC ATTTTGACACTAA AAAAGTAATG ACCAAATCGT AGAAACCATT AAAGATACA TCCCTTTATC ATTTTGACACTAA AAAAGTAATG ACCAAATCGT AGAAACCATT AAAGGTATCA TCCCTTTTATC ATTTTGGACAA AAAAAGTAATG ACCAAATCGT AGAAACCATT AAAGGTATCA TCCCTTTTATC ATTTTGGACAA AAAAGTAATG ACCAAATCGT AGAAACCATT AAAGGTATCA TCCCTTTTATC ATTTTTGGACA AAAAGTAATG ACCAAATCGT AGAAACCATT AAAGGTATCA TCCCTTTTATC ATTTTTTTTTT		AAACAACACC AAAATACTGG ACCCTTCAAT CATCAAGATA ATTTAAAAAG TGATGAAAAA	240
AAATTTATTT AATTTCAATA AAAACTCATA ATAATATTA AGTAAGTTAGCATTTTATTTAGGAA TTCGCTTATA ATTAGATGTT CAATATAGAC TTTTTTACAC ATACATGAA TAT (2) INFORMATION FOR SEQ ID NO: 908: (i) SEQUENCE CHARACTERISTICS:	15	GAGTTAATAA AATTACGCAA AGAAGTTCAA CATTTAAAAA TGGAACATGA TGTTTTAAAG	300
AAATTTATT AATTTCAATA AAAACTCATA ATAATATTA AGTAAGTTAG ATTGCTTTT GCATTAGGAA TTCGCTTATA ATTAGATGT CAATATAGAC TTTTTTACAC ATACATGAA TAT (2) INFORMATION FOR SEQ ID NO: 908: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 751 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908: TTTTCGGTTG AACATGATTN CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATT GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTTT AAAGCAATTAG ATGAGAACTT TGGTGTTATT GAACCACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGAAGA TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTTGGAGA		CAAATTITAA AGTTGATTTA GAAACTGAAC TTTTTAAAGA TACATTACTT GAAGATTCTA	360
AAATTTATT AATTCAATA AAAACTCATA ATAATATTA AGTAAGTTAG ATTGCTTTT GCATTAGGAA TTCGCTTATA ATTAGATGTT CAATATAGAC TTTTTTACAC ATACATGAA TAT (2) INFORMATION FOR SEQ ID NO: 908: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 751 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908: TTTTCGGTTG AACATGATTH CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATT GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGAAGA TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAA AAAAGTAATG ACACAATCGT AGAAACAATT AAGGATATCA TCCCTTTATC ATTTGGAGA		ATTTATCTGA TTATATAAAG AACCAACTTC CAACGATATG GAGAGACTAA GAAATAGTTT	420
(2) INFORMATION FOR SEQ ID NO: 908: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 751 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908: TTTTNCGGTNG AACATGATTN CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATT GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGAATGTG TTGCAACTGC AACAGAAGA TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGA	20	AAATTTATTT AATTTCAATA AAAACTCATA ATAATATTTA AGTAAGTTAG ATTGCTTTTA	480
(2) INFORMATION FOR SEQ ID NO: 908: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 751 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908: TTTNCGGTNG AACATGATTN CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATT GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT AAGCAATTAG ATGAGAACTT TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGAAGA TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTTGGAGA		GCATTAGGAA TTCGCTTATA ATTAGATGTT CAATATAGAC TTTTTTACAC ATACATGAAC	540
(2) INFORMATION FOR SEQ ID NO: 908: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 751 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908: TTTNCGGTNG AACATGATTN CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATT GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGA GAATTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGAAGA TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGA	25	TAT	543
(A) LENGTH: 751 base pairs (B) Type: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908: TTTTNCGGTNG AACATGATTN CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATT GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGGAAGA TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGA	25	(2) INFORMATION FOR SEQ ID NO: 908:	
AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACGA TACTGGAGTA TTCAGAATT GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACTT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGAAGA TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGA	3 <i>0</i>	(A) LENGTH: 751 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATT 40 GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGAAGA TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGA	3 <i>5</i>	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908:	
GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGAAGA TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGA		TTTnCGGTnG AACATGATTn CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGAA	60
GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGAAGA TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGA		AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATTA	120
AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGAAGA TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGA	40	GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACTT	180
AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTT TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGAAGA TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGA		GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTTG	240
TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGA GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGAAGA TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGA		AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTTC	300
TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAA AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGA	45	TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGAA	360
AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGA		GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGAAGAT	420
AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGA		TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAAA	480
	<i>.</i>	AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGAA	540
		GAAATTGGTA ATGCGGCATC TCATGGTGTT GCAGCTTTGT TAACATTATT AGTGTTACCC	600

	TATGTTATTT CTATCTTTAT GATGTTTATT TCATCTACTA TTTATCATTC TATGCAAAAT	720
	GAAACACCTC ATAAATATAT TTTAAGGATT A	751
5	(2) INFORMATION FOR SEQ ID NO: 909:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 394 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 909:	
13	AAATTGTCAC AATTCAGTCT AATTTAAAAG GAAGTTAATT ACAAAATTAA AAAATCATGC	60
	ATCGTGTCAT TTAGATATTG AAAAAGATGA GTCAAATTTG TTTCATATAT TTTCCAATAA	120
20	CAAATTATTA TATCTAAATA TACAATCAGA AATATATGAA TAGAAATATC AATAAGAAAA	180
	ATAATATGAT TAAAAATGAT GAATGGCATA CTTATAAAGT GTCTAAATAT TGGCGGTCAA	240
	TATTACTTAC AAACACGAAT GTTAAGTAAT GTAGACAATG cTGaAAAAAC AATAAGTAGA	300
25	AACTCTATAT AGAATGTTCG TTTTTATTTT TAATAATTGA ATAATCATTA TTGGGTGGAT	360
	TTTAATATGG NATTCCGGTC GGCACACGGA TTAC	394
	(2) INFORMATION FOR SEQ ID NO: 910:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1022 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(0) 20102001 2000000	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 910:	
	TANAGCTANG ANANAGANA ANCGTANNGC TTATANCCAN CGNATGANNG ANCGTNGGAN	60
40	AAATCAACCT AGCGCAGTTA GTCAACGTCG AATGAATTTT GAAGAGCGAC GTCAAATTTA	120
	CAACAATGAT ATTTCTGAAG AACGCAATTC AAGTGAAGTT AAGGACAAAA AAGAGCAAGA	180
45	ATAAATATTG ATGATACCCA GATTAGTAAG CAGAGGTCTT TTGCTTATTA ATCTGGGTTT	240
	TTATATGAGG TTAATTATCG ATAACGTTTA ATTAAAGTGT TTAGGTGTCA TAATTTTAAA	300
	TGACGATTTC CCCATTACKA TACACCTAAA TLATCATCAA TCTGAATTCA GATGTTTATK	360
50	ATAAAATTA GATGAAAAAT ATGTTAATAT ACAAGKAATT TAATGTGCGK ATATCTATAG	420
	GCTCGTAGTA TACTTATTAA AATATTAAAC AAAGAAAGGA TTTTAAGATG AATAGAAAAC	48

	GGCTATCCTA TTTTTCTTTA AAAAGTGGTA ATGCATCACA ACGTGAAGAA TTAGCGAAGC	600
	AATTATCTCA GAACGGTGGC AAGGTTTCTT TAGATATGCT TCAGACAACA ATGGGTGCAT	660
5	TAGCAATTAT TTTATTAATT TCAACACTTT ATGGTATATT TGCGACAATT TGTATTAAAG	720
	GACGTAGAAA ATTATCGATT ATACTTTTTG TTATCGCGAT AATTGTAAGT TTGATGGCTC	780
10	TTAATTTAAT TGCAATTGTC TTATGGGTTA TCGTGATGAT TATGTTGATT TCTAAAAAAG	840
	AATCAAAAGA AACAACACAT AAGGACGATG AGTATATTTA TCATTAATAT GTTCATAGCA	900
	AAAGAAAAC CATTAAAATG TTAAGTTGTT AATTATTAGA TACAACCAAC ATTTTAATGG	960
15	TTTTATTTTT AACTTTGTAG TTCTTGGAAT GTTTGAACGA TTAAATAGAC ATTTAAAATA	1020
	СТ	1022
	(2) INFORMATION FOR SEQ ID NO: 911:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 274 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 911:	
30	GGTACTTTAT TTTTATTTTT GGTCTTAGTG ATTTTTACAT TATTTACATA TAAAGCGCCT	60
	AATGGTATGC GTGCCATGGG TAGCATTAGC TAATGCAGCA ATCGCAACAT TTTTAGTGGA	120
	AGCATTTAAT AAATATGTnG GTGGCGAGTA TTCGGTATTA AATTTTTAGA AGAGCTAGGA	180
35	GACGCTGCGG AGGTCTAGGT GGTGTCGCTG CCGCTGGATT AACAGCATTA GCTATCGGTG	240
	TGTCACCAGT ATATGCATTA GTTATAGCAG CCGC	274
40	(2) INFORMATION FOR SEQ ID NO: 912:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 679 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	·
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 912:	
50	CTTTAATTGT TCACTTTATC ATTATTATCA ATCAACTCTA TGATATGAAA TTGTGTTAGA	60
	GATAAATCTA GTTCCTCATT TTCCTTTTTA TACTGTCTTC TTTTATCGGC ATTTTCTCTT	120
	TCTATAATAA ATTGTTGTAA TTTTAAAATA ACTTCTCTCT TCATATCCAC TATTATTCCT	180
55		

	TTGTTGTAAT TAACATATAT TTACTTAGTT ATGCACCATT TATTCCGCAT TTCACAAATC	300
	CACCTATAAT ACAAACTATC ATTTTAAATA AGCAGAATTT ACCCTGTCTT ECACACAAAT	360
5	TGTTTTCGAC ACTTTAATGT GCCTACTATC CAAAAAAGTT ACTCATAACA AATTGCGCAT	420
	TTTAATAAAT GTAGCAATGC CATTTGCATG CTGCAAAAAT ACTCGTATTC ATATTTATGT	480
10	TTTATATTAT TAAAGTTTTT TAAATCCATA TTTTTATAAC ACTTGCTATG TGATAAAATT	540
	AATNTTATAT ATAAAATCTT AAGATTCAGA TTATTTAATA GCAAAGGAGA TAGTGATATG	600
	GATGTTTTAA CAATAGAACA TTTAACAAAG AAGATAGGCA ACAAAACGAT TCTCGAAGAT	660
15	GTATCATTTA AGCTGAAAC	679
	(2) INFORMATION FOR SEQ ID NO: 913:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 564 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 913:	
	GCCATCCTTC AGTGCTAATT TTTTCAAATT CTAATGCAGA TGCACCACTA ACCATACCAT	60
30	ATATAAAGAA AAAGACCACG AAAGNAATAA GTAGTAGTAT AGATGCACAT ATCATAATGA	120
	CATTGGAGTT TTCAGCGCCA AATTTAAATG TCAATGSGAA AATGATAGAG TATGCCCCTA	180
	TGATACCAAA ACTCATTAAA CCTGACATAA TACCAATCAT CACACTTTGG GTCACAATCG	240
35	TAGTCACAAC TAATCCAATC ATTAAACTTG CACCGAATAA GATTAAATAA AAGGCAAAGT	300
	ATGACTTAAT ATAATCACTA CGTTTAACCG GTAAAGTAGA TACATAATAC ATCCATCTTG	360
40	AGTCTTTTTC aTGTTTAATA TTATCAGTAA TAGGTGTGAT TAACATAACC CCAGCCATKG	420
40	CCGAACTCAT CAACGGATTA AATACTGCAA AGTATCCTGC AGCTATAATA GCGACTATAA	480
	AATAAATATA TGTTTGCnTT CTCGTTGCAT AAAAACTACT TAGGAACATA CCTTTCATTA	540
45	TACTTCACCT CGCATTATGA TTTT	564
	(2) INFORMATION FOR SEQ ID NO: 914:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 643 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

	AAAGAAGAAG CAAGTGCAAA TAATTTAAGT GATATATCAC AAGAGGCACA AGAGGTTCAA	60
	GAAGCTAAAA AAGAAGCACA AGCAGAGAAA GACAGTGACA CATTAACTAA-AGATGCAAGT	120
5	GCAGCAAAGG TAGAAGTATC AAAACCAGAG TCACAAGCTG AAAGATTAGC AAACGCTGCA	180
	AAACAGAAGC AAGCTAAATT AACACCAGGT TCAAAAGAGA GTCAATTAAC TGAAGCGTTA	240
10	TTTGCAGAAA AACCAGTTGC TAAAAATGAC TTGAAAGAAA TTCCTCAATT AGTTACTAAA	300
	AAGAATGATG TATCAGAGAC AGAGACGGTT AATATAGATA ATAAAGACAC TGTTAAACAA	360
	AAAGAAGCTA AATTTGAAAA TGGTGTTATT ACACGTAAAG CTGATGAAAA AACAACTAAT	420
15	AATACAGCTG TTGACAAGAA ATCAGGTAAA CAATCTAAAA AAACAACACC TTCAAATAAA	480
	CGAAATGCAT CAAAAGCATC TACAAATAAA ACTTCAGGTC AGAAAAAGCA ACATAATAAG	540
٠	AGATCATCAC MAGGTGCAAA GAAACAAAGT AGTTCMAGta AGTCAACTCA AAAGAATAAT	600
20	CAAACTAGTA ATTAAGAnTT CAAAAACAAC AAATGCTAAn TCC	643
	(2) INFORMATION FOR SEQ ID NO: 915:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 915:	
	AGGTTTAAGG GAAAAATCCT ACCTGGAGAG ATTCAAAAAC TAAATGGACT ATTTCCAAAA	60
35	ATAAAGGCA ATCACATGGT GGTTCTTATT GGAAGTTAAT AAATAACAAA GGAAAAAGAA	120
	TAGCTTCTTT AACTAAAGAA GGAAAAATCT TAAGGGAATA AGGTGTTGTA AATTATGTGC	180
	TTTGATATAA ATAATTTGGA TATAAAAAAG TTGAATTTTA GAAAGGTAAA AAACGCAATT	240
40	CATTTAAGTT TAAGTGGCGA TAAATACCAG TTTTTGGAGG ACGGTAAAAC TATCAATAAT	300
	ACTTATTTT TAGCTGTATA TGATAATGCA ATAAACATTT TTGAAGATTT GTTTtCGCCT	360
45	tCTGATTCTA TAAATTTGGn TCATGTAGTA TATGTTTATA	400
	(2) INFORMATION FOR SEQ ID NO: 916:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

	CCCAAAGTTC GATAGTGTAT TAGTATTATC TTAATAAAAT GTTAGGTACA ATAAAGATGA	60
_	TTATATATCG GAGGTTAGTA TAAAAATGTA TGTAGATCGA AAACCATCAC TATATTTAGA	120
5	GGATTTGCGA CATGATTTTA AAAATAGTTT AAGTAAATTT GAAAATGGTG ATGAAGCATT	180
	TGATACGTTA TTAGGTTTCG TAGAGTTAGA TCATATTTAT TCGTCAGCAC TAAAGGAAAT	240
10	AAGCACTAAA CTGAGTATTT TAGATGACAA TTTCAATCAC ATTTATAWAC ACAATCCTAT	300
	ACATCATATG GAGCGACGTG TGAAAGAAAT GCGTAGTTTA ATAGAAAAGC TTAATCGTAA	360
	AGGATTACAG ATTAGCGCAG AAACTGCCAA AGAACATATA	400
15	(2) INFORMATION FOR SEQ ID NO: 917:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 917:	
	GAAAATTACT ATGAAGATTG CATTAGGATG CGACCATATT GTTACAGATA CAAAAATGCG	60
	TGTATCTGAA TTTTTAAAAT CAAAAGGACA TGATGTCATT GACGTAGGAA CATACGATTT	120
30	CACAAGAACA CATTATCCAA TTTTTGGTAA AAAAGTTGGC GAACAAGTTG TTAGCGGTAA	180
	TGCAGACTTA GGTGTTTGTA TTTGTGGAAC AGGTGTTGGT ATTAACAATG CTGTAAATAA	240
	AGTACCGGCG TTCGTTCAGC ACTAGTACGT GATATGACAT CAGCGTTATA CGTAAAAGAG	. 300
35	GAATTAAATG CGAACGTTAT TGGCTTCGGT GGACGTATTA TAGGTGAGTT ATTAATGTGC	360
	GATATTATCG ATGCCATTAT TAATGCTGGA TTATAAACCC	400
40	(2) INFORMATION FOR SEQ ID NO: 918: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1220 base pairs	
45	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 918:	
50	GTCTCCAGCC ATTWCACCAC ACATACCTGT CCATTTACCT TCTTTATGTG ACGCTTCAAT	60
	AACTTGTTTA ACTAAACGTA AGATTGAAGG GTTATATGGT TGGTATAGAT ATGATACACG	120
	CTCTGACATA CGGTCAGCAG CTAATGTGTA TTGAATTAAA TCATTTGTAC CGATACTGAA	180
66		

	GATTCCTAAT	TCTATATCAT	CCGAAATGTC	ATGACCTTCA	TTTTTAAGGT	TTTCTTTTTC	300
-	TTCTAATAAT	ATAGCTTTAG	CTTCTCTAAA	TTCGTTAATT	GTTGCAACCA-	TTGGGAACAT	360
5	GATATTTAAC	TTACCATAAA	CTGATGCACG	TAATAATGCA	CGTAGCTGTG	GTCTGAAAAT	420
	ATCTTGTTGC	GCAAGGCATA	AACGAATCGC	ACGGTAACCT	AAGAATGGAT	TCATTTCTTC	480
0	AGGCAAGTTT	AAGTATGATA	ATTCTTTATC	TCCACCTATA	TCTAAAGTAC	GTACAACAAC	540
	ACGTTTACCG	CCCATTGCTT	CTAATACTTC	TTTATAAGCT	TCAAATTGTT	CTTCTTCTGT	600
	AGGCATTTGG	TCACGACCCA	AAAAATATAT	CTCAGTTCTA	TATAAGCCGA	TACCTTGTGC	660
5	ACCATTTTCa	ATAACACCTG	GCAAATCATT	AGGTGTACCA	ATATTTGCAG	CAAGCTCTGC	720
	GTGAACACCA	TCAACTGTAA	CAGTATCAGC	ATCACGTAGW	TTTTGTAATT	CTTTCTTGTC	780
	AGCAAAATAA	CGCTCACGTT	TATCTTGATA	AGCGATTAAC	TCATCTTCAG	TTGGATTAAC	840
20	GATTACATCA	CCATTTAATC	CATCTACGAT	AATCATGTCG	CCTTGTTTAA	CTTCTTGAGT	900
	AATTGATTTT	GTACCAACAA	TTGCTGGaAT	TTCTAAAGAA	CGACTCATAA	TTGCAGAGTG	960
25	aCTTGTTCTT	CCGCCAATGT	TTGTAGCAAA	ACCTTGTACG	AATTCTTTAT	TTAATTGAGC	1020
	AGTATCAGAT	GGCGTTAAGT	CATTCCCTAC	AATAACAACG	CTTTCATCAA	TCATACTCGG	1080
	ATTCGGTAAT	TCTACACCTA	AAATATGTGA	TAACACACGT	TTAGAAACGT	CGCGAATATC	1140
30	AGCCGCACGT	TCTTTCATGT	ATTCGTTATC	CATAGATTCA	AAAATTGTAA	CAAATTGTGT	1200
	TGTnACATCC	GCTTAATGTG					1220

(2) INFORMATION FOR SEQ ID NO: 919:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 919:

TTAGATTGAC TGCAAATGCC GACTCAAAAG AACAAGCACA ATCATTGATT CAACCTGTTA 60

AACAAGAAAT TCTTGATCGT ATTGGAGAAT ATTATTATGG TTCAGATGAC ACATTAATTG 120

AGCAAGCTGT AATAAAGAAA ATTCATGAAC CTTTTGTAAT ATATGATGGT ATTACTAATG 180

GTGCTTTATA TCATCGATTG AAAGAAGTGG ATTTAAACGA TGTTCTAAAG GGTATGATTA 240

ATCACAATGA AAACTTTGTL GATATTAATA AACCTATTGA GCAGCAATTA AAAGATGCAG 300

TGCAATTTGT TAATA

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(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 433 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 920:	
	ACTITIGIAAA CCTACAAATG TAATGAATAA TCCTATACCT GCTGAAACAG CCATCTTCAT	60
	TTGATAAGGA ATTGCATTAA TAATAACTTC CCTAAACCCT GTGACGGTTA ATATCGCAAA	120
15	GAATATACCT GAGAATAAAA CGCCTGTTAA ACCAACTTGC CAAGGAATAC CCATGGTTAA	180
	CACAACAGTA AATGCAAAGA ATGCATTTAA TCCCATACCT GGTGcTAACG CAATTGGATA	240
	TTTAGCTATT AGCCCCATGA ATAGCGAGCC TACAAATGCT GCTAATGCAG TCGCTACAAA	300
20	AATGGCACCT TGGTCCATTT TCATATCTTC TGATACGCCT TTAACACCTG CTAAACTTAA	360
	AACTTGCGGG TTAACTGCTA AAATATAGGC CATAGATAAG AAAGTTGTGA TACCGCCTAA	420
25	GATTTCTCTT TTA	433
25	(2) INFORMATION FOR SEQ ID NO: 921:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 439 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 921:	
	CTATTTTATT TGTATAGCGC TTGATGTAAA GTTATTTTAG CTGTCATACT ATGTGCTAAA	60
	CCAAATTCAG TTGTGTCATA TCTTCGCTTT TTTGTCACTG TTATAATAGG TATAATCGGA	120
40	TATAATGAAA AGGKGAGGGA GGATTCAAAA TGCGTAGGTT ATTATATTCA TTTCTTTTTT	180
	ATATGATCAT AGGTTTATTT AGTGGCTTTT TCTATAGAGA GCTAACAAAA GCATATGATT	240
45	TTACTGGTAC AACACAATTA TCACTTGTAC ACACACATAC ACTTATTTTA GGTATGTTTA	300
	TGKKTTTAAT ATTATTACCA TTGGAGAMGT TATTTAAATT ATCAAGTTAC TACTTATTTA	360
	ACTGGCCTTC TATGTATATA ACATAGGTGT TATCGTTACT ATAGGTATGA TGGTGACAAA	420
50	AGGATTCTTC CAAGTCACT	439
	(2) INFORMATION FOR SEQ ID NO: 922:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 474 base pairs	

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 922:	
	GTAATATCTA TATACGTATA TTTAAATGAT ATATCTGGGT ATTTTCTTTT TAATAGCGGC	60
10	TGTAGCCAGT CATAAATATC TETCGaTGTT GGCGCATTAA CGCAACTTGC ACATATAACA	120
	TCTGCCCCAT AAACTACCAC ACTCACGTGC TCCATATATT TATCCCCCAT TGGTTTGATA	180
	GATTTTATT ACACTATCTA TTATAATATA STMATAAAGA TTATCAAATT CATCTCTCGA	240
15	AAGGAGACTT GCCTGATGCC TACTGAAGAT ACAACGATGT TTGATCAAGT AGCAGAAGTT	300
	ATTGAACGTC TTCGTCCATT TTTATTACGT GATGGTGGCG ACTGMTCATT GATTGACGTG	360
	GAAGACGGTA TTGTAAATTA CAATTACATG GTGCATGGTG GNACATGCCC CAAGTTCTAC	420
20	AATCACTCTT AAAAGCTGGG TATTGAGCCG TGCATTACAC GAAGAAGTGC CTGG	474
	(2) INFORMATION FOR SEQ ID NO: 923:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 554 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 923:	
	TCAACTTGTG AAGAAAATTT ATTAACTTTA GTAACTCTTC CAACAAAACC TTGTGATGTC	60
35	ATCACAGCCA TATTTGAAGT TATACCTGAT TTAGATCCCT TATCAATTAC AATTGTATTC	120
	ATCCACTGAT CCGGATTTCT TGCCAAAACC GTAGTAGAAA TAGGATCAAA TTTTGAAATA	180
	TCTTTTAAAT CAAGCTCTTT TTTTAATTTT TCATTTTCCG CTTCTAATTG TTGGTTCTTA	240
40	GATTCTAACT GGCTAATCTT ATTITTAGAT TCTTTAGAAT CTCCTTTTTT AAAAAAGTCC	300
	CCAATCGTAC CAGCAACAAA ATTAACTGGA TAACTCACAA CTCGTTGTCC AAAAGACACA	360
45	GAATCACCTA TATATTGTTC AGGAGGTGAT TGAGATTGTG AACGTATGGA CAGCCCAATT	420
	AATGCAATAA AAACGATAAT TGCACATAAA ACAACAATTA ATTTGGTATT TITAAAAAAC	480
	TTAAGCACCC AGAACACCTC TATTATGTCA NAATATTGTA TATCCTTTTC TAATTNATAT	540
50	TACTCCCATT ATGA	554
	(2) INFORMATION FOR SEQ ID NO: 924:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 575 base pairs	

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	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 924:	
	ATCTTTAGGC ATTAAGCAAG TTTATGTAGA AGACTTTGAA CATAAATCCT TTAGCAAAGC	60
10	TAAAAAAGCC TTAGAAGAAA AAGGGTTTAA AGTTGAAAGT AAGGAAGAGT ATAGTGACnA	120
10	TATTGATGAG GGTGATGTGA TTTCTCAATC TCCTAAAGGA AAATCAGTAG ATGAGGGGTC	180
	AACGATTCA TTTGTTGTTT CTAAAGGTAA AAAAAGTGAC TCATCAGATG TCAAAACGAC	240
15	AACTGAATCG GTAGATGTAC CATACACTGG TAAAAATGAT AAGTCACAAA AAGTTAAAGT	300
	TTATATTAAA GATAAAGATA ATGACGGTTC AACTGAAAAA GGTAGTTTCG ATATTACTAG	360
	TGATCAACGT ATAGACATTC CTTTAAGAAT TGAAAAAGGA AAAACAGCAA GTTATATTGT	420
20	TAAAGTTGAC GGTAAAACTG TAGCTGAAAA AGAAGTCAGC TATGATGATG TATAAATATA	480
	ATTGAAGTAA ATGTACCGAG GTTTCTATTT GGAAGTCTCG GTATTTTTAT GTTGGAGATT	540
	GCGGTAGTTT TAAAATGCnT CnTGTCnTCA TATAC	575
25	(2) INFORMATION FOR SEQ ID NO: 925:	3,3
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 307 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 925:	
	AAAAACGCTG CTGAGTTTAA AAAGCAACAA TTAAATGAAC AAGGTATTTT CAAGAAACCA	60
	GTGATTACAC CTATTAAACC ATATAAAAAT TTCTATCCAG CTGAAGACTA CCATCAAGAT	120
40	TATNACAAAA AGAACCCCGG TACATTATTA CCAATATCAC CGTGGGTCAG GTAGAAAAnC	180
	GTTTATAGAT CHCATTGGGG GGATCCAAAG CTTAAAAAGA TAAAAGTGAC TACCAGATAT	240
45	AGATATATTG TTACACAAGA AACGGCACTG GACCACCATT TATGAATGAT ATTGGACCAT	300
45	TTGCTAA	307
	(2) INFORMATION FOR SEQ ID NO: 926:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
EE		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 926:	
5	CTCTACGCAC TCATTCAGAT ACACACATTG CGCATTGCTC ATAGAATCAG GTGTACACAT	60
	TAAAGAAATA CAAGAACGAT TACGGCATAA AGATATCAAT ACCACTATGA ATATCTATGC	120
	TAAAATCACA AATTCATACA AAAAAGACGC CTCCCATAAG TTTAGTCACC AAATGGAAGA	180
10	CGTCTCGTAA TTAAAATATA TTTGCGTGCA TTCTAATTTA TACTTAGAAT GAATCATACT	240
	CGTGCATAAT GTAATTTTCT AGTTAGTCAA AACTATAAAC AGTTTTACAT CATTCCTGGC	300
	ATGCCACCCA TGTTAGGTTG GTCATTATTT TTTTCTGGAA TTGATGCTAC AACCGCTTCA	360
15	GTCGTTAAGG ACATTGCTGC AACACTTGCA GCAGTTGNAA	400
	(2) INFORMATION FOR SEQ ID NO: 927:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 809 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
?5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 927:	
	TTTAGGTGGT TTTAATnGTT ATGGTCATTC TGGACACCTA CTTATAATAA AATTTCAAAT	60
30	CAAACTGAAC nTTTTGTACC GTTTGATTAA ACTCAAATTT ATTAGCTCCG TATTTAAATT	120
	TTGGTTGGGC TATATTCGTT TCGGTACTTA TTTCAACACC GTTTTTATAA ACTCGGAAGC	180
	TATCATAAAC AATTCTGTCT CCAGCTTTTA GTTTGATCCC TTCGATTTTC ATTATTTCAG	240
35	CATGCGTTAA ATTCCATACA AACGATTCTG TATCTTCGCC TAAAATAATT GTTATCTTTT	300
	TATACATGTT GAATTGGTCG TTAGGAGCAC TACCATGATA GTAAACTGTA CCTTTGCTCA	360
	AATTTTCAAA TGTATACTTT CTTTTGTCTC CGCCTGCATG CCAATCAATA TTAAAATCAA	420
ю	ACGACCACAA TCCAACCTTT TTGTTTTCTT CTAACTCTAG GCTTGTTCCA ATACTTTCAC	480
	CGTATGGTAA TTCTGTAGTT TCGAATTTTA GTTCAAAAGA AACTTTATTA CCTTTTTGTT	540
5	TAGGGTTTAT AACTCCGTTA AAAATAACTT TATACTGTTT ACCATTTACA TAAATTTGTT	600
	GATCGTGTCT TGAATATTCG TAATCCGGGA AGTTGTTTTT ATCTAATTTC ACGTAATCAT	660
	CAGAAGTTGG TTGAGTAAAC CTGTAATTCA ACTCTTCTTT TCTTCTGATn TCTCGCAAAT	720
o	ACATAGGTTC TATGTCTGTC GTTAACGAAT ACAACATATC TCGCATATAA GCAATGTCTG	780
	AACGATTTT AACTTTACAA AAACAAGGA	809
	(2) INFORMATION FOR SEQ ID NO: 928:	

(A) LENGTH: 1016 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 928:	
10	NAAAACTATT ATCGCATCTA CAGTAATCGC TGCAGGTCTT TTAACTCAAA CTAATGATGC	60
	TAAAGCTTTC TTTAGTTATG AATGGAAAGG TTTAGAAATC GCAAAAAATT TAGCAGATCA	120
15	AGCTAAAAAG GACGATGAAC GTATTGATAA GTTAATGAAA GAGTCTGATA AAAATCTAAC	180
	TCCTTACAAA GCTGAAACTG TTAATGATCT GTACCTTATT GTTAAAAAAT TÄAGCCAAGG	240
	TGATGTGAAG AAAGCAGTTG TCAGAATTAA AGATGGTGGT CCTAGAGATT ACTATACTTT	300
20	TGACTTAACT CGTCCTTTAG AAGAGAACAG AAAAAATATT AAAGTTGTTA AAAACGGTGA	360
	AATCGACTCG ATTACTTGGT ATTAAAAAAC ATACTGAATT AAATAGTTGT ACGCCAAACG	420
	TTAGAAAACA ATGCTAACGT ATTGGCGTGC TTTTTTATTT TAAGTAACTT CCAATTTATT	480
25	TAGCATCTTT ACGACTGTTT AATAAAGCAC GTATGATTAA CACGGTTGCC ACTATATCCG	540
20	TTACAATTTT TATGATTGTT AATACATTCG ATTTCCTTTT CACAATAGCC ACCTCGCTTG	600
	TTCAAAACAT AAACAACTAT TGCATTCACT TTTAAGTAAT TATTTATATT ATTTATCCCA	660
30	ATAAGCTCAC CATTCAAATA AACACAATAT TATAAAATAA TTATACCTTT GGATATAGCA	720
	AAAAGCCACA CTCTATAGCA TGGCTTCTAT CAATTATTTT AAAGTATTAT ATTTTAAAAC	780
	TAGATCGATT TGTCTTTGTA ATTTTTTCTT TTCATAACTG TGTTGGAAAT GAATTAAATT	840
35	AACAGCTCTT TGTGCTTTAC GGTGTGTTGC AACAGTTCTT GTACGTTTGA AAAAGTTTAC	900
	AGCTTTTTGT GCATCCACAA CTTTTttATT TACTTGWTTT KTAAAGTTTG TTGATACTGA	960
40	TCATATTTTT TAGCAGCTTC ACCGTTnTTA GTTGTGCATG AGATCACCGG CAACCG	1016
	(2) INFORMATION FOR SEQ ID NO: 929:	
4 5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 929:	
	AAATGAAATC ATACCTAAAA GAGATATTAT TACAGAATCA ATGATTTGTG ACTGTATTCA	6
	AAATGCAGGT ATTGATTTAG AAGTATTTAA AGACGACTTA CAAAAAAGTA AACTAACCGA	12
55		

	CGTTTTCTTT AGTGAAGATG TTCATGAAGA AGGTTTAAAA GTCGAAGGAT TATACCCATA	240
	TCACATCTAT ACTTATATAA TTAATGAATT GATGGGTAAA CCTATCGAAA AGAATCTTCC	300
5	TCCTAAATTA GAAACTTATA TACAGCAACA ACAACTTGTA ACGATGGAAG AATTACTTAC	360
	TATTTATGAA TGGCCAGAAA AACTTTTAAA CAAAGAGTTA	400
	(2) INFORMATION FOR SEQ ID NO: 930:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 930:	
20	TATTTCTGAC ATGTATCATG CTCCTTCGTG CTTTATTCTA ATGTAATATA CACAATTATA	60
	CATTGAAATT CAAATTTGTG AACACATTGT GAACTGACAT AAATTATACA CAATTTCATA	120
	GCGCATAATG TTTTAAAAAT ACACATTATA GCAATTATAA TTAAGTTCAT TGTGTTGTCA	180
25	TCAAAAAAA AAAAAGGTGA TGTTTTAAAT GGATACAGTT GAATCAGTCG GTTTTTGACA	240
	GCATGACTTA GCAGTTCATA TCATTTTGCA ACGATGGTGT GGTATGCTTA ATGTCGCAAT	300
	TCAGATTTTA GGATCGCAAA ATGACTCATA TATAGCATGC CAAGTGGCAA GTATCATACG	360
30	ACATGGnGTG TCAGGCATAN GGCTCATACT GTGCAATATG	400
•	(2) INFORMATION FOR SEQ ID NO: 931:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 931:	
	CCAATCAATG TTGCCAATGG ATCACCTAAT GACAACCAAG TAATTGCTAC CATAGTAACT	60
45	GCTGTTTTAA TTTTACCTAA TTGACCAGCT GCACTTACGA ATCCTTGTTC AATTTGTAGT	120
	AAACGTAAAC CAGTTACGGC AAATTCTCTG GCAATAATAA TGATTGCTAC TACAGAATTT	180
	GTTAGTCCTA GTTGCACAAG TACAATTAAA GCACTTGCAA CTAATAATTT ATCCGCTAAT	240
50	GGATCCAAAA ATTTCCCCAT ATTTGTAACT AAATTCCATT TTCTAGCTAA ATAACCATCA	300
	ACAAAATCGC TAAGGGAAGC CAATATAAAA ATAAAACCAC TGATTAATAA CTCAATTCTT	360
55		

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	ATAAAAACTG GTATTAACAC TACTCTAAAA ACCGTAATCT GGTTCGGAAT ATTCATTATA	480
	CATCCTCATT TCTCACTAAT TTATTTCTGT TAAAAATATT AAAACTAACC ATGATCCATA	540
5	ACC	543
	(2) INFORMATION FOR SEQ ID NO: 932:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 932:	
	GATTGCGAAT GAGATTAGTG GGATGATACC GGTAGAATGG GAGCAAGTAT TTACAATAGC	60
20	TTATGTAACT GATCAAGCTG GAGAAGTCAT CTTTAATTAT ACTAAACCAG ATAGTGATGA	120
	ATTAAATTAT TATTCAGmCA TACCTAAAGA TTGCAATGTC TCAAAAGATA TTTTTAAGAA	180
	TTCATGGTTT AAAGTTTATC GAATGTTTGA TGAGTTAAGA GAAACTTTTA AAGAAGAAGG	240
25	GCTTGAACCA TGGACATCAT GCGAATTTGA CTTTACAAGA GATGGCAAAT TGAATGTATC	300
	TTTTGATTAT ATAGATTGGA TAAATACAGA GTTTGATCAA TTGGGCCGTC AAAATTATTA	360
	TATGTACAAA AAATTTGGGG TTATACCAGA AATGGAATAT	400
30	(2) INFORMATION FOR SEQ ID NO: 933:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 759 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 933:	
	ATTTTTACAA AGAAATAGTA GTCTTATATA TCTTAACATT TAATAACTAA ATCAAACATA	60
	TTTTGAGCCT TTTTTTGAAA ATTAACATTT TAACCTTTTT GATTTTACAA CAAATTATAG	120
45	CTACGTATTG AAAATTAAAG CMTTGGETTA AGTGTTGTGT TAAAAAGYTTT TATGTTTAGA	180
	TIGITATATI ACTATGTATI CITAAATTIG TITAAAAAAT TAATGCTITA AATTGATGTA	240
	TAATGGGAAT AAGAAATAAA TAAAAACGAC CCGCACGATT AACGTACGGG TCCACTACTA	300
50	AAGGGAGTCA AATTTTTACC TCGTTTGTAT CATGCAGCGT TTTACACATA CTTTTAAGAG	360
	ATGTTTATTC GTTATCGAAG GTACACCTTT ATTATAACTT ATATCATTTT TATTAAAATA	420

	ATAATGATTA TTAAATAGTA ACTAAATACA AAATTACATG GGGTGAATGA TAATGAAACA	540
	ATACTTAATT ACTGGTGGGA CTGGTATGGT TGGATCTCAA TTAGTTAATG-AAATTAAAAA	600
5	ATCAGATTCA CATATCACGA TATTAACGCG ACACGACCAA ATTTCAAATG ATAAGAAAAT	660
	TTCATATGTC AACTGGGCTA AATCTGGGTG GGAACACAAA GTTCCTCAAA ATATCGATGT	720
	GGTCATCAAC TTAGCAGGTG CTACATTGAA TAAACGATG	759
10	(2) INFORMATION FOR SEQ ID NO: 934:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 934:	
	GATCAAGCTG GGGAAGTCAT TTTTAATTAT ACTAAACCAG GTAGTGATGA ATTAAATTAT	60
	TATTCAGACA TACCTAAAGA TTGCAATGTC TCAAAAGATA TTTTTAAGAA TTCATGGTTT	120
25	AAAGTTTATC GAATGTTTGA TGAGTTAAGA GAAACTTTTA AAGAAGAAGA GCTTGAACCA	180
	TGGACATCAT GCGAATTIGA CTTTACAAGA GATGGCAAAT TGAATGTATC TTTTGATTAT	240
	ATTGATTGGG TGAATTCAGA ATTTGGACCA ATGGGAAGAG ACCATTATTA TATGTATAAA	300
30	AAATTTGGna TTTGGCCTGA AAAAGAATAT GCCATAAATT GGGTTGnAAA AATAAAGnTT	360
	ATGTTAAGAG CAAGnTTGAG CTGAACTATA GGGGAGATAA	400
35	(2) INFORMATION FOR SEQ ID NO: 935:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 345 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 935:	
45	CTGAATATAA TTTTTnCAAC TACATCTCGT TTATTAGACA CCGTGCACTG ACTAAGAAAA	60
	TTTCTCTTGA CTCCATTAGT CCTGACGAAT ACTAACATTT AACTACCTTG CTCATCGATA	120
	GAAACAACTT GTAATGTTAA TTTCCCTTAT TTTCTTAGTT TTAATCTATC AGCGATTAAT	180
50	TCGATTGCAT CTTTTTCATA AGCAATTGGA TAAACTTGAC CGCGGTACAC CTAACGCTCG	240
	AAATATGATT TTnTATCGTC ATAATCTAAA ATATTATnGG CAAAATCACA GCAGTTTTCA	300

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(2) INFORMATION FOR SEQ ID NO: 936:

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 619 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 936:	
	GTTATCATCA TCTTCTGAAG TATCATCTTG CCCATCGACT TGACTTGCAT CAGTTCTCTT	60
	TAAATCATCA AACTCTGGAC TAGCTAATGT ATTATATAGT GTTTTAGGTA AGTAATAATA	120
15	TTCGTTTAGC ATATCTTCTT TTAAAATATC ATCTACTTGA TACATAATTC TTTGAGCCAG	180
	ATACATATTA TCTTCAGAAT TTTGATTTTG GAAAAAATTA GGTAAATATA AGAACATATT	240
20	TACTAAAATA TCATCTAAAT CTGAATGTAT AGATGGTATA TCAAAGAAAT CTTGGCTTAA	300
	AAATGCATGT TCTAAATACA AAAATAATAA ATCTGTATAT TGTGTTTTAG TACGATACAC	360
	TTTAATTTGA GATTCCGTAT ATGATATACG TGTATCTAAG CGAAGATCAA TTAATTTAGC	420
25	AGTACTTGGG CGCTCAACTT TAATAGAATT TAATACGCGC ATATCTTCTA ATAATTTAAA	480
	AAGTTGTTGG ATAAAATTTA GGGLGTTTAA AAGTTTTATC TTGLACTACT TCATTTACAA	540
	TTTGtACATC CATCATATGA TAACCGTAAG CAGCTAACAT AACATCTGTT TTTAAACCAG	600
30	CCATTTCGAT ATGGCTTGG	619
	(2) INFORMATION FOR SEQ ID NO: 937:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 615 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 937:	
	TAATCCCTTT CATAATGGGC ATCAATATCA TATTAATCAA TCTAAAAAAC TTACAAATGC	6
45	TGACGTTACT ATTGCAATAA TGAGTGGTAA CTTTGTCATG CGTGGCGAAC CAGCAATCTA	12
	TAATAAGTTT ACTCGTGCAA AAATGGCATT ATCAACAGCT GATTTAGTTA TCGAACTACC	18
	AGCAACTGCC AGTTTATCAT CTGGCGATCA TTTTGCCGAA CTAGCAGTTA AAGTCGCnGA	24
50	TTATATGAGT GTCGATACAA TTGCATTTGG TAGTGAAAAT AATGALATCA AAACATTAAA	30
	rCmATTAgCA CACAGCATTA ATGAAATTGA mCAATCTGAA TCCTTTTCAC AAAAAGTrAA	36

	AAGTCCTAAC AACATACTTG GTATTAGTTA CCTGAAAGCA ATTGCTAAAAA ATGCTAAAAA	480
	CATCAATGCA ATTTCTATCA AACGAGAAAA TGCTCAACAT CATGATTCAT TAATTCAACA	540
5	CCATCAGTTT GCAAGTGGTA CATCTATTAG AACATCAATC ATTAGTCAAG ATGATCATTG	600
	GCATCATGTG GTACC	615
10	(2) INFORMATION FOR SEQ ID NO: 938:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xT) SEQUENCE DESCRIPTION: SEQ ID NO: 938:	
20	AGAATTGAAG ATGGTAAAGT TTCAAAATAT CATTCGGTTA TCATAAAAGA CGCACAAGCA	60
	ACTTCACCAT ATTCAATTTT TATCAGAGGT GCTATTTATC GCTTTGAACC ATTAGTATAA	120
	ATATACGTAA GTGCTATGAG CGAGAATGCC CATATGAATA ATGACAAGCA CAATGGAAAG	180
25	AATCGTAATA TATTATTTAA TCGTGATGCT TAATTAAAAT GAAAAAGATT GATAATATAA	240
	ATGTGAAAAA GTAAGTATAC CCGTAAACTA AAGTATTCAC GGTGAGAGGT GCTCATGTCA	300
30	TAATGATGCA CGTGTCATAA TTATAATAGC TTANATATGT CCATACAACA CCATGTAGAT	360
30	ATGCATATAC AGGGTATGAT AGACATAGNG TCTGNGAAAT	400
	(2) INFORMATION FOR SEQ ID NO: 939:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 466 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40		
	(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 939:	
	GTACAGGTAT GATTGGTGAT CCCATCAGGT AAATCAGAAG AACGTGTGCT ACAAACAGAA	60
45	GAACAAGTAG ATAAAAATAT CGAAGGTATT AGTAAGCAAA TGCACAATAT TTTTGAATTT	120
	GGAACAGACC ATGGTGCAGT GCTTGTTAAT AATAGAGACT GGTTAGGACA AATCTCATTA	180
50	ATTAGTTTT TACGTGACTA TGGTAAACAC GTCGGCGTTA ATTACATGTT AGGTAAAGAT	240
	TCAATCCAAA GTCGTTTAGA ACATGGTATT TCATATACAG AATTCACATA CACGATTTTA	.300
	CAAGCTATTG ATCTCGGTCA TTTGAATAGA GAATTGAATT	360

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	GTAGATAAGC AAATGATTAA TAGTTGAGGG GTATGTCGAT GAAGCG	466
	(2) INFORMATION FOR SEQ ID NO: 940:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 329 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 940:	•
15	ATGAATCACC CATTGATACC AATCATTTAC ATCACTGTCA TACGAACATA TATTTAAATA	60
15	GAAAAAATT ATTTTAAAGA TTATAACTAC TCTTAATCAT TTTAGTGAAT TAAAAAAAAGT	120
	AGTGCAAAAA GCAAAATATA CTTTATACAC TACAAATCAT TTATTTAT	180
20	CCAAAAAATG TTCCAACTAA TGAAACCGCT TGTTCAGCAG TATGATTATN ACTGTCAATC	240
	AATGGATTTA CTTCAACTAA ATCCATTGAG GAAATTAAAT GTGATTGATG CAGTAATTCC	300
	AATGCNAAAT GGCTTTCTCT ATNACTAAG	329
25	(2) INFORMATION FOR SEQ ID NO: 941:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 941:	
35	CGATATAGTA CCAATTTATT TGAAGAAAAA TCCGAACTTC AAATTTCCGA TGAAGCAAGA	60
	TATACCGGTT ATTATGATTG GACCAGGTAC TGGAATTGCT CCTTTTAGAG CATATTTACA	120
40	AGAACGTGAA GAACTTGGTA TGACTGGAAA AACATGGTTG TTCTTTGGTG ATCAACACCG	180
•	TAGTTCTGAC TTTTTATATG AAGAAGAAAT AGAAGAATGG CNTGAAAATG GAAACTAACA	240
	CGCGTAGATT AGCATTTCCA AGAGnCCAGA CACAAGATAT GACAGCCnCG ATATGGAGAA	300
45	GTAACGTTCC ATGAT	315
	(2) INFORMATION FOR SEQ ID NO: 942:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 699 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 942:					
	TACCAATAAT CAACTTGTTT TACATCATCG TGTGTTTCAA TCACTTTCCT TTTTATACCT	60				
5	TTCTTACCTT TAAAGAATGC ATCAACATCT TTTATTGAAG ATCCTTTTGA ATCTTTAGTA	120				
	AATCTATAAT CTGCAAGTTC CACTTTACCC ATTAATTCTT TGTAATCTTT CCATCCTTGA	180				
	ATCCCTTTAC TATTCGTAAA CGACTTTTCT GTCATTAATG GATCCAACTT ATCAAGAGAT	240				
10	GGCGCATCTT TAATTCCTTT CATTTTCTTC TCTATTTCTT CATATTTCTC TAAATCTGGA	300				
	TCTTTCTCTT CTTCCGATTC TTTTTTTACA GTTTCTTGTT TTGATTCTTC TGATTTCTTT	360				
15	GATGATAATT TATGATTCCC ACCAAAAGAA CAACCTGCTA CGACTAAAAG CATAATTAAA	420				
,,	AGTAAACATC CCAGTGTCTT TTTCATAAAC TTTCTCCTCT TAAGTTATTT TGTTTGAATC	480				
	AAATAAACAT ACATAAATTT AAAAAACTTA TITATATTGA TATTITACAT TAACCATCAA	54 0				
20	TATTTTAAA TACTTTAAWT GATAATTTAA GAAAATTGTT TTGTCTAATA ATTTAAGTAG	600				
	TTAAAACATA GATAGATATA AAATAGTTTA TAGCCATTAA TTTATAAGTT TAAAATTCGC	660				
	ACTATTICAA TITGCCATTI AAAAATAGIT TGTTTAATC	699				
25	(2) INFORMATION FOR SEQ ID NO: 943:					
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 					
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 943:					
35	CGCTCCATAA ATCAACAATG TTCGAGTCTG TAATCTAGAT GATAAAACGC CAAGAATGAT	60				
	CATAAATGGC ACTTCTAAAC CAGCACATAA ACTAGCTAAA TAACCGACAT GTTGTTCATT	120				
40	TTCTTTTAAA TAATCAGTAA CAAATAAAGG CATATTCATC GTATACATCC ATTGTCCAAT	186				
	GTGTAATAAA ATAAATGCAA TAAATGGTAA TAAAAGCGTT TTGTCTTTAA ACATATTAGG	24				
	AGCAATTTTT TCAACATGTT GTTGCGTACT AATAGGGTGT TTAATGTTTA AATCCTTATA	30				
45	GANAAACACT TGAAGTACTA AAGTAAATAA AATGATACTT ATTGGGCCAC CAAACAATCC	36				
	AGCATAGCCT TTTAATCCGA TTAATTGGGC ACCAATAAAT					
	(2) INFORMATION FOR SEQ ID NO: 944:					
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 570 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double					

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 944:	
5	AAGATGACAA TACTTTGTTT CAAGAATTGA AAAAAGAATT AGAACAATGG GATTTTAATG	60
	TTGCTGGTAT TGAAGATTTC GGCAAAGTAA TGGATACATT TGAAAGTTTT AATCCTGAAA	120
	TTGTTATATT GGATGTTCAA TTACCTAMAT ATGATGGGTT TTATTGGTGC AGAAAAATGA	180
10	GAGAAGTTTC CAACGTACCA ATATTATTTT TATCATCTCG TGATAATCCA ATGGATCAAG	240
	TGATGAGTAT GGAACTTGGC GCAGATGATT ATATGCAAAA ACCGTTCTAT ACCAATGTAT	300
15	TAATTGCTAA ATTACAAGCG ATTTATCGTC GTGTCTATGA GTTTACAGCT GAAGAAAAAC	360
	GTACATTGAC TTGGCAAGAT GCTGTCGTTG ATCTATCAAA AGATAGTATA CAAAAAGGTG	420
	ATCAGACGAT TTTCCTGTCC AAAACAGAAA TGATTATATT AGAAATTCTT ATTACCAAAA	480
20	AAAATCAAAT CGTTTCGAGA GATACAATTA TCACTGCATT ATGGGATGAT GAAGCATTTG	540
	TTAGTGATAA TACGTTAACA GTAAATGTGA	570
	(2) INFORMATION FOR SEQ ID NO: 945:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1241 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 945:	
	CCGAGNCCAC CGTTCCAAAG TCCATTTTTA TCCCCATCCC TCTCTGAATT GAACTATAAT	60
35	TTTTGAATTT ATTAATAATG CTATTTTTnT TATTTTATCA AAAACTGATT ACAAATACAC	120
	ATAGAAAATG AAATATATTT TTCTTTGACT ATACATAACT GTTATTTCTT TGGATATTTA	180
40	TATTAAATGC ATTGGTAGTA GTTGTAGCGC ATTAATGTTT GACGGTGTAT AGTATTAATT	240
	ATATTGAAAG TTAGTTGGAA GTTGATAGTA GGAGTGGGAG CATTGAAGCG ATTTGTGGCG	300
	ACGGTATTAT TATTACTAGT CTTTATATCA GGATGLGGTA ATGTTAAATA TGTGAAAGAA	360
45	ATAGATGAAG CAGTTAAAAT TCAAAATCAA AAACAAGAAC ACTTGCCCAA AAAAGGCAAC	420
	GGTGATCGTG TTGATCATTT TGAACGCAAA GATGCTAATA TTTATGTCTA TGATAAGGAT	480

AAAATTATCA TTTTAGCTTA TAAACCTTTG AGTAATGATG ATGAAGTGCA TTATTATGCA

TATGATTTTA GTGATAAACG TGTATCATAT AAGCAAGATT TTGATTCGAG ACGATATTAT

CAACAACATG ATGCGGATTA TCATGAAGAA AATATGACGA ACTAGATATG AATAGGAGTT

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GGTAA	AAAAG	AATCAGCAAC	GACATCTTCG	AAAAACGGCA	AACCATTAGT	TGTCGTATAT	780
GGCGA	ACTATA	AATGTCCTTA	TTGTAAAGAA	TTAGATGAAA	AAGTCATGCC	-AAAGTTGCGT	840
AAAA	ATTATA	TAGATAATCA	CAAAGTGGAA	TACCAATTTG	TCAATTTAGC	TTTCTTAGGT	900
AAAGA	ACTCAA	TTGTTGGTTC	GCGTGCGAGT	CATGCAGTAT	TGATGTATGC	ACCTAAATCA	960
TTTTT	PAGATT	TTCAAAAGCA	ATTATTTGCT	GCCCAGCAAG	ATGAAAATAA	AGAATGGTTA	1020
ACAA	AAGAAC	TATTAGATAA	ACATATTAAA	CAACTGCATT	TAGATAAAGA	GACGGAAAAT	1080
AAAAT	AATATT	AAGATTACAA	GACAAAAGAT	AGCAAGTCTT	GGAAAGCTGC	AGAGAAAGAT	1140
AAAA	AAATAG	CGAAAGATAA	TCATATAAAA	aCGACACCAA	CTGCATTTAT	TAATGGCGAG	1200
AAAG	TTGAGA	TCCATATGAT	TATGAAAGTT	ATGAGAAGTT	Α		1241

(2) INFORMATION FOR SEQ ID NO: 946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1057 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 946:

TAATACAATG ACACCATTTA GCATGACCGT TATCCCTGTA ATTCAGCTGA TATTATCTGT 60 TGCAATTTTA TGTGACGAAC TGTTGCACTT AATTTGATAA ATCNACAAAT ACAAAAAATC 120 TAAGTTGAAC AATTATGATA CAACCGTGCA AACGATATGT AGTATAACTT GTCAACTTAG 180 ACTTATTGAT AAATATATTA ATAGTGGTTT ACCATAGCAG GAGATTTCAC ATCAAAATTT 240 TGAAGTAGCG TATCAATCTT TGAATCATCA ATATATACCL TATGTAAATT TTTCATATAC 300 ATCGAATGAG AAAGTGCTTC ATAATTTAAT GAAAAAGATA TATGATCTCC AACTTGATAG 360 TGTCCTTGAC CATTTAAATC AAGCATTAAA TGATCACTCG AAGCGCCTAA AATATTGATA 420 TGCTGATCCA TAGGTGAAAT ATTATCGACT TTTGTAYCTA AATAACCAAT ATCTACAATA 480 GCTTGTAAGA ATGATTCATG CGTTTGTGTA TTAACTCGAG GTTTAATTTC TAAAATCTCA 540 600 GCCTCCAATG TAATCGCATC TIGATATAAC ATAGCGATCG CTTGATITGT CGTTGTATCA ACACCTCTAA ACAACGTTTC ACCTATTCGC AATTCATTTA TTTTACCCAA ATCATTATAT 660 AAAAGTTGTG GTAACATGCT CGAATTACCA CCTGAAATAA TTTTCAATCG ATATCCTATT 720 TCTCTTTCAA CAGCTGAGAC GAATCGATTA ATCATAAAGA TATCATCATC ACTTGGCGCA 780 TCAGATTTAA AACACATAAA ATTGAATGCT AAACCTACAA AATGGATATT TTTCAAGTGA **B40**

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	CAATCTACCA TTAATAAAAT CTTATGTTTT TTTCCTAAAA CTTCTGGCTA CTTCATTTAT	960
	TTGATGTATG GGTAGATAAT TCCGGTTTGG GATACCTCCA TATCNAACCT TTTTTCCTAA	1020
5	TCAATATCCT GGAAAAnCCC TTTTTTTGGG CAGGGCG	1057
	(2) INFORMATION FOR SEQ ID NO: 947:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 649 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 947:	
	GATATCCGCT CGATGAATAT ACCTTTAAAG GTGTTGGTGC AAATTCTGAA CAATTAAGTG	60
20	CTATGAATCA TGATTCTTTA AAAAAGGAGT ACATTTCAAA TGACTGTTAA ATATAATCAA	120
	AATGGCGAAT TAACAATGGA TGGTATTAGT TTAAAAACGA TTGCACAAAG CTTTGGTACA	180
	CCTACCATTG TTTATGATGA ACTACAAATT aGAGAACAGA TGCGCCGTTA CCATCGCGCA	240
25	TTTAAAGATA GTGGATTAAA ATACAATATT TCATACGCCT CAAAGGCATT TACTTGCATT	300
	CAAATGGTCA AACTTGTAGC TGAGGAAGAT TTACAGTTAG ATGTTGTTTC TGAAGGTGAA	360
	TTATATACAG CTTTAGAAGC AGGTTTTGAA CCGAGTCGCA TCCATTTCCA TGGTAACAAT	420
30	AAAACGAAAC ATGAAATTAG GTATGCTTTA GAArATAATA TCGGTTATTT TGTTATAGAT	480
	TCATTAGAAG AAATTGAATT PATAGACCGC TATGCTPATG ATACGGTTCA AGTTGTATUA	540
35	CcGAGTTAAT CCcAGGTGgT TGrAAGCcAC mTrCaCaCgA aTTTATTCaA ACyGGGcaaG	600
	AAGGATAGGT TAAAGTTTTG GGATTAAnCC nnTTTCCCAT TAATGGGCC	649
	(2) INFORMATION FOR SEQ ID NO: 948:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 472 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 948:	
	TACAAAGCTT AAAAACAGAG CTTAGTYTCG TTGAACCATT AATTAGCCGC TTAGAATTAG	60
50	AAGAAGCTAA TGATAAACTA GCTAATATCA ATGATAAGTT AGATGACATG TATGATTTAA	120
	TTGAACATGA AGTTAAAGCT AAAAATGATG TCGAAGAAAC AAAAGATATC aTTACGGATA	180

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	AAAACTACTA TATAAATGAA TCTGATGCTC AGAGTGTTCG TCAATTTGAA AATGRAATTC	300
	AAAGTTTAAT TTCTGTATAT GATGATATTT TAAAAGANAT GTCTAAATCT GCTGTGCGAT	360
5	ATAGCGAGGT TCAGGATAAT TTACAATATT TAGAAGATCA TGTCACAGTT ATTAATGACC	420
	AACAAGAAAA GCTACAAAAT CATCTGATTC AATTGCGTGA AGATGnGCAG AA	472
	(2) INFORMATION FOR SEQ ID NO: 949:	
o 5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 949:	
0	AGAGGATCCC AGGCGTTTGT TGATCCAGCA GCCGATnCAG AATACATCTT CTATGCATAT	60
	AAACGTTTCA ATTTCGAATT GAAAGATCCA AACTTCACTA GTGAAGAAAA TATGTTTAAA	120
	GATGTATCAG ACAAACCATT AATACCTGCT CGTAAAGCTC AAATTACAAA TGCGAACTAT	180
25	AAACGACATG GTATGAAGTT GATGATTCTT GGGAATGACG AACCATATAA CAATGAGTTC	240
	AAGAAAGATG ATCGAAAATG CGAAGAATGA GAAATTTCAA AGGTGCGCAn GTCAAGCCAT	300
	GTGTCAGGGG GGCATATGAT TTCnGGTCAT CAGTAAGGAC TGTGTCATGC CATGGCCATC	360
30	TGTTGTACnG ATCTCTAATA GAATCTCAGA TGCCCGGCAA	400
	(2) INFORMATION FOR SEQ ID NO: 950:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 556 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 950:	0.
	AAAATCTTCG ATGACAAAGA AATCTAATGA TGTTTCTTTA AAATGACCAA ACTGCAACGG	60
45	AATGATATAA CCACACTTGA GATATGGCGC TTCTTTTTTC AACTTAGTCA TCACATCATA	120
	ATCCAAAGAC ATCACACGAT ATTGATGTTC AACACCATGC TTTTTCAAAA TATCAATAAC	180
50	ACSTTGTGTA TAATCTGCTG GTTCTTTACC ATGTGGCTTT AACTCTACTA GTAGCTTCAC	240
	ATTTGATTGT TTAGCCGTTT CAATAAATTC GTCTAAGGAT ACAAATTTTG CTTCATGTCC	300
	ATTTTGACGC ATTTTCAAAC CGACGATATC TTTGAAATTA GATTCAGAAA TATTTTTATT	360

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	CATAATTGTA TCTAACTCAA CGTATTCGAC ATTCGCTTTT GCAGCAGCTT TCAATGACGG	480
	AATAGAATTT TCAACACCTT TATCTTCGAA ACCACGTGGC CAATAATGGA GATATTGTAA	540
5	TTGATAGTAT TATTGG	556
	(2) INFORMATION FOR SEQ ID NO: 951:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 469 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 951:	
	TTGTGGTAAT GATGTTAATC AGTATATTTC TACTTTTGAC AATGACATCT AAAGGATTAA	60
20	GCAATCTTAG AGTAATAGAT GATGAGGCAA ATATCATTTC TTTTATTACT GAATTGAATT	120
	ATATTAAGTC GCAAGCTATA GCAAATCAAG GATATATCAA TGTTAGATTT TATGAAAACA	180
	GTGACACTAT TAAAGTAATA GAGAATAATA AAATACGATT TCTAAAATTA AAAGTAGGCA	240
25	AAATAATTAA TGTTGCAAAA GTTGATATTA TTGCCTTTGA TAAAAAAGGG AATATCAATA	300
٠	AATTTGGTAG CATAACAATT TACAATAACA ATTCAATTTA TAGGAATAAT ATTCCATATT	360
	GAAAAAGGCA AGAATTCGTT ATGAAAAGCT ATAAGTGTAA AGGTTCATTC TTAATAGATA	420
30	GTATGGCTGG nTTTTTGCCA ATTGGGATTG NATTACATTA CTATTGATT	469
	(2) INFORMATION FOR SEQ ID NO: 952:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 730 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	,
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 952:	
	ACATHTATAA THOTTATTTG CTTGCTCCTT TCACTTTTTA AGAGTAAAAH ATAACCTGAA	60
45	ACATAACTTT AACATCCAAG TTTCAGGTTA GTGTAATGTA AATGATTTAC TTTGTTNTAT	120
	TATGATTAAA CATCTAATTC TCTGCTTGTA AGTGCTTTAA TCATCTCTGG ATCAGCATGT	180
	GAGAAAAATT GGCTATTACT TTCTTCTAAT GTCGCAATTT GTTGTTTATC TTCTTCTGTA	240
50	AGTICAAAAT CAAATATATC TAAGTTITGA GCCATACGTT CTGGATTTAC TGATTTTGCG	300
	AGTACAACAA TGTCACGTTC TACTAACCAG CGTAAAATAA CTTGTGCAAT TGATTTGTTG	360

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	AATGGTGCCC AAGCTTCTAC CACAACATTT TCTTGTTGAA GTGCTGCAAC TTGTTCTTCT	480
	TGTTGATGGA ATGGATTAAT TTCTATTTGG TTCACTTGTG GTTGAATTTG ATTGTGAATA	540
5	CCTAAATCTA CAATTCGATC AACGCCGAAG TTAGATACAC CGATTGCTTT AAATTTTACC	600
	ATTTTCTTT AACTCCTCCA ATGCACCCC ATGGAGCCAT ATACHGCCAT TGGTAAAGGT	660
	TGGGTGGAAT NAAGCACCTA GGATCCAGGA TAGGTCCCAA ATTTTAATCC GGTGGGNAAT	720
10	GGATCGGTTC	730
	(2) INFORMATION FOR SEQ ID NO: 953:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 953:	
	ACAAATGACA ACGTACAATG ACGTCTTCAC AAACATGCAT TTTAGGAGAT TGATTATTAC	60
25	AAATATCCAG TTTTTTGTTA CATCTATTTG CAAATCTGCA CTTATTAACG TGAAATGCTT	120
	GGATTGATGG CACAATTCCT TCTATCGTTT CAAGTCGTTT CTGCTCTTCT TTAAGTTTTG	180
	GAATTGTTGA TAATAATTTT TGGGTATAAG GATGTTTCGG ATTGTGTAGT ATTTCTTTTA	240
30	TGCCTCCAAA TTCTACAATT TGACCTGCAT ACATAACTAA GACTTTATCG CAAAACTCAG	300
	CAACTACACT CAAATCATGT GTAATCATCA TAATTGCCAT TTGCGTTTCC TTTTGCAATT	360
3 5	CTTTTAATAA GTCTAATATT TGCGCTTGAA TCGTGACATC	400
	(2) INFORMATION FOR SEQ ID NO: 954:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 251 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 954:	
	TAAATCTTGA GGACGTTTGG TCTGAAAGCG ATGCTCAACT GTTGATAAAT CCAATTCGAT	60
	AACATCTGTA TAATTAGGAT CTTCTTTCTC AACATCAAAn ACATATGGTT TTGTTTCAAA	120
50	TATTCTTTTA CTAGCGCGAT ATGTTCGTCT GATCTACCAG TTAACTTCAT ATATTTAAGA	180
	ATTCTCATCA ACTGGGGAAG AATCCGCAAG TTGCTCCATA CTCTGGTGCC ATGTTTnCAA	240

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(2) INFORMATION FOR SEQ ID NO: 955:

(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 514 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 955:	
	AAACATTTAC ACAAGTAGTA GAAGCAATTT ATGATGAAGA AGGTAACAGC TTaGamgCGG	60
15	CGCGCCATCC ATTACAAATC GTTCAAATTA AAGTGGATCG CCCGATATAT CCAAACAACA	120
15	TGATGAGAAA GGAAATTGGC TAATGAAAGC TACTACAATC ATTGGCATAG CTGGTGGATC	180
	TGGCTCAGGA AAAACAACTG TAACTAACGA AATTATGAAA AACTTAGAAG GTCATAGTGT	240
20	CGCTTTACTT GCTCAAGATT ACTATTATAA AGATCAAAAG CACTTGACTT TCGACGAGCG	300
	CCTAGAAACC AATTATGACC ATCCATTTGC ATTCGATAAT GATTTATTAA TTGAAAATCT	360
	TAAAGACTTG AAAAATGGTA AAGCAGTAGA AGTACCGACA TATGATTATG CLAGTCATAC	420
25	AAGAAGTGGA CATTACCATT GGATTTTLAA ACCTAAAGAT GLTTATTTAT CGTAGAAGGG	480
	CCTTTTCGC CTTTAGGAAA ATAAGGGTAT TTAC	514
	(2) INFORMATION FOR SEQ ID NO: 956:	
<i>30</i> <i>35</i>	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 388 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 956:	
40	ATTTTAACGA ATATCTTGCC GTACGATGCC CAAGCTGCAT CTGAAAAGGA TACTGAAATT	60
	ACAAAAGAGA TATTATCTAA GCAAGATTTA TTAGACAAAG TTGACAAGGC AATTCGTCAA	120
	ATTGAGCAAT TAAAACAGTT ATCGGCTTCA TCTAAAGAAC ATTATAAAGC ACAACTAAAT	180
45	GAAGCGAAAA CAGCATCGCA AATAGATGAA ATCATAAAAC GAGCTAATGA GTTGGATAGC	240
	AAGCCATAAA GTCTCACCTG AATGACGGTC AAGTGTATAG CATAATAGTC ATGCTAAGTT	300
	AATGAGTCTC AATGTGTAGG GCACAAGTGC GGGCGTCTAT GCATGAATGT TGCCACGCTC	360
50	ACAACTGGGA AGTGTAAATG TGACTGTA	388
	(2) INFORMATION FOR SEQ ID NO: 957:	

(A) LENGTH: 394 base pairs(B) TYPE: nucleic acid

5	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 957:	
10	AACAAAGTAC ATCGCAGTTA CGAGAAGAAA TAAATGCATT GTATAATCAA GTTATAGAGG	60
	TTGGACAAGC GTTATCAAAG CAGCGTCGTA TAGTCGCTAG GGAGTTAAGW GACCACATTG	120
	TATCGGAAAT TCAAAACTTA CAAATGAAAG ACGCAAATCT TGAGATTTCA TTTAAAAAAAT	180
15	TAGAAGAACC GAATATTGAT GGAATCGAAT TTGTAGAATT TTTAATCAGT CCAAATAAAG	240
	GGGAACCATT AAAAAGTTTA AATAAAATTG CGTCAGGTGG AGAACTTTCT AGAATTATGT	300
	TAGCGTTAAA AAGTATTTTT GTTAAAtCGa GAGGTCAAAC TGCAATTtTr TTcGATGAGG	360
20	TTGaCTCAGG TGTATCtGGr caAGCTGcAC CAnA	394
	(2) INFORMATION FOR SEQ ID NO: 958:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 503 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 958:	
	CCGCCATTTT TTTCGATTTC TTTTTCAAGT TTTTCACGGT CTTTTGAAGA TAGACTATTG	60
35	AAATCTTTTG CACCACTATC ATCAAAATCA ATATCTGCTT TCAATTTTGT GCTAGATTTT	120
	AAAATGAAAT TAATTGGTTC TTCAGCATAL TTGATGCCGA TATYTAACGT AGATTTCTGA	180
40	GTGTTATTYT TTACGTCAGA ATCTATATTA TTTTCAAAAG TGAATTCATT TTCGTCGCTA	240
40	TATTTATCTA ATGCGACAGT GATTTACCT TTATCTTGAC GTTTTGTGCC ATCTACTTTT	300
	TCTTGGTTAT CTAATTTGAT TTTTGATTCA TCATATTCTG TCTTTTTACC AAATTCGTAT	360
45	TTATCATTAT ATTTATCATC TTTWTCTTTA GAAGATACGC CTTTAATTGT ATATTTCGCT	420
	TCAGCATACG TGTATTTATC TTGATCGAAA TCAAGTGCGT AATCTAGTTT TAACTTATCG	480
	TCTTCTAAAG TATTAGTACC TTT	50
50	(2) INFORMATION FOR SEQ ID NO: 959:	
55	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 307 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 959:	
	TCAAACGTAC AGAGCTTGTT AAGTGTTTAG ATTATTTACG AGAGAGCGAC ACATTAGTTG	60
5	TCTATCAACT TGATCGGTTA GGTAGAACGA CAAAACTATT AATTGAATTA TCACAATGAT	120
	TCGATGATAA CGGAATTGAC TTACCANATT AGTAACCTGA ACATTTCCAC GAAAGACCCC	180
10	ATGGGGCCAA AATGTTTTTA CCGATGATGA GTGCCTTTTT CCGGGTTAGA AGTTAATTTA	240
,,,	CTATGTGAGT GTATAAAATA GACTNAGCAG CCACAAGNCG AGAGGCCGAA AAAAGCGGGC	300
	GCCCTCT	307
15	(2) INFORMATION FOR SEQ ID NO: 960:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 960:	
	ATAAGGACAT TTATAGTCGC CATATACGAC AACTAATGGT TTGCCGTTTT TCGAAGATGT	60
	CGTTGCTGAT TCTTTTTTAC CGCAAGCTGT TAAAATTAAC ATGCTCACTA TAAATAATGT	120
30	TAGTAATTTT TAGTCCATAA TTACTCCTAA TCCTAACCAN GTCNGCNAAA TTTCCTCCAT	180
	GATAATCCGC ATCATGTTGT TGATAATATC GTCTCGAATC AAAATCTTGC TTATATGATA	240
	CACGTTTATC ACTAAAATCA TATGCATAAT AATGCACTTC ATCATCATTA CTCAAAGGTT	300
35	TATAAGCTAA AATGATAATT TTATCCTTAT CATAGACATA AATATTAGCA TCTTTGCGTT	360
	CAAAATGATC AACACGATCA CCGTGCCTTT TTTGGCAAGT	400
40	(2) INFORMATION FOR SEQ ID NO: 961:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 961:	
50	ACAATTAGTT ATACCCAAAA GAGTTATGTC AGTGAAGTAG ACAAGCAAAA CTCAAAATCT	60
	GTTAAATGGG GTGTTAAAGC AAACGAATTT GTTACGCCTG ATGGAAAAAA ATCTGCGCAT	120

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	GCTCCTGATA ATCAATTGCC ACCTTTAGTT CAAAGTGGCT TTAATCCATC GTTTATCACT	240
	ACACTATCAC ATGAAAAAGG TYCAGTGATA CGAGTGAATT TGAAATTTCA TATGGTAAGA	300
5	ACTTAGATAT TACCTATGCG ACTTTATTCC CTAGAACTGG TATTTACGCn GGAAGGAAGC	360
	ATAATGCATT TGGAAATAGG AACCTTGTAN TTANGTATGG	400
	(2) INFORMATION FOR SEQ ID NO: 962:	
10 <u>,</u> 15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 358 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 962:	
20	CTTTTACAAA GACAAATTAG CGGTAATCGG TAANGATCGT TGTTGATCCA GTTGCACTAT	60
	TGAAAGAATT AGACGGATTA AATGAACGTG GCATTCCTAC AAGTAATTTA CGTATATCTA	120
	ATCGTGCGCA AGTGATTTTA CCATATCACT TAGCACAAGA TGAATATGAA GAACGTTTAC	180
25	TGGTGACAAT AAGATTGGTA CACTAAAAAA GGTATCGGTC CAGCATATGT AGCCAAGTCA	240
	CGTATCGGTA TCGTATGCAG ATTACTTGAA AAGAACATCG AAGATATTAA ATCAACATGA	300
30	TATAACCAGC TATTCAAGGA TGTTACGAAC ATGnCACATT GATGAAnCTT GAGATATA	35B
	(2) INFORMATION FOR SEQ ID NO: 963:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 258 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 963:	
	AGTGAGCAGG TTGAAGTAGT AGGGCCGATT CAAATGGAAA GAGATACACA TAAAGATGGT	60
45	AAGGTAAAGT GGCAATTGCT TTATATAATG AATCAGGATG ATGATGAAAT TAAGCCACCA	120
40	TTTTTTATTC AATGGGAGGA AAGTGATTCC ATTGCGTACT AAAAAATTGC AAAAATATTT	180
	TCAAAACCAT TTTCAATTGA AACTGTATTG TGAAAGTAAA ACCGTCACAA CAGTATCGAT	240
50	TGGTTGAAnT GGTTGnAT	258
	(2) INFORMATION FOR SEQ ID NO: 964:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 388 base pairs	

(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 964:	
	TTATCAAACC GCCATAGCCA CATCTCGATT CAAGGATAAA TTTGTTTTCT CATATCTTAT	60
10	CTCTCATGAC AGTGCACGAT ATATATCTTT TCCAAATATT CATCACTTTT TTCCTGTTAA	120
	AATCATTTCT ATTATTAATG CTTTAATGAC AACTTATTTA ATTTATTGCA TTTAATGCCC	180
	TGCTTCATTT TCAAATATTA ACTTTAATCG ACTAGCTCAT CACACTATTT ACCCTTTCCA	240
15	CCTATCACTA CTGAATTCAA AACGATTTGT TTACAAATCC CCTTATGCCA ACGGTCGAAT	300
•	TTCATCATGT TTACATTTAA TTGCAAATGC CCTCTTGAAA TATTTTAAAA TTAATATTAT	360
	TCTTAGCATA CTAGTCGGAA TTATATTC	388
20	(2) INFORMATION FOR SEQ ID NO: 965:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 602 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 965:	•
	AAAGTGAGGT ATAGTCCGAC CATACTCTAA AAACGTAGCG AGATAAATAT ATTTCAATCC	60
	TAACTTTTAT GTTTTGAGGC ACTTGCCATT TAGGATATTG TCGTTCGTAA TACGACACTT	120
<i>35</i>	GTTGTATAAA TACACCTAGT CCAAATGGCA GCATCATGAG TAAGATACTT CTTAAATAAC	180
	TTAAACCAAT ATCATGCCAT ATGTGTCCAA TAATCAATTG AAAGACAATG ATAGATACTA	240
	TTAAAACGAT TATATTTATT GTCACTTGTT CAAACGCACT CCTTTTCCAA ATAATAGAAT	300
40	TGCTGCTTGC ATGACAACCA TAAAACATAC AAACATAGCA GTTTTAAGCG TTAGACTTTC	360
	TAGAATGTGA TTTAGAACAT GTAAGGGCTC ATTAAAGAAA TAAACGGAAT GTAAGCGTAA	420
45	GAAACGACCA ATATAAATTC CGAATCCATT TAAAAACATT AGCACGACAA CYATTAATCT	480
	ATTAAGCCAA CGGTGAGAAG TCAATGTTAG TATTTCAAAA TAGATTNAAA TCATCACATA	540
	AACCGCTAAG AAGACACCAA GCAGTAAATA GGTAAAGTAT TTCCACTCAC TTAAATTTAG	600
50	тс	602
	(2) INFORMATION FOR SEQ ID NO: 966:	
	(i) SECUTENCE CHARACTERISTICS:	

(A) LENGTH: 744 base pairs

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 966:	
	GTCCTAAGGT AGATTTATCT ACAACTGTTG TTATTTTANC AATTATTGGA GCGATTTTAT	60
10	TAATGTTTGC TAGCATATAT TTTATnAAAA TTGTGACATC ATACTTTACT AAGAAACTTT	120
	TAGAAATTAA ATTTAATTCG AAATAGTATT TTCAATGAAG TGCTTCAAAG CTAAACTTTC	180
	ATGACATTTT TTTGAAACTA GAGAAAATGG CTCATCAACT TCTAGCLGAA TGCCTTCTTG	240
15	AAAATGTATT AATGTTGAAT TCTCTATGGC AGTCATACCA ACAATATAAT GTGCATTGAT	300
	ATAAATTTGT ATCGGTGCAC GTTTATGTTT TAACGGAAAA AGTATAGTTT TTGGGTTGAT	360
	GTAAATAGGA ACCAGTTTAT TAATATTTAG TATGTTTTTT GCAGTCTCAA TTAGCACACT	420
20	TTGTGATGAT AAATGCAATT TCGCATAATA TGrAACGAGT TTGTTAATTG GAACTTTAAG	480
	AATGTAATCG CAATGTAAAA AGACACAATT TGTTTCGAGA TGGTTTGAAG TAGCAGTTTG	540
	GATATAAAGT AGATATTTAG TAGAATTGTC TTGCAAATAT AGTACTCCTC GTTTAATAAG	600
25	TTGTTAATTT AATGGTTAAA ATAAATTTAT ATGAAGATGT TAGGGTGTTT CAACATCATT	660
	AACACATCGA CCGAAATTTC ACAATAAACT AATTAAAATT ATGTTGGCAT TTACGCTTAA	720
30	CGGACATCTT AATTAATTTA ATCG	744
	(2) INFORMATION FOR SEQ ID NO: 967:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 503 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 967:	
	TACTTTGCAG GAGCATTAGG TATTCTAGCA TTTATAATGT CAATTGTATT GATTCACGAT	60
45	CCGAAAAAGT CTACGACAAG TGGTTTCCAA AAGTTAGAGC CACAATTGCT AACGAAAATT	120
43	AACTGGAAAG TGTTTATTAC ACCAGTTATT TTAACACTTG TATTATCGTT TGGTTTATCT	180
	GCATTTGAAA CATTGTATTC ACTATACACA GCTGACAAGG TAAATTATTC ACCTAAAGAT	240
50	ATTTCGATTG CTATTACGGG TGGCGGTATA TTTGGGGCAC TTTTCCMAAT CTATTTCTTC	300
	GATAAATTTA TGAAGTATTT CTCAGAGTTA ACATTTATAG CYTGGKCATT AWTATATTCA	360
	GTTGTTGTCY TAAWAWTAWT AGTTTTtGCT AATGGACTAT TGGGTCAATA ATGGTTAATC	420

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	TTTTCCnAAn ATTGCnGGGG AAG	503
	(2) INFORMATION FOR SEQ ID NO: 968:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 465 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 968:	
15	TACAGGTAAA AAAGGTGGTC CGTTTATCGA TTCATTAAAC CATCGTAGTT ACACGAAAGC	. 60
	ATATGTTTCA TCAGAAACCG ATATTCCATT TTATGCTGAA GCATTTGGAA TTAGAGAAGA	120
	AAATGTTGTA CCAACAGGTG TACCACGTAC TGATGTACTA TTTGATGAAG CTTATGCAAC	180
20	ACAAATTAAA CAAGAGATGG AAGATGAATT GCCAATTATA AAAGGTAAGA AAGTTATTCT	240
	ATTCGCACCG ACATTTAGAG GTAATGGTCA CGGTACGGCA CATTATCCAT TTTTTAAAAT	300
	TGATTTTGAA CGTTTAGCAA GATACTGCGA GAAGCATAAT GCAGTTGTGT TATTCMAAAT	360
25	GCATCCGTTC GTAAAAAATa GmCTTAATAT TCaCGTGAAC CATAGACCAT ACCTTAATCC	420
	GATGTGGTCC AGATCCATCC GTGGAAAGTT AAACGGATAT TCCnC	465
30	(2) INFORMATION FOR SEQ ID NO: 969:	•
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 300 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 969:	
40	AATTCGGAAC AACGAGCTGG CAACAACATA AGATGACAGA GGCGAATGGT CAATCAATTC	è0
	AAGTTAACTT AAATAATGCG CAANGCGATT TGGGATATTT AACTGCTGGT AATTACTATG	120
	CAACAAGAGT GCCGGATTTA CCAGTAGCGT TGAAAGTTAT GAGGGTATTT ATCGGTATTC	180
45	GTAAAGATGA TACAACAACN ATTTACTCAC ACCTATACTC TAAAAGATTN CACACGTCAT	240
	CACAACGGCG ACTTGAGCAA CATGGACAGT TCCTAATGAA CATAATCAAC GGTATTGTTC	300
50	(2) INFORMATION FOR SEQ ID NO: 970:	
50 55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 970:	
5	ATACGCGAGC GAACGGTGAA GCGACTTGCT GCTGCAAAAC GTCTGCGACC TTGAGCAACA	60
	ACATGAATGG TCTTCGGTTT CCGTGTTTCG TAAAGTCTGG AAACGCGGAA GTCAGCGCCC	120
	TGCACCATTA TGTTCCGGAT CTGCATCGCA GGNATGCTGC TGGATTATCA TCCGATTTTT	180
10	AAAACGTTAT TAGGCGTTGT CGTTGCAATT CAATTTACAG TACCTGCTTT GATTGGTGCA	240
	TTGGTTGCCA TGAAATTTGA CCTATCGCCA TTAGCAATTG CTGTTGTGGC AAGTGCAGCA	300
	TATGTAGGAA GCGGTGCAGC GCAGTTTAAA AATGGTGCTT GGATGATTAC GGGTATTGGT	360
15	GATTTAATnA ATACAATGAT TACAGCAGCG ATTGCAGTTG	4,00
	(2) INFORMATION FOR SEQ ID NO: 971:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 251 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 971:	
	AAGTGTAAGA TTAGAATAAA AAATTTATAA ACGAATTGAG AAAGACCAAA GCTAGCAATT	60
30	ATTCAGAAAT TAAATCGAAG AGTCCTACAG TTAATGACTT ACCTGAACGA GATTTATCnA	120
	ACAAATCTCA GTATGACCAA TATGGCAAAT GCCGTGTCCA TGTTAACTGA TGAAAAGTAC	180
35	TTTGGTGGTA GTTTTGAAAG ATTACAAGCA TTGACGACAA AAACAACATT ACCCGTATTA	240
	TGCAAAGnCT T	251
	(2) INFORMATION FOR SEQ ID NO: 972:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 414 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 972:	
50	TGAAGCTCTT AATAAATCTT TTCTTGAACA CACACCAACA AAATCGTTAT CTTCATTAAT	60
50	AATAAATAAT GTACTTACAT CTTCTAAAAA AATTGTACAA ATAGCGTCAT AAACTGTTGT	120
	ATTCTCTCTT AGCACAACAG GTTGAGACAT ATAGTCCTTA ACCTCAAATT GTCGAAGTTT	180
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TTCTAAAAAA CCTGACATTG TTAATATCGC TAAATCTGGT CTAAGCGTTG CTCTTGTTAA	300
ATTCAACTTA TCTGCTATTT GTTCACCAGW AATGGGTCCT TTAGTTTTAA CAATTTCGAT	360
GATTCGTTCT TGTCTTTGAC TGAGTTCTrw AGGKCTTCAc CCCTTTtTAT GCnC	414
(2) INFORMATION FOR SEQ ID NO: 973:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 747 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 973:	
GAAATCGATA CTAATATCTT CTTTATTTAC ACCTGCTAGT TCAGCTTCTA AGTAATATAA	60
TTCGTCTGTt CATALATATE CGTtACAAAT GAAGGTGTtG AAAAGTAATT AAATACTTGT	120
TTACCTAAAT CTTTAAATGT ATCACTTGGA TTACCGTTAA AAAAGTTTTG ATTCTCGAAT	180
TGATTGAAGT TCALATCATC ACTTCCATTA TAGAAATTTG TATTACAAAG CCATTATATG	240
AGTAGTATTA AAAAAGTTAA AGTAAAAGGG GAGATAAAAA AGTAATAAAT GGGTAGATTT	300
GTGCCTGATA AGGAATCAGG GCAAAAGAAC TGAGCATCGA GATTTATACA AGCAATAAAG	360
ATAATGAATA AACATATCGA TGCATACTTC TGCCCATCAC CTTATGATAG GGAGTTATTT	420
TTTGTCGGAA TAGTCAAAAT TTTTAGAAAC AAAATTCCGC AAATTATTAA TTATATCTGA	480
TGCTTCTCGT TCTGAAATGT TGAATTCATT AAAGACCTTA ACAGAAATTT CAGCAAGAGG	540
GCTTTTATT GCTTTACCTT GTTCTGTTAG AGAAATTTGT AGGTTTCTTT CATCTTTCTC	600
TTCACGTGTT CGAACAACGT AATCTTTCTT TTCTAATTTC TTTAGTAATG GKGTCAGTGT	660
TCCAGAATCT AAGAACACAC GTTCACCTAA TTTTTTGATG TTAAGTTTTT CATCATTTTC	720
AATCGCCAAT TAAACCANGG TANCNGG	747
(2) INFORMATION FOR SEQ ID NO: 974:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 257 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 974:	
TGCTTCCAAG TAATGTGGAC ATTTAATACG AGCTGGGATT GAGATACACC TTGCAATGCT	. 60

	TCTTGGnCAT TTGCATTGCT TCTCCCAAGT GAATGCCTTT AACAGCTTGT GTCATCATCG	180
	ATGACTTGCC ATTGAAATCG ACAACCTTCA CCTTCAAACT TAGCATCTTT. TATAATGCCG	240
5	nCTTCTATAT CAAATGT	257
	(2) INFORMATION FOR SEQ ID NO: 975:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 451 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 975:	
	CAATGGAGCA TATTTTACGT TCGGCAATGG ACATTGATCA NACAACAAAA CATTATATAA	60
20	mTAATAAAGT AGAAGTTATC AAAGAAATTA TTAAAAAAGT AAGAGGGGGA AATCACGTGA	120
	CATCACAAAA TCCAGAAGTT AATTACGAAG CATTAGCTAA ATATGGCCGC GACTTAGTAG	180
	AAGAAGTTAG ACAAGGTAAA ATGGATCCTG TTATAGGAAG AGATGAAGAA ATTCGAAATA	240
25	CGATTCGTAT TTTAAGTCGT AAAACTAAAA ACAACCCTGT GCTCATTGGT GAACCAGGTG	300
	TTGGTAAAAC TGCAATTGTT GAAGGATTAG CGCAACGTAT AGTTAAGAAA GATGTGCCAG	360
	AATCATTATT AGATAAAACT GTTTTTGAGT TAGATTTAAG CGCATTAGTA GCGGGCGCTA	420
30	AATATCGTGG TGAATTTGAA GAGAGATTAA A	451
	(2) INFORMATION FOR SEQ ID NO: 976:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 571 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 976:	
•	AACTATTAAT AATATTAAGT TCACTACAGA TGTTGCTAAT GGACCATAAG TTTTAAAGAC	60
45	ATCTTCACTT TTATAACCAA CAATCGCATC TAAAAATTGA ACTAAGATCA TTGCAATGGA	120
	TATAGTTATC AAAAATATAG CACTATGAAT GACTAAAGAA ANAATAGCTA ATAAAAATAA	180
	AGGTAAGCTT CGACTAAGTG CATAATATGC ATTTATATTA TGGCTAGATG CACATGCTTG	240
50	AATTGAATAA CCTAAACTTA CACTGGCACT GATTATTGTA AATATTGCTA AAACAAAATA	300
	CATGTTAATC CTTCTTTCTA TATTTGGATA TAAACAAGTA CTTGTCTAAA GTTATTTAAA	360
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TATAACTATG TCATAAACTG AATTTGTTGA AATTTTTCAT TATGCAAATT TATTAATAAC	480
AAACAGCTCG AACTATAGCA TCATTTTACT AATGAATGCA TTAAAGTAAC TATGACTAAA	540
AATGCATATT AATTATCATT ATTAAGACTA T	571
(2) INFORMATION FOR SEQ ID NO: 977:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 274 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 977:	
CCCGAAAAAA TTTAGACATT TTCAAACAGT AACATTTGAA GATTTGTCTA AGCTGGAAAA	60
GAGTAGTATG CCATCAGGGG TCGGTATATT AGGCTATGCT GTTGACAAAG GTGTTGCTTT	120
AAACAAGGGG CGCATTGGTG CAAAAGAAGG ACCAGATGCG ATTAAACAAG CATTTGCAGG	180
TTTGCCGGAT TTGAATCCAT GTGnACTTTA GTCnGATTAC CGGAATGTTT ATCCTGGTCA	240
TGGGGGAATT AATTGGATAC CCCAAAAAGG AATT	274
(2) INFORMATION FOR SEQ ID NO: 978:	*
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 877 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 978:	
nTnTTACTTC TTCTTTTAAT ATTTCTCGTA TAGCTTCAAA TTTTTCACTG TCAAACAGTG	60
TTCTTAATAT CCCTTGCTTT TCACGACTGT TTGATATTAA AAAGCGTTTG AATTCACCTT	120
GAGGCAAAAT AAACAATTGT CGGAATTGAT CTGCATTTAC TCCTAATAAT TCAATAATGA	180
ATTGGGTACC TGAAATTACT TTACTTTCTC TAATTTCATA CTTGCCATCC ACCATCTCAA	240
ATACATCAAA TTTAGCGTTC GTTTTTGTTG TATTACCTTC TTTGATATAA GGGCCTTGTC	300
TATGCACTTT ATAAATTCGA TGATTTAATT GAAATTCAAA TGTTACTGAC ATCGGCTGTT	360
TACCATCAGC GAAATGACTT CTCAAATCAT TTTCTTCTCT TTGTTCAGTT GATGCTTTAC	420
CAAACAAGGC ATAAGTCATT GCATCAAAAA TCATTGTTTT ACCCGATCCA GTCTTACCAC	480
TTATTAAAAA CAATTCATTA TTATCAATTT TAGAAAAATC AATTTCTTCT TTTAAAAAGG	540

	CGTTTTCTAA AATATTTTTT ATCTTTTTAG ATTGGATATC CGATAATTCT TTATCAGTTA	660
	TATGTTTATA AAACATTTCG ATAATTGACA TGTCaTCTTT TTCACTTATT TCYATAGCAT	720
5	TATTTTCTTC ATMGTAATTA AAAGTTTCAT TCGTCAGCGC TAAAGTATTA GGATAAATTM	780
	GTTTTAAACT CATCATTGGA TCAGTAATAT GAGACATATT TTTAAGTTTA AAATGTAAAA	840
	TAATTATCGT TATNTTTCAC ATGAACTTNT TCATTAA	877
10	(2) INFORMATION FOR SEQ ID NO: 979:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 624 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 979:	
	ATTGGTACTA TACCATTTGT CCATTTTAGC GAAGACGTTA AACTATCGAT TAGCTAGTGA	60
	AGAAATTAAT CTCACTATAC CTTCTATACA TAAGCAAATT AAAAATTTAG AACAGCATCT	120
25	CAATGTGAAA CTATTTGAAA CTTATAAAAA TCAAATTATC TTGACTGAAG ATGGTCATAC	180
	ATTTCTTCCA ATTGCGCAAA GTTTTATTGA ACAATATGAA AGTGGCATCA AACATATCCA	240
	ACTTAAAAAA ACGATGTTTC AATCGAAATT AAATGTTGTC GTGTCTTCAT ATATCGCGAC	300
30	ATTCATTATG CCCAAATTTT TAAAATCTTT CTTTAACGAG CATCCTTTTA TCGATGTTTC	360
	TCTTCATGTC AAAAATGAAA ATATTGAAAA AGATATTAAT AATCATACGT ATGACATCGG	420
<i>35</i>	GATTAGCAGA AATCAACCTA AACTAAGAGA AGTTCATTCT GAAAAAGTAT GCGAAGGTAA	480
	AATTGTATTG ATTGCTCCCA ATAAAGAGAA TAATCATCTT CTAACTGAGG CATCTTTATT	540
	TGAAAAATAC AAAATAATAA GTGATAACCA TCCAGAATAT TGGGTCATCA CTTAAAAATA	600
40	ATATTITAAA TATTTATGAA AAAG	624
	(2) INFORMATION FOR SEQ ID NO: 980:	
4 5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 457 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 980:	
	TTTGTCCTGT TGCATAAACT GCAGCTAGCA TAATGTTAAT TGTTGCACCT ACGCTAACCA	60
	TITALCTAL TACULUMCE OCUACINACE TENTOTTALE TOLIGONICE TENTOTTALE	,

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TKGATTCATC	AATTTCAGCA	CCTAAAGCTT	TAAATCCTTT	aatatgttga	TCAATTGGAC	180
GTGGCCCAAG	TGGACATCCT	CCCGGTAAAC	CAATCACACA	TTTTTTAAAT	CTACCTAACA	240
TGGCACCCAT (CATATAGTAT	GAAGCACGTA	ATGATTCAAC	TTTATTATTT	GGLAATGCAG	300
CATTTTGLAT	TTCAGTTGTA	TCAACTTCTA	AWTCCGTACC	ATTTAGTGaw	GCCTTAALAL	360
TTAAAtCtkC	LAALAAACT C	aCTAAAGTTT	TAACATCAGA	GATTTnGCGG	TAACCCTTCT	420
AATTTCACAT	GTCCTTGAGC	TAATAATGTT	GCAGGAA			457
(2) INFORMA	TION FOR SE	EQ ID NO: 9	81:			
(i) SE	QUENCE CHAP	RACTERISTIC	S :			

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 981:

(A) LENGTH: 997 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

ATTGCAGCAA CGCCCCCTGT AAAACTACGT ACTCTTACAT TTATGAAACC TGCTTCTTCA 60 AACATGCGCT TCAACTCTTC TTTTCCAGGA AAATTAAACG TAGATTGCTG TAACCATTCA 120 TATTCTTCTT TTGATTTTGC AAATAATTTT CCAAAAATAG GCATAACAAA TTTAAAGTAT 180 AGTGCATACA TTTGTTTAAA GACTGGCAAA GTTGGTTGGC TCGTTTCAAG ACATACCACC 240 ATACCACCTG GTTTAAGTAC TCTATTCATT TYTTTTAACG CGACTAAATA GTCTGGCACA 300 TTTCTTAATC CAAACCCAAT TGTTACATAA TCAAAAGAAT TGTCTTCAAA CGGCAATTCC 360 420 ATTGCATCAC CATGAACAAG TTTAACATTT TCCATTGAAG CAGTTTTTTC TTTTCCTACT TCTAACATAT TCTCACTAAA GTCAATACCA GTAACTTCAC CTGTTGGTCC TACAGCTTTG 480 CTTAATGCGA TTGTCCAATC ACCAGTACCA CAACAAACAT CTAATGCTTT CGTCCCTTTT 540 CTAACACCCA TGTCTTTCAT GACGCGTTTT CTCCATACTT TATGCTGCTC AAAACTAATA 600 ATATTATTTA ATCTATCATA TTTTTTTGAA ATATTTTGAA AAACGCGATG TACTTGCTCT 660 TTATTTGCTT TATTGTCAGC CATGCTTAAT TACCTCTACT TTTTAAATAA CTTTTTTGGA 720 TATOGTGTAA GTAATGCTTT ACTTCACTTT GATTATATTT CTTGAAGTAT GATGGATAGT 780 AATCAGACAT ATCTTCAAAT AAATAATTAT ATATTTCCGA CTCATCAATA TTGATACCGA 840 AATGAGATAA CGTAALATAT GGGAAAAGTG LTTCAATTTT TACTATTGCT TGAGAAATTT 900 CATAATCATT TAAAGCTTGA TGATGTAATG AAGATTTCAA TTCATTAATT TCAACAATTG 960 CTTTACTAAT TTCATTTTGA AATGATAAAT CATTGAT 997

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(i)	SEOUENCE	CHARACTERISTICS
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(A) LENGTH: 1118 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 982:

10	CATTCCCTTT	ATCGGnACAA	TTATTTTAAA	TAATTGGTTA	ATAAGTTTTT	CTATTAATTG	60
	CTGTTTTACT	TTCTAGAGCA	ACAATAAATG	TTTTCAGTTT	AAAATAATTA	AGATTGTCAT	120
15	TTACTAATTT	GCTTTTTCCA	TTCTTTAACC	ATAAATCAAC	TTGTAATTGC	CACTCAATAG	180
15	GATGATTTT	AATATAAATT	TGCTCTGGAA	AAATATAACC	ATAATTGTGC	ACTACTTCTT	240
	GATCAGTTAA	CTGTAATTGA	TACATTGCAC	TTAAAGTGGG	TTCTAAAACA	GAATTTTGCC	300
20	AGCGACAATA	TTTGATATAT	TGATTAATTG	CGAACTTTGA	TAATTTATAA	ACAGCATGAT	360
•	AATCACAAGG	CGCCTCATTA	AACAACTCAC	TAATTTTGGC	ATTTCTTTTT	TCAGCGACAT	420
	ATTTGTGCCC	GCCTAAATAT	TGTATTTGTT	GAAACATCAT	TATTTGTTTT	TTCTCTAAAT	480
25	TGAACGTATG	AAGTTTTCGA	GTGAATGGAT	TAATAAACAT	ACTTTGAAAA	TGATTGAACT	540
	TCACTTTATT	ATGACAATAA	TCAACATCAT	TTAmTAACCA	ACTTACTTTA	TATCCCATTT	600
	TCTTKAAACC	TTCCGTTCGT	TGAAGAATCT	GTTTATAAGG	AATTGGCGAA	TACTGTAGCT	660
30	CAATAACATA	TTTATTATTA	ATCAAAATAT	CCGGAATTTG	TTTTATTTCT	TTTAAAAATG	720
	GCTCTATCTC	TACTTTACAT	CCTTGTTGCI	GTATCATCTO	TGCTAAAATC	AATTTACTTT	780
35	TATAATGTTT	AATCGTTTCA	TTATTAAAAC	ATTTTGTT	CGCTAAATGT	TTATGTGCAA	840
	AATGACTAAT	TACTTTGAGC	CCACGCTTT	AAATAACTTO	CTTGCCACAC	ACCGGACAAA	900
	AATATTGTGT	CTTTCTCAAT	GCAGTAGTT	CTAATACGC	TTCCTTTTC	T TCATTTAAAG	960
40	CTACTAACAT	ATCTTCACCT	CAAAATATT	A CACGTAAGT	TAACTACTA	r TACTTTTTCA	1020
	GCTTTGGAAI	A TCCATTAAA	AAAAGGGAC	CCCAAAGGA	G GCCTCCTTT	C ATANGTGCGG	1080
	ጥርርርርጣን እጥ	T ABATAATCC	TTAATTCCA	G GTGGnCnC			1118

(2) INFORMATION FOR SEQ ID NO: 983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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	CATCCCCTGT TAAAAATTGn TATTTGTGTA TTGATGCTTC TCAGnCATTA TTACGAGTCC	60
	ATATTCATTG CTTCAGTGAA ATATCAGTAG CAATAACATT TAAATCCGGC TTTTCACATT	120
5	TCAAGGTAAT TGCAGTACAC CACTACCCGT TTCCGATATC TACGGATTGT TGCATCATCT	180
	TCTAACTGTT GGTAAGAAAT GCAACCATTA CTGCTTCAGT TTCAGGTCTG GTATCAAACA	240
	ATTTGAGTTT ACATCAAACG GTCTACCTT	269
10	(2) INFORMATION FOR SEQ ID NO: 984:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 298 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 984:	
	AACCCAAGTG GAAnnGGTTT TGGTGGAAAA ATTTTAGGTC CTTTATCTGT CGTGCGAATC	60
	ATTGTATTTT TTAAACTTTC CGCATAATCT TGATGGTCGA TTAACTTTTC GCGATAACAA	120
25	TATTCAATCA CTTCAGAAAT CGCTTGCTCT GATATCTCTT CTTTTTGTAA ATATTGTATA	180
	ACTTCTTTTT CAGTTCTCTT TTTATATGAT AAATATTGGA TTGCTTTATT TAAACCTATG	240
30	CGATAATGAT CATACTTTTG AATCTCTGCC ATGTCAGCAG CnTCAAGTTG TnGCCCTT	298
	(2) INFORMATION FOR SEQ ID NO: 985:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 431 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 985:	
	CCATGCGATT CCACCTATTA ATAGTAAGAC AATAATAATA GGAATTATAA TTTTTAACTT	60
	TTTAGACATT TTGCTTCCTC CCAATTATTT ATGAGTTAAT CATATCAGAA CAATACATTT	120
45	TATTAAATGG TTTATTTTAA ATTTTGTTTA AATTAATAGA ATTTTAGTTA TAATAATGTT	180
	TAATAAGTTA TTGGrAATCY AATAAACTAC MAAAAATAGT TTGATTACAT AATGATTCET	240
50	GAAAAATGKT GGKTAACYTA ATAATATGCA TTTTTTKGGC GArGArGATT tATTtAACYT	300
	ATAAAAATAT KGAAGTAAGA TEGGGGAGAT EATGAATTEA TGGTATEGAA AGTCGATGAT	360
	TTTGTAAAGA ATATAAAAAG ACCATACTTG ACTGTATTGG GAGTATTTGT AGTTGCAGTT	420
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(2) INFORMATION FOR SEQ ID NO: 986:

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5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 329 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 986:	
	AAGGTTAGGn TGGAGTACCC AAAGTAGGTT TTAAAGGTTG GAAATACNAG GAGGATGAAT	60
	AACATGAATC AGTCAGTCAA ATTACTTAAA CATTTAACAG ATGTAAACGG CATTGCTGGT	120
15	TATGAAATGC AAGTTAAAGA AGCAATGCGT AACTATATAG AGCCTGTCAG TGATCAAATT	180
	ATTGAAGATA ACTTGGTGGC ATTTTTGGAA AGAAAAATGC TGAGAATGGT CAATACTCAT	240
20	TATGATTTCT GGTCTATGGA TGAAGTGGTT ATGGTAACAA GATGTAAACT GTTATTCATT	300
	ACGCGTGGTG TGTGATCAGC nGCACTCAA	329
	(2) INFORMATION FOR SEQ ID NO: 987:	
<i>25</i>	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 545 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 987:	
35	CATATTATTT nTATATGAGT TTACCAGTGT CAAAAAAACA ATTGCTTAAT GCCAACTATA	60
	TTACATGCAT TGTTTTAACA TTAATTGGAA CGCTTGTTAT TAGTTTATAT GCTTATGAAG	120
	CAGATGTGAT TGAACCAAAT TCAATCTATT TTTCAACTGC ATATGCATTT GTCATATCTA	180
40	ACTTCTTGTC TATACCAATT GCATTTAGTC AATTTACAGA ATTGCGTAGA GTCAAAGTGC	240
	CATATGGTAT ATACGTGTTT ACTATTATCA TTTTAGTTCC ATTTTTATTT TCAATTGCAA	300
	TAGTATTGGT GAATTATTTT GTTCTAAGTC AATCATCATT CCCAGATTTA TATTCATATA	360
45	TTTTAAATAT TGGTTTTCTA ATTATAAGCA TTGTTATACT TATTGTTAAT TATTTTAAAC	420
	AGCTCAATAA AATAAATACT AGAAAATTTA AAGGAGGCAG TCGATGAAAT TAGAACATAT	48
	TACAAAAAA TACGGCTCAA ATGTCGTTTT AAATGATATI GATTTTGACT TTGGCGAnAG	54
50	TAGAA	54
	(2) INFORMATION FOR SEQ ID NO: 988:	

5	(A) LENGTH: 607 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 988:	
10	ACCTAGCATG ACATAATCAA ATATATCAAA AACACCTTTC TGAACTGATT CAACCGTTCC	60
10	AATAGTTAAT GGTCTTTCAG AATCAGATGT CTTTCCACCT TGAACAGTCA GATGACTAAT	120
	TAAAATATTG ACGGCATCTT CATCAATTTC CGGTGCTATT GTTTCAATAC AGCGCGTAAT	180
15	TCCCTGTTGA TGTGTTTCAA TGGTGTCATC TTCAAAGTAG TGTTTCATTT CGCTCACAGT	240
	AGCATARGGG AGTGTATARA RATTRACCCC ATTTATCTCT ATTGGTGRAT TRATCGATGT	300
	AAAATCTGTT CTTATAAATA ACTGATTATG TTCAAACCAA CTCGCCCCAT AGTTTAACCT	360
20	CTCTTTACCA TCGTGATTTC CACTAATAAT AATTATTGGT ATACGCAGTT CTAAATTTAA	420
	CTTTCCAATC GCTTGTTCTA ATAACATGAT TGCATCTTTA CTTGGATATG TTGTGTCATA	480
	TAAACTCCAG CTATCACAAT GYTATCAGGT TCTTCTTCTT TCATTTTTTC TACGAACATA	540
25	TCTAAAATAT ACGCTTGaTC TTCTAAAAGC TGTTTGCCAT CTAATATTTT CCCTAAGTGC	600
	CAGTCTG	607
30	(2) INFORMATION FOR SEQ ID NO: 989:	•
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 722 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	*
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 989:	
40	ATCGCGTTAA GCAACAATTA CAACAATCAT CATATAAGCT AACGCCACAA CGCGAACTAC	60
	TGTTAGAGTT CTAATTGAAA ATGAAAAAGA TCATCTAAGT GCTGAAGACG TATATCTGAA	120
	AGTAAAAGAT AAAGCGCCTG AAATTGGCTT GGCGACAGTA TACAGAACGT TAGAGTTGTT	180
45	AGCTGAACTA AAAGTTGTCG ACAAAATTAA CTTTGGTGAT GGCGTCGCTC GTTTTGATTT	240
	AAGAAAAGAA GGCGCAAAAC ATTTCCACCA TCATTTAGTA TGTATGGAAT GTGGTCGTGT	300
50	AGATGAAATC GATGAAGATT TGTTACCAGA AGTTGAAAAT CGAGTTGAAA ATGAGTTCAA	360
	TTTTAAAATT TTAGATCATC GTTTAACTTT CCATGGTGTG TGTGAAACGT GCCAAGCTAA	420
	AGGTAAAGGA TAGTAAATTG CGTAGGTTAA ATTAACCTTC GCTTTTTTTA GAGGTGTGGT	480
55		

	TAACACAATT GGTGCTTATA GACGTGATTT GAAAAAGTAT CAAGATTATA TGACTGAACA	600						
	TCATATCTCG CATATTGATT TTATAGATCG ACAATTAATT CAAGAGTGTn TGGGGCATTT	660						
5	AATAGACCAA GGGCAATCTG CTAAATCTAT TGCGCGATTT ATTTCAACAA TCCGTAGTTT	720						
	TC	722						
	(2) INFORMATION FOR SEQ ID NO: 990:							
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 366 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 							
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 990:							
20	ATCCAAAAAA TACGAAAGCG CTTTCTATAT TGGTATGCAA GTATTTCAAA AAGAATAAAT	60						
	TTAATTTTCC TACTTTTCTA AACATTTATC TTTATGTATA ATGTTTTCAA GTAACTAAAT	120						
	TATAAATTAA ATAAAGGGAG TGTTTATCAT GCTTACAATG GGGACAGCAT TAAGTCAACA	180						
25	AGTAGATGCC AATTGGCAAA CTTATATTAT GATTGCCGTC TACTTCTTGG GTnATGACTC	240						
	CAACTTATTG ATAGTGTTnT TATGTTTCAG ATAATGCCCG ATGACTTTGT CATGCCAGCT	300						
	CCACCGATTT TGAGnAACGA CAGCGACTTC CGTCCCCAGC CGTGCCAGGT GCTGCCTCCA	360						
30	GTATTC	366						
	(2) INFORMATION FOR SEQ ID NO: 991:							
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 338 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear							
40								
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 991:							
	TGACTACAGT AACATTACCT GTAAATAATG ATTGAATGGC TTCATTTTCA TCATGAATAC	60						
45	CTGTAATAAA TTCTAATTCT TCATCTGAAA CTTTTACAAT ATGCGCCAAT GGCAAAAAGG	120						
	TATGAATAGT TTGTCTTAAA TCTTCAGCGT TATCCCATAA TGGCAATCTT ACATTAGGAT	180						
50	CAAATACGAC AGTACCATTT GCATTTAATG TTTTGGTAAT CAATTGATAA TGTGCATCTC	240						
	TCATCGGACT ATCGACCAAA TCAACAGAAC AAAAATGTAC TACATCATTT TCATTCACAT	300						
	CaATATCATT CACAAAACTK GGKTCAAATA aCATATCn	338						

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5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 371 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear				
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 992:				
10	AGTTCATCGT ATTCTTAATA CCTATATGCT ATCGTTCACA AACTTTTGTT CTTTTCTTCC	60			
	AACATACCGC CTATAATGCT CAAAAAGAAA TCAGCAGTGG AACCACTACG TTCCCTACCG	120			
15	CTTTATCATT TTCAGGCTTA AATATTTTTA AAATTTTGTG AGGAATCCGC TTAAAAAAAC	180			
	TCATATCTTC AAAAAAAATG ACAAAATTTA AATTTTTGAA TAACATCATT TTTTAGTAAA	240			
	TGTTATAATT TCTTTATAAT ACAAATATCG AAAGAAGGCG ACTGACTTTG AAAAAAATTAT	300			
20	GTTCATTAAT TGTAGGTAGC ATTAGTTTGT ATCCTTGCCA TTATCAGCTT GTGGNAAAGA	360			
	ACnAACCnAA A				
	(2) INFORMATION FOR SEQ ID NO: 993:				
25 30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 530 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	·			
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 993:				
35	ATAATGATTT ATCAATCGAT GTTAGATGCG GTTCAATTAT ATCCTAAGTC TATCGTGGTT	60			
	GATTATACTG TGGATGGACA ATACAAAAAT GATTGTCACT ATTTCGGTCA ATCATCGATC	120			
	AACATTGCCG ATTGGGCTCA AAACAATAAT TATTATCCTA ACCTGATATA TGCGATTCAA	180			
40	CAGACTCTTG ATTTAATACA TTATTACTCT GTAGAAACGA TTTTCGATTT AGCTTTATTG	240			
	ACACTTCTGA AAGGTGATTT ATCAATCGAT GGTCATGTCG TTTTTGATTT TAAAGCCCCT	300			
	ATAGCAACAA GTGCTTCAAT ATGGGAAACT ATTAAAACTA TTGAAGATTT TGATATGATG	360			
45	TCCAGTTTT: TTGALAAALG GCTTATATLG ATCATCATCC TATACCTTTT CGCAACCTTT	420			
	TTATCGAGGA TTCAGAACAA CTTAATTCGC CAGATAATTG GTTGTATTCT ACCAAGTTTA	480			
50	TGCTACCTAA ATGGGNTATA TAAAATAAGC AAAGCAACGT GCTGATAACA	530			
	(2) INFORMATION FOR SEQ ID NO: 994:				
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs				

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 994:	
	TATTGGATTN TTNCCACCAA AGGCAACGGT TCCTTTTCTA ATTCTAATAA TCAAATCCCC	60
10	ATTAATATCA ATCCCACTCA AATTCTTTCA CATCATTGAG TATAAAATAA TATGGTGATA	120
	TACGTTGAAG TTGATTnTCT TATTTAAGTA TACTCCAACA GTATTTTATA AAATTATTTA	180
	GTCATCATCT TCAGTGTTTA ATTCAAAAAT ATAGAATCTA CTGTATTGCA TAATAAATTG	240
15	AAATGCCACA AATTGTGTAC AAGCAATAAT AATGATACTT ACCATTATGA CAAACTTGGA	300
	TTCTACGACA TTGGGCACCA ATATATATTC GATAATTCTT TCAATATATA TAAATGCGCT	360
	CAACGCGGTT AATAATAAAC CGAAATGTGT TTTAGTTTTA CCACCCCAAC GTTTTGTYAC	420
20	TTTAGGTAAT TTTAATAACG TGAACATTCC GCCAATTACT AATAACAAAT AACTAATTAT	480
	GATTGAAATC GTACCCATCA ACCAATAATT GAATAGGTCA TAATGATTTT GTACAGCAAC	540
25	AAAATAATAA A	551
	(2) INFORMATION FOR SEQ ID NO: 995:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 729 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 995:	
	ATTCGCCACC ATTAGGTAGT GGAACACGAA CTTCATCATC TAAACCTTTA CCAATTAACG	60
	CTTTAGCCAT TGGTGATTCA TTTGAAATCT TACCATTAAA TGCATCTGAT TCAGCTGAAC	120
40	CAACGATTTG ATAACTTTCC TCTTCATCAC CTGGTAATTC TACAAACGTT ACTGTTTTAC	180
	CAATTTTAAC AACGTTGTTA TCTCCAGTAT CTTCAATGAT TAATGCATTT CTTAACATAT	240
45	GCTCAATTCT TTGAATATCT TGTTCGATGA ATCCTTGTTC ATCTTTTGCT GCATCATACT	300
	CAGAGTTCTC TGATAAGTCA CCAAATGAAC GTGCAACTTT AATTTTCTCT ACAACTTCAG	360
	GACGCTTAAC TGTTTTTAAT TCTTCAAGTT CACGCTCTAA TTTTTCAAAA CCTTCTTGAG	420
50	TCATTGGATA TTGCTTTTGA TTTTCCATAT TGTCATCTTC CTTTACTGAA TTATACTATT	480
	GCTTGCTAAC TAAAGACTGA ATTTTTGTTG TCATAATATC TATTGCAACT TTATTGCTCC	54

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CACCTTCAGG AATAATTATA TCAGCATATT TCTTAGTCGG TTCAATAAAT TGGTCATGCA

	TIAGRATUTE GIGITGAAAC GGCGTAATAT HETCAAGTET GGCATEIGIA TCAACATATA	720				
5	TnTTnAACA					
	(2) INFORMATION FOR SEQ ID NO: 996:					
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 325 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 					
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 996:					
	GACAAATATA CTGCTTCTAC TCAAATATTA GTGAACATGA AAAAGTCCTC AAGTGATTTA	60				
	GCTTTCCCAA AATGTTCAAA GTAGTTTGCA GTCTGTTAAT ACATATACGG AAATTATCAA	120				
20	AAGTCCTAGA TTCTAGATAA AGTATCTAGA GAATTGATGG TCAGTATTCA ACAGCTGAGT	180				
	GAAATCATTT TAAAAGTAAC CATCCAACCA ACTCTCAAAT TATTACTGTA CAGTTACACT	240				
	GGGATAATCT GATCTGACAA ATGTATAAAT ACTAAGTTTT GCCAGCAGCT AAATAGAGGT	300				
25	GTATGTACGA CTTCCAnCTG TAGnG	325				
	(2) INFORMATION FOR SEQ ID NO: 997:					
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 271 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear					
35						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 997:					
	CTTCAGTTGT CGGCAAATCT TCTATATTGG AAATACCAMA TACATTTAAA AATAAATCAG	60				
40	TAGTAATTAA CTGTTGGCTA CGCTGTTCAT TAACCACTTT AGCCTCAACT AGTCCTTTGG	120				
	CAATCAATGT CTTAACTGCA CCATCTGAAT TGALACTACG AATTAATTCA ATATCACTTC	180				
	TTGATAATGG CTGGTTATAA GCAATAATTG GATAGTACTT CCATTGCTGC TTGTGALAAT	240				
45	TTCATTTGTG aCTTTTGTTC AATTGAATTG T	271				
	(2) INFORMATION FOR SEQ ID NO: 998:					
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 498 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 					

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 998:	
5	TTTATGTGCT AATTTGTAAT TGAGATTCAT AATGGTATTT AAATCATTAT GGTGCGGGAG	60
	TTATGGTATT GCCATAATAT GAGAGTGCAT CCACTTCTAT AAGTAATGCA TATTGCGAGT	120
	GCAGGATGA ATGAGTGCTT GATTAAAATC CTTATGGGTG GTTGACATAA TTAAAAGAAA	180
	CCACATTTAA AATTTCTTAA TCACAAGCGG TTAACTAGGT ATAGTTTAGT TTTGAGTAAA	240
10	TCTTTTTAAA GGTGTACTTG TGCATTTTAC TTAATTAAAG ACATAAGACA TTTAATCGGC	300
	CTAAAATAAA TAAAAAACTA CCTGTTTAGG TAGTTTTTTT AATGTAATAG ATTAAAACAC	360
15	TAGTTCATTT CTTATTAAAG ATGGATAGTT ATTTTATAGA TAAATTTGTC CTTTAGTGTA	420
	GCGGTAATTT TTAGGACTTT TTGGTGGNAA AAATGTTCTT AATAAAAGTA ATAGTCCTAC	480
	TTTACCGCCA AAGCCATA	498
20	(2) INFORMATION FOR SEQ ID NO: 999:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 568 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 999:	
30	TGAGCTGGTT GTTTATTATC ATCAGTTTTC TTCTGATTAT CATCTGATTT ATCTTGAGAT	60
	GCTTTGTCAT CCTTATCTTT CGACTCATCC TTTGATGCTT TATCATCATT CTCTTCTTTA	120
35	GCAGGACGTT GCTTTGTAGG TGCTTGTTGC TGAGGTGGCA CATATTGATA TTGATTCTGC	180
	TGTGGCAATT GCTGATATTG GTTTGCTTGT GAATCTAGCT CATTCTGCTC TTTTTCCTCT	240
	TGTTGCTTTT TCTTTCTCC TTTTTCTGCA TTTTCTTTTT GACGCTTTTC TTTTTGTTCC	300
40	TGCTTTTGTT CGTTCAACAT ACGTTCTTTA GCTTTATTCG AATGATCTAC ATATGCAAAA	360
	ATTGCAAATA CTAATCCTCC GAGTAATAGC AATACCGTCG CAATGCTAAC TACTTTCGCT	420
	GTTGTACTCA TTTTCTTCTT ACTTCCATCT TCATTTTTAT TGTAGTCGTA ATTTTGATTC	480
45	GACATACTCT CCCTCACTTC AAACTAATTT AAATATAGAA ATTATCACGC AACCATTAAC	540
	ATTTTCACAA CTAATTTGCG ACCNAGTA	568
50	(2) INFORMATION FOR SEQ ID NO: 1000:	
50	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 1441 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	

	(xi) 5	SEQUENCE DES	CRIPTION: S	SEQ ID NO: 1	1000:		
5	AGTGTTTCTA	ATTGCAAAAT	TCCAAATACA	GTGTCGTTAT	TTACTTTTTT	CATGCTAAAC	60
3	ATCTCCCAAT	TAATAATCAC	ATATTTAGCT	ACTATACAAG	TATTAACAAA	CATCCCAACA	120
	ATCCCAAAAC	TTGTATGTGC	TAACTTATGC	ATAAAACTAC	AAGTGTAAAT	AAACTTGCTT	180
10	TCTATTCAAT	TGTCAAAGTT	GAATAAAATT	AAATAAGTAT	AAAAACCAAT	AATCAATAGA	240
	GTTAATATTT	AGAAATAAGA	TAATAGTACA	TAAAACAAAT	CACTCTATTA	CATATTAATT	300
	TTATAATTTA	TATACAAAGA	AAATATATCA	ATATTACCAT	TAAATTGCAA	CAATTCTACA	360
15	TATATTTCTT	CAAAAAAGAT	ACGCATTGAA	TTTTTATTAC	ATATAACTCT	CATGAAAATT	420
	GATTAAACTA	AATTAATTAG	TTAGCCTTAA	ATTTAACAAA	TTAAATCAAA	CCGAATGAGG	480
	CTAAATTGGT	TATTTTTCAA	GATATGATTT	GTATAAATCA	AAACATTTCT	TACAAATCAA	540
20	ATGTGTATAA	AATGTGATAT	ACATTTTCAA	CCTTAAAAAA	GTTCTAAAAA	AAGATGAGCA	600
	TCTACTGTCT	CATCTTTCAG	TTCTTTTTTA	CGGGTCTGTT	TTCTAATTTG	AGCACAATCT	660
25	TCGATTTCTT	TATCTAAATG	ACTACCAATT	AAATCTATTT	CTTCTATTGT	TAAATCGCTA	720
25	TCTCCATCTT	CTTTTATCTC	TGGTATTATT	TTTTCTTCAA	CTAAGTCACG	ATATAGTGTT	780
	TTTGAATTCT	CGTTCAATTT	CGATTCGTGA	TTTTGAATAC	TTTCTTCCGC	ACCAATGTAT	840
30	ATCTATTGGC	ACTAGCTTCT	ACTITIGIAC	CATCAATAAA	AATTGAATTA	TCATCAATAA	900
	GATTTTGCTT	TAAACATTGA	CTATAGAACT	GAATAAATAA	AGATTCAATT	AACGCATCAG	960
	TATTAGGATT	CACTCTAAAA	CGATTAATAG	TTTTATAAGA	AAGTGTTTGA	TCTTGGGCTA	1020
35	ACCACATCAT	TCGAATACTG	TCATGAAGTA	ATTTCTCTAT	TCTACGACCA	GAAAATACAG	1080
	ATTGAGTATA	TGCATATAAG	ATGATTTTTA	ACATCATTT	TGGaTGATAG	GATGTTGCAC	1140
	CACGATGATG	TCTGAATTCA	TCGAATTCGC	TATCAGGTAT	CGTTTCAACA	ATTTCATTAA	1200
40	CATATCGCGA	AATATCATTT	TGAGGAATTC	TAACGAAGTT	TCTATTGGTA	GTGTAAGTTG	1260
	GGGTCATGTT	ATAATTTTTA	TACATAAGGC	ACCTCTTTA	TTTAGTTTAG	TAGTATTTAT	1320
	TAAATTATAC	GaAGGGACCC	AACACAGAAA	ATTCATTTT	TTGAATTTTA	CATTTATGTG	1380
45	CAAGTTGGGG	AAAAATGTCT	TATTTTTTC	A AAGTATTTA	A AAGTAAAATT	ACATGTTAAT	1440

(2) INFORMATION FOR SEQ ID NO: 1001:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 587 base pairs

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(C) STRANDEDNESS: double

(2) INFORMATION FOR SEQ ID NO: 1003:

	(D) TOPOLOGY: linear	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1001:	
10	TAATAATATC TGTCATATTA AGTCTCCCTC ATTAGAACTC ATTATAAATG AAGTTATTGT	60
	GTGTGTCGCC ACTGCCATAA ATTAAATATA AAGTAATAAA TATTGCCAAA TACAATAGTG	120
	TTAATAAATA TGGTTTGAAT GCTTCAACAT ATTTATTAGG TGGCTGTTTA CTTTTAGATT	180
	TCATATTGCA CCTCTTAAAG TTCTTAGTAA AAACGCCTTT ATAAAGACCG TTCAATATAA	240
15	AATACGTTTT AAAATTTGTT TTTTACAATT CATTATATCG ATATTCATAA TGAAATTCAA	300
	TTTTAATTIT ATAGATTCAA CATAGTAATT GGTTGTCATC ACTCAAKTAT TGTAAATGAT	360
20	ACACTTTGTT GAGRACATCA TTCATTTTAA AGGTTATTTA AACAATAAAC AATTACAGTC	420
	TATATAACAA TTTTGTTATA TACGTCAAAA TCAAATAAAC TCATCACATT AATATGACGA	480
	GTTTATAATG TTATTGAATT ATCATCAGCG CAAATATATA CATTCGCAAG TCAAGCATAA	540
25	CATATTTAAC AATTGCTTTG CTTGGTTTTA CCAATGGATT AAAAACC	587
	(2) INFORMATION FOR SEQ ID NO: 1002:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 522 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1002:	
	CAATTGTGTC ATAATTTTGC TGATGATAAC TAATCGTTTT GGAGTAGCTA TTTGATGAAG	60
	TTCGTCCAAT ACCTTTGTT GAATCGAATT TACCACCTGA GCGTATATGA AAATGTACTG	120
40	TCTACTTTTG CAGTTGAAAT TTTATTTTTC GGCAATTGGT CTAATATTTC AGTTTTACGA	180
	TTTCTTTTTA CTTGAAAATC TACATGGTAC ŢCACTTGGAT ACTTTAACCA ATTTGAATTT	240
45	TTTTCTTCTT TATGAGATTC AAACTTTAAA TTTGAATGAA TTGAGCCTTG TTTTTTAACA	300
	AGTAATACAT TCTTGTCATA AGTTGGATCA TCGATAAAGT CGAATTGTAA ATTTTGGAGT	360
	ATATTEGTWT TCTCATCATA TACTGTTTCA GTTCGTTTTG TGATTTTACC GTTTTTCCCA	420
50	ATATCATCCG GTGCTGTTGA ATTTTTATCT TTATTAGTAA CATTACGTTG CTTTTGTGAn	480
	CTTATCAACA TGTCTTCTAT TTGGCTGAnG CTTATGGnGA TT	522

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5	(A) LENGTH: 323 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	-
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1003:	
10	TCTTTGTTTG AGACATAATG TCATGTAAAG TTTTCACAAT GCGTTCTTCA ACTTGTTGCC	60
	TTGCCTCTCC TTTGAAAGGA ACAATTCGAT CTCCGAATAA GTCCTCAGGC TTGTATAGAT	120
	TATCAAATAG ATAGACTGAC TCACCTTCAA ATATTCCAAA ATGCCATTCC TTCAGTCCCT	180
15	TAAAACGTTG ATACGATTGG WTAGGTGCAA CATTTTCAAG TGTGTCACTT GCGCGTTCTT	240
	GCGTTGATGA TGCATATAAA TCGAAGTTTA TCCCCTTAGT TTCATAATAA CTACGTGCCT	300
	TTmGAGCTTG AGCAATTCCA AGT	323
20	(2) INFORMATION FOR SEQ ID NO: 1004:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 320 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1004:	
30	TTCTAACTTG ACGTGACTGG GCATTTCTGT GNAAATNTTC TGACATTCTT TTTAATATCC	60
	GCAACGCAAT TGCTTCAGTT AAAGATTGNA ACTTGCAACA TTATTTGGTA CGAAAAAGTC	120
3 5	AGTTTTAATG TCGATATAAG ATTTATTTTT TTTGTTATAT AGTTTCGCAA CTACATTTGG	180
	TTGTCTTACT TGATCATATT TTGCAACCGT ATCGAATGCC GTCTTTTCAA ACAGCTTTAC	240
	GAGATACGTA AACCATGACC CATCCATCGA AGTCCTTGGT AAAAACCCAG GGTTTCCGAA	300
40	GCCGTAGGGT TTGAAAGATA	320
	(2) INFORMATION FOR SEQ ID NO: 1005:	
4 5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 305 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1005:	
	NATTAATGCT AGCCAAAACA GANTTGCAAN ATGTAAAGAC ATGTGAAACC CTCCTTATAT	6

	CGATATTTAT AAAAAATAAT ATTTCACTTA ACCAGTTTTT AGTTATCATT GCAATGGTAA	180
	AGGATACGAT GAGTATCACA CCACAAATGA TAATACCAGG CAGGAGCCAA CATAAATCAT	240
5	CTARATCTTT ATTATATGTG ATTARAATAT TARAGATAAC AARAGTGGTA GTARTAACTA	300
	TATTG	305
	(2) INFORMATION FOR SEQ ID NO: 1006:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 334 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1006:	
20	TTCAAGATAT CAGTATAAAT AAAAACTTAA TATGCTCATT ATAGACAGCT ATAACTATAT	60
	TTTCTCGTCC CACTCTATAG AAATCAATTT CATTTATTAC CATTTTCTCT ATTTAAAAAC	120
	ATATTTTGG TATTAACAAT TAAAAGTGGG TATATATATT TAATGAACCA ATTTTTTAGG	180
25	AAAGTAGGGC TAAACCTATG GAAAATAAAT TATACCACAT GGTGTCCTCT TTTACCATGA	240
	ACACAGTGAA TTAAAAAATA TTAANCAAGG TATTGGGGAA GTANCACCAG CATTAGGTCC	300
	AATTGGTAGC CACCTTCCAA TCCATTGGGG GNAA	334
30	(2) INFORMATION FOR SEQ ID NO: 1007:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 565 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1007:	
.•	AGAAAATTIG TTATATTAGA AGCGAATAAT TTTAAAACAT ATTATGAAAT GTAAGAAGAA	60
	ATATTATGAA ACTAGGAAAA GTAGATTGTT GAAAATTCCA TACAATAGGN GANGTAAAGT	120
45	GAATAAATTC TGGTATTACT AAAGCTATTG ATTGTCCTAA TTGTAATAAA AAGTTGGATA	180
	GTGTAGTTGA GGGGAGAAAA ACTAAAATGC AAAAATATAT TCTCAATGGA TCATTATAAA	240
	TACCAATTAG ATTAAAGTAT TGCGAACATT TACAATTAGA AATCAGTATT AATCTGCCAT	300
50	AGATAATTGT ATTAATGTAA AAMATAAAAT AGAATGAGAA TATACGGAAA TTTTTTATAC	360
	ATTTATAACC AATTCTGTTA AACTGTGAAG AGTAGAGTTA AAAACGAACT TTTTGTTTAT	420

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	AATGATTGAA CGCTATTCTA GAGAAGAAAT GTCTAATATT TGGACTGATC AAAATCGCTA	540
	TGAAGCCATG GTTAGAAGTG GAAAT	565
5	(2) INFORMATION FOR SEQ ID NO: 1008:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1008:	
15	CAACATTAGC GTCTAAACAA ATCTTTGACT AAACGTTCAC TTGAGCGACC ATCTTGATAT	60
•	TTAAAATGTT TATCTAAGAA TGGCACAACT TTTTCAACCT CATAATCTTC ATTGTCCAAA	120
20	GCATCCATTA ATGCATCAAA GGACTGTACA ATTTTACCTG GAACAAATGA TTCAAATGGT	180
	TCATAGAAAT CACGCGTCGT AATGTAATCT TCTAAGTCAA ATGCATAGAA AATCATCGGC	240
	TTTTTAAATA CTGCATATTC ATATATTAAA GATGAATAAT CACTAATCAA CAAGTCTGTA	300
25	ACAAAGAGAA TATCGTTAAC TTCACGATGA TCTGACACAT CGATAAAGTA TYGTSTATGT	360
	TCACGTGAAA TAYYAAGTCY ATTLTTTACG AACGGATGCA	400
	(2) INFORMATION FOR SEQ ID NO: 1009:	•
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 454 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1009:	
	TATTGTAAAA ACTGTGGTTC TTACAATGGC GAAGAAGTAG CAGCTAAATA ATTTTAGTTA	60
40	CTCAATATAA AAAGTCCCGC TTAAAATGAT TGTTTTAAGT GGGACTTTTT ATATTGCGAA	120
	AAATAATTGG CGAACGAGGT AACTGGATAC CTCATCCGCC AATTAAAATT TGTTAATTTA	180
45	ATAATTAAAT ATAAAGACGA TITATTAGTT TITACGTTTT CTAGGTAATA CGAATGCAAC	240
.=	GATGCTACTT AAAGCTAATA ATGCCATTAA TGGTAATGTC ATATCTnTAT TTGATTCTTC	300
	ACCAGTTTGT GGTAATGATT TTGCTTTATT TTCTTGTGTA TTTGTATTGT TTTGGCTTTG	360
50	GAGTGTGTCC ATCATTTGTG TTTTTAATGT TTGCTTnTnG TAATGGAGCA CTAATCTTTT	420
	GCCTCGCTAG AACCTGCCGG AGGTTTGGAA CCAC	454

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5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1010:	
10	GGTACAACAA CTTTAGACAA TGAAATATTA AAAGATACGG ATGATAAAAA GTCGAGTAAA	60
	ACTTTTGTTG GCGGAACAAA AGTTGATGAC CAACATGCTA GTATCGGAAT GGATTTTGAA	120
45	AATCAGGACA AAACTTTAAC TGCCAAAAAA TCATATTTCA TATTAAACGA TAAAATTGTC	180
15 .	TTCTTAGGAA CTGGCATTAA AAGTACTGAT TCATCAAAGG ATCCCAGTTA CCAACCGATG	240
	AAAATCCGCA AGCCGATGGG GAATACGGTA TTTTCCGGCC GTTAACCAAC CACCCATTCC	300
20	GGTTATCCGG GAAACCATTC CATCCTTTTA GGAGnCnCCG GTnCCnAAAA GGACCTCGGG	360
	TATCCTTTTT TTAACCAACC CGAAATTACT GGTAAAAAAG	400
	(2) INFORMATION FOR SEQ ID NO: 1011:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1011:	
	TTAGGTATTC GCAAAAATGA TCTTCAATAT ATAGCTATGG CCAAAAGATG GGCTAAAGCT	60
<i>35</i>	TATACAATTA CTGTAGCAGT GGGAGTTGTT ACAGGTACAA TTATAGGACT TCAATTATCA	120
	TGATTTGGCC TACATTTATG GAAATGGGTG GACACGTATT GCACTTCCCT TATTATGGGA	180
	ACATTGCGGT CTCTTGGAGC TATTTCTTAA GTATATATTA TATACTGGGA TCGTTTAAAA	240
40	TAATGGCACA TTCTTAATAG TATACCAGTA ATTATGGGGC CTTCTCAGCA TCTCATACTC	300
	AGGAATCATT ATGAATACGC CTGCAGGTTT GAGTGAAGAT GGAAGTGGCC ATGTCACCnT	360
45	AGAGCGTGTT ACCCACGTTA AGTCGTCATT nCGAATACAC (2) INFORMATION FOR SEQ ID NO: 1012:	400
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1012:	-
	CTTTATGGGA TACACTACAA ATCGAGACTA TAAGGTTTTT TATTTATTT ATŢATTACAT	60
5	TATCAATAGT TTTATAATCG AGCTTCAAAA CTTTAGAAAA TAGTAGAAAT AGCATTCAAT	120
	ATAGTGCAAA AGTGCAAATT GATAACTTGA CACTTATCTC CTATAAACCG TACAATTAAT	180
	TTGTATGATT TATATATAT TTCATAAAGT CATATTGAAT TTCATATAAA GAGCAAACCC	240
10	TAGAAAANGA GGTGTTGTGG AATTATTAAG CTCCTACTCA TTTGCGGGGT CATCTAGGGT	300
	GTGGAGGATG TGTGCCGAAT TGTGCTCAAA nATCCCAGCA GCAACGCGAG TTGAACAGCC	360
•	TAAGACGCAA CAAAGGATCT GnnAAGGACC ATCAGGCACG	400
15	(2) INFORMATION FOR SEQ ID NO: 1013:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 353 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1013:	
25	GTCGTTGCTG ATACCACGCC AGTATTGGTT TTAAATGATA AAAAAATCTG TGAGATTGCA	60
	TCATTGAGAC AAACATCGCT ATTTGAAATG GCCGAATATA TAGGGTTTAG CGAGCCACAG	120
30	AAATTAGTAC AATTATTTAT TAACCATGAT AGGAAGGTGA GACGCCAATG AATCAATATA	180
	ATACTATAGG TTTTCACCCG GGAAATAGTC GTATTCATCA ATTAAATGCG ACTGTTAAAC	240
	TTTTATnCTT ATTAGTTGTT CTATTCTGCA ATGGTnCTAT GCACAGGTAT TNATTTAATT	300
35	AGGCTCACAT TTATGGGCAA TTCTCAATGA TGAACAGTCG TTGTGTAATC TCG	353
	(2) INFORMATION FOR SEQ ID NO: 1014:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 627 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1014:	
	CAAAGCCTTC AACAAATAAT CUTTTATTAG TACTGATTGG TTGCACAACA TAAGTTACAC	60
50	CAGGTTCATC TTTAAATGTA ACTTCCTTAT AGAAGAGACC TTTTTTAGCA CTATACTCTG	120
	TTTTTTCTGA TTTAATTTTA TCTTTTAGAT TTTTCTCTTC CAAGTAACTG TCAATTAGTT	180

	ATGAAATAAA TAATATAATG ATAACTTTAA TCGCGTTTTt TTTCTTCTTC ATTATGTAAC	300
	TCCTTTTTGC TTATCTATTC AGTATGAACG AATCAATTTA TTTAATAAAG AGTTTTTACC	360
5	AGATTGTAAC AAATTTTTTT ATTCTCAATA TTATTATAGA AATCGAATTA CATACACGAT	420
	GCTTTTAAAA AATTTAATAA CAAATTTTAT TTTACTATCT ATCAAAATAA TTGACTACTT	480
	TTAACAATTA AGGATGATAC AATTACATTT TTTTCAATTT AAAAAATCAG TCATATCAGT	540
10	AATTACCGAT GAAAATACTA AGATATCGAT ATATTTTGCA TTATTTAACA TTTAAATTCn	600
	ATTATAGACA ATTCAATAAT TGCGATG	627
	(2) INFORMATION FOR SEQ ID NO: 1015:	
15 20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 462 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1015:	
	TAGTGTGACA TTAACACTGG AACAAAAGA AGCTGCAATT GCAGAAGTTA ATAAGCTTAA	60
25	ACAACAAGCA ATTGATCATG TTAACAATGC ACCTGATGTT CATTCAGTTG AAGAAATTCA	120
	ACAACAAGAA CAAGCGCATA TTGAACAATT TAATCCAGAA CAATTTACGA TTGAACAAGC	180
30	AAAATCAAAT GCAATTAAAT CGATTGAAGA TGCAATTCAA CATATGATTG ATGAAATCAA	240
	AGCTCGTACT GATCTAACAG ATAAAGAGAA GCAAGAAGCT ATTGCTAAGT TAAATCAATT	300
	AAAAGAACAA GCAATTCAAG CGATTCAACG TGCGCAAAGC ATCGATGAAA TAAGTGAGCA	360
35	ATTGGAACAA TTTAAAGCTC AAATGAAAGC AGCTAATCCA ACAGCAAAAG AACTAGCTAA	420
	ACGCAAGCAA GAAGCTATTA GTAGAATTAA AGACTTTTCA AA	462
	(2) INFORMATION FOR SEQ ID NO: 1016:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 235 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(wi) SPOUPMOR DESCRIPTION, SEC. ID NO. 1016	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO. 1016: TGATTGGTCC CATCGACTCG TTATAACAAA TTGAAGGTAC AAAAGTATCT TGTGATTTAA	
50	TAAATTCAAG TAAATTCGTA CCTGGTTCTA CAAGGTAATT CTTTTCCATC AAGTGTAACC	60
		120

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	ATAAATTGCG CATATCCACC NAAAATAACG ATGCCCCACA CATCTTTCAG ATAGG	235
	(2) INFORMATION FOR SEQ ID NO: 1017:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 227 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1017:	
15	GTTGAAAACT ATAAGATCAN ATAAAGGTAA AACAGTGGTT TGTGTCATTA GTGGTGGTAA	60
15	TAATGATATT AATCGAATGA AAGAAATTGA AGAACGTTCA TTACTATACG AGGAAATGAA	120
	GCATTACTTT ATCTTAAATT TCCCTCAACG TCCAGGTGCA TTGAGAGAAT TTGTAAATGA	180
20	CGTATTAGGA CCTCAAGACG ATATTACTAA ATTTGAATAC TTAAAAT	227
	(2) INFORMATION FOR SEQ ID NO: 1018:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 284 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1018:	
	GTCTTACTTG CACAAGGTAT TATTTCTATC TTACTCGTTG CTTTCGCAAT CATGCTATAT	60
35	ATCATTAATA TTTTAGATGC ATATCGTAAT GCTGAACGAT TTAATCGCAA TGAGGAAATA	120
55	AAGGATCCGA AGCGCGTATG GTGGCACATG GGACAAGACG TTCCCATACT TACTAATCTC	180
	ACCAGGTACA TACTTATTGA TATTGTAGTG TAATTCCATT ATATTATGTT GGAGTAGCAT	240
40	TACAATACAA TTATACACGC GCCTCGAGAC nACATAGATG GGTG	284
	(2) INFORMATION FOR SEQ ID NO: 1019:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 779 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1019:	
	CARTCATCAC ACATAAATGT TCGAATAGGA TTGTTTTTAA GTCGTTTAGA CTCAGTTGTG	60
55		

CACCTCAATA	TGAGTTACAT	GGTTGATTCG	ATATGAATAA	CCATCTTCTT	GATTGTAAAT	180
AAAACTATCT	ACACCATTAT	CGCTGTAAAG	TCGTTTACCG	TCTTTTGCAA	ATTGGAAAAA	240
TAAATAGGGT	AATAGATCTA	TCGGTATATC	TAAATGATCA	TGCTCATTTG	ATAATCGAAT	300
AGTAGTTGCA	GAGTCATGTG	GTTCGGAATG	TTTGAAAAAT	GGTGTCATAT	TAATGACAAA	360
TGAACCTTCT	AACATGGCAC	GTTTTTTATA	TTTTATTTCT	GAATTTAAAG	TAGGCGGATT	420
AGTTTGTCCt	TCtAGGATAG	CaCGATTCCa	TTCaTGaTTA	TCTTCAAAGT	CGATTGGTTT	480
TGAACCATCa	AATACACCTT	TTTCTAAATC	TTCGATGCTA	ACTTTTCTAT	CATCGAAAAT	540
CCAAGTCGTA	CTATCTAATG	TTATAGGAAA	CTTTACGGCT	CCTTTAATTT	GTATCATTTT	600
CCCACTCCCT	ATCAATGTAT	ATAGCATTAT	TTTAACACAA	ATTGCTAACG	ACACATTTTA	660
AATCTACTTG	CTTTTTAATA	TTTAGTAAGA	TAAACTTTTA	GTAAGACTTG	AGAATTTATA	720
TAGAGGGGGA	GCGTGTCATG	GCGAAACAAG	CAACAATGAA	AAATGCAGCT	TTGAAACAA	779

(2) INFORMATION FOR SEQ ID NO: 1020:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 950 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1020:

TTAATGGTCC ATTAAGAATA ATGGCAGAAA ACCGTTTGCA TAAATCAAAC CTTGATTCAC 60 TAACTTAAGT AATACTCGCT TTTCnTAAAT CCTTTAGAAA GGAACTATnT ATCATGATTA 120 CTTCATTCAG ACATTCTGAA GATATAGATA AACATATTAT AAAAACACCA TTAGATCATA 180 CAGCGTCATG GATTAATGTA GTAGANCCAG ACCGAGAAGA AATTGAAAAT CTTATGGAAC 240 AATATAATAT ACCTGAAGAC TTTATACGTG ACCCTTTGGA CTCAGAAGAA AGTTCCCGTA 300 TTGAATATGA CGAAGATACT GGTTACTCAT TAATCATTAT TGATTTACCT ATCGTCAATT 360 CAACTAATCG TAGCGTTCTA TCTTTTGTAA CGATTCCATT AGGCATTATT ATTGGCAACG 420 GTATTATCGT AACAGTTTGT GACGCTGAAA ATGAATTTT AGAAAATTTA CCTAAGCGTG 480 ATATTAATTT AAAATTTCAC AGCAGATTTG CATTAGAAAT TTTAACTACT ATTGCCGACC 540 ATTATAATUG TAACTTACGA TIACTIAATA AAAGTAGAAT TCGTATTGAG AAAGAACTAA 600 AAAATAACAT TACTAACAAA CAACTTTTCA AATTAATGGA AGTTGAAAAA AGTTTAGTAT 660 ACTITITAGC TGCCTLAAAA GGTAACGATA CAATTATTAA AAAGTTATTC CGTTTACCTG 720

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AAGCCATCGA AACAACAGAA TTACATCAAC GTATCTTAGA AAGTATCACA ACATCATACG	840
CTTCCTTATT ATCTAATGAT ATGAATACGA TTATGAAGAC ATTAACACTT TTCACGGTAC	900
TATTAACGTT ACCAAYACEC GTATTTAGTT TCTTCGGTAT GAATGTGTCG	950
(2) INFORMATION FOR SEQ ID NO: 1021:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 528 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1021:	
AATATATAAA ATGAATACAT TGTGAGGCAA TTATCAAATG AAATTTAATA AAGTAAAACT	60
AGTTATACAT GCGTGTGTAC TATTATTTAT CATTATTTCT ATAGCGTTAA TTTTTCATCG	120
ATTACAGACG AAGACACATT CTATAGACCC AATACATAAG GAAACAAAAT TATCAGACAA	180
TGAAAAATAT TTAGTGGATC GTAATAAGGA AAAGGTTGCG CCGTCTAAAC TAAAAGAGGT	240
ATATAATAGC AAGGATCCTA AATATAAGAA AATTGACAAG TATTTACAAA GTTCATTATT	300
TAACGGTTCA GTAGCTATAT ATGAAAATGG CAAATTGAAA ATGAGTAAAG GTLATGGATA	360
TCAAGATTTT GAAAAAGGTA TTAAAAACAC ACCGAATACG ATGTTTTtAA TnGGTTCAGC	420
TCAAAAATTT TCAACAGGGT TACTGTTAAA ACAGTTAGAA GAAGAACATA AAATAAATAT	480
CAATGATCCA GTAAGTAAAT ACCTTCCATG GTTTAAAACA TCTAAGCC	528
(2) INFORMATION FOR SEQ ID NO: 1022:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 713 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1022:	
GCATTnCGGT TAAAGTAKGL TTCAGCTTCT CTCaTTTTAG AAGTACCGaA AALTGGTTGG	60
TTALCTGGAT TTAATYLCAC GATAAATATT GCTTACTTTG TTACTTTGTr AAATGTACCC	120
ATTACGAGTC TCAATGTTAT TCCAATAAAT ATCACTTGTT GGTGCATGGT TTGGATATGC	180
ACAATGATIT CTTGAAATTG TTTGAACGAT TTCTAATGGA TCACAGCCAA ATGTACTGTT	240
TAATACTTCA GAGTCTCTGA ATAATGCACA AANTGAAATA CAAGTTGTCC AGTTTGGTAA	300

	AGTATCTTGC GTATAACCAG CCTCTATACG AACCATTTTA AATTTTGTTT GAATTAAATC	420
	TGTAAAACTC TGTCTATCCA TTCTGTTATC TACCTTTCTG TTTGGGGAAT TTTATCCGGA	480
5	CACAAGAAAT TGCAATAATA CACATTTCTT GAAACACAGA TTACATCTTA ATATATTTTT	540
	AATAAAATGA AAAGAGTCAA TTTCACATTI GTATTAAATT TTGATCAAGT CAACAAGAGT	600
	TAAGTTTACT TTATAATGAA GCGAAAGTAA ATGAAGTAAA ATTTTATGCA TAATCACTAG	660
10	ATTTGATAAA ACTTACACTT TTATAATGAT ATCAAATTTA CAAAGGAAAA CTG	713
	(2) INFORMATION FOR SEQ ID NO: 1023:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 570 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1023:	
	AATAAAATAG AAATGATTAT GGGTACAATT ATCGCTATCA TATCCTTGTT ATTAATTATA	60
25	TTACAAGCAT TTAATATTAC TTGGGGCGTT ATACCAATTA CAAATTTTGG ACATCAATTT	120
	TTCTTTTTCA TTGGTATTAT TTTAGTAATT GCCGGCATAT TTTWYAAGCG ACTEGAGTTT	180
	TCGGGAATCG GGTTATTATT TTGTCAAAAA ACCGTCGATG CAATGATTCA TAATCCACAA	240
30	TCAGCCCAGA TTTTTCATT AATTATATGG ATATTATTAG TAGTTCTAGT TATATATTTC	300
	ACAATTAGAT TATCTTCACG TACAAGATTA TAAATATGAT AAAACTATTC ACTTGATTAA	360
<i>35</i>	TTGTATTAAT TGAGATGAAT AGTTTTTTTA TTGTTGGAAT AACTTTTGGT AATTTATAAA	420
	TAATTTAAAA AAATTGTTTA TAAAAGGAAG CGTATATAGA ATGAAGGTTG GGTATATAGT	480
	TTATTGAGGG AGGTGTCACA ATGAATAAAG TCACAATTAA TCCTCAAATC CAATTAACTT	540
40	ATCAAATTGA AGGTAAAGGG GATCCTATAN	570
	(2) INFORMATION FOR SEQ ID NO: 1024:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 487 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1024:	
	CTTTGTTGTG CTTGAGCATT ATTAAAAAGA GTATTTAAAT TTAGTTGTTG GTTTGTAATA	60

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	TCAGAATTAT TAACACTATA TTTCCCTTTA AATAATGGTG ATTCGrAATA ATGCTTATCT	180
	TTATCTGCAG CTAACTGGAA TTKCCCTAAT GCAGAGTCTG CGATTGTTGG TTCAAGATTA	240
5	ATCATTGATT TCTCTTTTTT AGGATCATGT CCATATGACA tGTAATTTTC GATGCATTAA	300
	CAACAGATTT AKGAATGCCA AGCCCTTTAA CAATTTCATC TGATGCATCT GCGCTTAATn	360
	CTAATGAAGA TAAAAACGAL TALCTITCAT CKKTTCTTGG AACTTCACTT CATTTTCAAA	420
10	ACGGTCATTA AAATAATCTT TATACATTTT TGCTGTTTGT TGTTCACTTT TTAGGTATGT	480
	ATTTTC	487
15	(2) INFORMATION FOR SEQ ID NO: 1025:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 364 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1025:	
25	ATATGTTATA AACAATTTTA CAGTTGTATC ATCTACTCGT TCTATTCTCA TATCATCTCA	60
	CTCCTTACAG TCGATGAATA GTATCCACAT TGTATTAAAG CATCAAACAA AATACAATTT	120
	ATTTGTTTGA TTTCTTCTC TAAAMTATTT TGGTAACTTA TAATAACATA TTCGTTGTAG	180
30	CAAAACTATT TAAATGATTT ATACAGTTAA AGCATTAAAG CACTTTCTTA ATTTAATTTT	240
	ACCTTATCAT AGCAAATGTT TCATCCAAAA CACTCTAATA TAGAGCTATA TTAACAATTG	300
35	CACATTTGAT TTAAAAGATA CTAAGCAATT ATTGLAAAAT TAAAACCAAA AAAGCAACAC	360
	TATA	364
	(2) INFORMATION FOR SEQ ID NO: 1026:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45		
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1026:	
	TGCCCCAGGG GAGTACNAAA AAAAAGNGGG GTGGGGAATT GGAAACCGGA ATTAGTGGTT	60
	AAAGGGGTTT ATTGGATGTT GGGTCTAAAG TATTCCCAGA AATTTATCCA TCnATGATTG	120
	CTTTAGCCAA GTTTTTTCC AACCCATCTT TATGGAATTT AGTTATCTCA ATTACATTAA	180
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	CTTATATAAA AATGGCACAA TTATTTCATG TACCAACAAG AACAATATTA ATACGTCATT	300			
	TAACACCTAA AATTATACCG GCTATTATCG TTG	333			
5	(2) INFORMATION FOR SEQ ID NO: 1027:				
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 450 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 				
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1027:				
	TGTTCCATTC GTTTTAATAA TGGTGATACT GTACCAGTAT CGAGTGCTAA TTCAGTTACG	60			
	ACTTTCTTGA CGTTTACAGG AGATTCATCC CATAAAATTG TTAAGACAAG AAATTGTGGG	120			
20	TATGTTAGAT TGTACTTCTT AAAAACTTTG TTAGAGTAGT AGCGATTAAC TTGTCTTTGA	180			
	GCATTGTACA AACTAAAGCA TAGCTGTTCT TTTAAATTAT GTTGATCAGA CATTAAAGTT	240			
	CTCCTCCAGA CATACTATCC GTTTTTnTCT CTTTTCGGAT TGGTAATCAT TAAAAAGTTG	300			
25	ATTGTTTATT AATTCACAAC TTTCTTTGAT TCAATGCCAT GCNAAAATTA AAGTATGTTT	360			
	AAAGTTTAGA AGATATTTTT GATTAAATCA AGCAAAAAGA TAATTTAATA TATATGTGAT	420			
30	CATTTTAAA AATAACTGTn ATAGAAAAGA	450			
50	(2) INFORMATION FOR SEQ ID NO: 1028:				
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 535 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 				
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1028:				
	TGCATCTATA CCTAGAACTT TAATTTCGGA TTTTATTGCG TCTGTAATAT CTTTAATACC	60			
	ACTITICGATA GGGAAACTITI CGTCACCTIC AACATATITA ATACCAAAGC CACCACCAAG	120			
45	GTTTAATAAT TCAACTTGAA TGCCTTGctC TTTAAGCCAA CGTAAAmCAA TTTTAGCAGT	180			
	TTCAATAAAL GCTTCTGTAC CTTCAALCTG TGYACCAATA TGACAATGTA CACCTTTTAA	240			
50	TTTTAAGTGT TTAGATTGTT GGACTTTGTC AATTGCTTTT TTAGCTAAGC CATATTGAAT	300			
50	TGATAATCCA AACTTACTAT CTTCTTGCCC AGTTTGAATA AATTCGTGTG TATGTGCTTC	360			
	aACACCTGGa TTAACTCGTA ALACAACTTG aACCGTATCA TTAGCATAGC GGTCTATTAA	420			

	AATTTCATGT TTCGTTTTAT TGTTACCATG GAAATGGATG CGACTCGGTT CAAAA	535
	(2) INFORMATION FOR SEQ ID NO: 1029:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 359 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1029:	
15	GAAGATGATT GAATTATGGA ATTTTTTTCG AGATATGTTA TTTCGGGGAT CAGATTTTGC	60
	GATTTTGCCT TGGATAGAGT AGTTGCGATT TGTAAATACG TTTTTCAGGT TCGATTCAAT	120
	TTCGTTGTTA AGATAATATG GATTAGTTTC ACTGACATGT TGATGCATGT CTTTTTTGTT	180
20	CTGATAAAGT ATAAAATGTT TACTTAACAT TACTTAGTAT GACACCTGCT AATTCAAACA	240
	TTATTTGAGA CATTCTTTC AAATTAATTA TAAATTTTTA CCLATAGACT AGTTTGATAT	300
	TTATCTACAT CTCAAAATTC TCATCAACAA TCTGTCACAT CCAACATTTT TACTTNAGT	359
25	(2) INFORMATION FOR SEQ ID NO: 1030:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 341 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
3 5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1030:	
	TACATTGGTA AATAATTCTC ATAGTTTATG TCTCGTTGAT TAATCCAATC ATTGTTTTTA	60
	TCGGGTAAAA CATTCAAACT TTTCAAATTC ACAATTGATT GATGTTTCAT TAAAGTATCT	120
40	AATTTTTGCT CTCTAGTTAA ATATTCACCA ATGTCATTAT AATAGATATC GTGATTGTAA	180
	CTTCCATCTT TAACTAAAAT AGATATAGCT ATCGGTGCTC TACTTCCTGA TCCAAATATT	240
	TTTCCACCTT CTTTTCTTGa TTTTTCACCC TGTGTTCGTT GGTCGCCTCT CAAATTAATT	300
45	ATGLACAGAT AGTTAAATTC ATCGATAAAA CTTTTCTAAA T	341
	(2) INFORMATION FOR SEQ ID NO: 1031:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 326 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1031:	
	GTCTAACTTT AATGTTTAAA AANCTTAGAA ATTTTCTACT CATAAATGGA TGCTTTATGG	60
5	AATATTATTA ACAGGCCCAG CTTCAATGCT AGCTATAGAA TTTGGATGGT TCTTAACAGA	120
	GATGGGTAGA CAGCCTTGGA TTGTTCGTGG TTATATGCGC GTGGCAGAAG CAGCAACACA	180
	GCAGCGGAAT AACCTTCGTT ACAATTTTAT TTGGCATATG TACATCATTT AAGTATACAG	240
10	TGCAACGTAT ATCGTAGTTA AAATAACCGC GTAGAGAGTA ACGTAGCAGA GCAGAGGAAT	300
	GAAAnATTAG CTTATGRAAC GGTAGG	326
15	(2) INFORMATION FOR SEQ ID NO: 1032:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 263 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1032:	
25	ACAATCAGGC TTGTGAAGAA TGAATTGCAT GACGTTTGTG TAATTGAACT GCGAGGTTTA	60
	ATTTCTAAAA TGCTCCAGnC CTCCAATGTA ATCGCATCTT GATATAACAT AGCGATCGCT	120
	TGATTTGTCG TTGTATCAAC ACCTCTAAAC AACGTTTCAC CTATTCGGCA ATTCATTTAT	180
30	TTTACCCAAA TCATTATATA AAAGTTGTGG TAACATGCTC GAAATACCAC CTGAAATAAT	240
	nTCAATCGAT ATCCTATTTC TCT	263
	(2) INFORMATION FOR SEQ ID NO: 1033:	
<i>35</i>	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 514 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	•
	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1033:	
45	TTTCTATAGA GGATCCTGTA GAGATGCAAA TTCCTGGTAT CGTCCAAATT AATGTGAATG	60
	ATAAAGCTGG CATAAACTAT GTAAATTCGT TTAAAGCTAT TTTAAGATGT GATCCTGATG	120
	TTATTTTAAT AGGTGAAATC AGAGATAAAG ATGTTGCCAA GTGTGTTATA CAGGCTAGTT	180
50	TAAGTGGTCA CCTTGTTCTG ACTACATTGC ATGCAACTGA TTGTAAAGGT GCTATTTTAA	240
	GGCTATTAGA AATGGGCATT TCTGTACAAG AATTGATACA GGCAACTAAC TTAATTATAA	300

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	AGCAACAACT CCGATATTTC TTTTCCCATA ATCATCCATT ACCATCATCA TTTAAGAACT	420
	TAGAAGATAA ACTTGATGAT ATGACAAAAG CAGGTGTCAT TTGTGAAACT ACAATGCATA	480
5	AATACATTTA AACTACATTC TAAGAAGCGA CAAT	514
	(2) INFORMATION FOR SEQ ID NO: 1034:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 598 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1034:	
	TTTTTCACGA ACATTTTGT TTAAAATTTT CTTTCTTAAA CGTATACTTT CTGGTGTAAC	60
20	CTCAACAAGT TCATCATCAT TAATGAATTG TAACGCTTCT TCCAATGTTA GAATACGCGG	120
	TCTATTCATT GTTTGTGTTT GGTCTTTCGT TGCAGAACGT ACGTTAGTTT GATGTTTTGT	180
	TTTAGTGATG TTAACAGTTA AATCATTTTC ACGATTATGT TCACCAACAA TCATACCTTC	240
25 .	ATAAACTTCA GTACCAGGTT CCATGAAGTT TACACCTCTA TCTTCAAGTC CCAAAATGGc	300
	ATAAGTACTT GCAGAACCTT GATCCATTGA AATTAATGCA CCATTACGAC GACCGCCAAT	360
	TTGTGCTTTA ATACGTGGTC TAAATTCYTC AAATGTATGG TTAATAATAC CGTAACCTCT	420
30	TGTCATTGAC ATAAATTCAG TCGTATAACC AATCATACCA CGAGCCGGTA CATTAAAGAT	480
	TAAACGTGTA AGTCCATTAT CAGTTGTAGT CATATCAACC ATTTCACCTT TACGTGCACC	540
	TAAKGATTCa ATAACAGCAC CTGcATTTtC TTGTGGCACT TCACATTGCA CACGTTCA	598
35	(2) INFORMATION FOR SEQ ID NO: 1035:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 313 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1035:	
	AAACAGTGCT TCATTATCGG TATTGATATT GATCCACAAG CCGTTGACCT AGGGCGCACA	60
	ATCGTTAACG TCTTAGCACC AAATGAAGAT ATAACAATTA CGGATCAAAA GGTATCTGAA	120
50	CTTAAAGATA TCAAAGATGT GACGCATATC ATATTCAGCT CGACAATTCC TTTAAGTACC	180
	AGCATTTAGA AGGAATTATA TGANTTAACC AATGAAAATG TCCGTAGTGC CATGCGCCTT	240

	AAGTGGGCCA TGT	313
	(2) INFORMATION FOR SEQ ID NO: 1036:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 235 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(b) Topologi. Timeal	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1036:	
15	AATAATGAGT AGGTTTTGAT TACTTACGAG ATAACATGGT GAATTATTCT GAAGATAGAC	60
	TAATGCGTCC ATTACATTTT GCAATCATTG ATGAGGTTGA CTCAATTTTA AATCNACGAG	120
	GnCGACGCCA TTAATTATTT CTGGTGAACT GAAAAGTCAA CGTCACTTTA TACACAAGCA	180
20	AATGTTTTG CGAAAATGTT AAAACAGGAC GAAGATTATA AATACGATGA AAAAC	235
	(2) INFORMATION FOR SEQ ID NO: 1037:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 263 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1037:	
	nCAATATACC TCCTATCATC ACACAAAATG CGTTGTTTCG TATGATTTTC TCAACATCGT	60
3 5	AGACTAATGC AATCAGACAC AACACCATGC TCTATATCCA ATATTTGCTT TATTGCCTAT	120
	CAATGAGCGT ACTGCGTGCT TTTAAATAAT CATCATCAAT TAATGACTGT ACAGGCACCT	180
	CATGAAAATT ATCATCCGCC AAGTATTGCG CACGATCACT ATATGCTAAA TGCATCGCTT	240
40	GTATCARATG ATGCAAGTAA TCA	263
	(2) INFORMATION FOR SEQ ID NO: 1038:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 218 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1038:	
	ATTGTACCTG GCACAATCTC ATTATGTATT GGATTATCAT CATTACGAGC GCCAAATATT	60

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	ACCOTTATGA CATGTTGATC ATTTTTAGTN AATGTTAAAG CTATAACGTG TGATATTGCG	180
	AGTCTGTCGG CATTCAATAT CTTCnAAATG CCCTACAT	218
5	(2) INFORMATION FOR SEQ ID NO: 1039:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 396 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1039:	
	GTTTAGACGC TAATGnTGGC ATATATTACT TGCCATGCAA ATGAGTCATA AGGCATAGTT	60
	TTCAAGAAGG GTTCTGACAA TGAAGTGAGC AACATGTCAT GATGAGAAGC AGGACTATAC	120
20	AATGAGAATA ACCTTTTGAT TTTTCATGCA TAAGGCGATT CAATCAAAAG CAATCACCTT	180
	CCAACTGAAT TGTCATTTTG TAAAATAAAA TAATCGATCC AATCGTTATC TAATTCATAA	240
	ATGTGTAAAC ACATACGTTA TGAATGGATA ACGATTTTTT GTTATGTTAA AGTGGTACAT	300
25	TAATCATGTA TTTCGTATGA TAATTAACGA CAAGTGTAAT GGTTAAATGT ATTTTATGGA	360
	TGGAAATGCn ATAATAGGCC TGGGTTACCA TGGnGC	396
	(2) INFORMATION FOR SEQ ID NO: 1040:	
30 35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1040:	
40	AGCATTTGT TTAAAAGCTG ATGAAGCAAT AATAAACTCT TCATATCCTC TGTCCATTAC	60
	AATTTGACCT TGATATACAA TTTCTTTAAA GTTTTCGATT TCTTTAAATT CTCTGCTATC	120
	ATTTARANTA GGTGCATTCG TAATAACATT CGCTTCCTTC TTATATCCTT TAGATTGATA	180
45	ATATTCTTTT GCTGCATGAC TTACTGTTAC GAAGGCATTA ACACGATGTT TTACTATGTG	240
	TTTTTCTATA CTTTCTACAA ACTTTGAAAT AAGTGGAACT TTATTAATAA AGGCATTTTT	300
	CGCATATAT' TCATGCGCAT CATAAACAA' ATTAGCTTTT TLATAATTGC TTAAATAGAC	360
50	CATTAATAAT ACGTCGAAAT CATTTGCATG AATCACGTCA	400
	(2) INFORMATION FOR SEQ ID NO: 1041:	

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5	(A) LENGTH: 268 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
•		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1041:	
10	ACTTGCGTTT CTATTTAGCT CAGACAGGAA AAATATTCGC TGGAAATATG TAGGAATTTT	60
	ACTTGCAATT CAGCTTATCT TTGCATTTAT CTTGCTTAAA ACTACAATGG GAATCAAGGT	120
	TATTGGTGGT ATTTCAAACG GTTTTAACTA CTTATTATTA AAAGCAGCAG ATGGTGTTAA	180
15	CTTTGTATTC GGTGGTATTC AATATATCGT CCCTAAGCAC CCACCCATTC CTCCTCCGGG	240
	GAATAATAAC CAACnGAATT AATTCCGn	268
	(2) INFORMATION FOR SEQ ID NO: 1042:	
20 25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 277 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1042:	2.
30	GTGAAGATAA GAAATTAAAG TTAAGACAAG GTTAAAAATA AGCAAAAAAT ATTGAAATTA	60
	CAGATCATTG GANTGGTATT CCAGAGGAAG ATCAAGATTC ATTTTTGATC GCTTTTATCG	120
	ATGGATTAAA TCTCGTTCAA GAAGTCAAGC GGTAATGGAC TCGATTATCT ATTGCTCAAA	180
35	AAATCATCAA TTAAACGGnG ATCGATTAAA ATTAAAGTGA ATTAACAAGG AGCAACGTTA	240
	AATCTATTTT AATCAGACTG AGACGTCATC AAGTCAT	277
	(2) INFORMATION FOR SEQ ID NO: 1043:	
40 45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 379 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1043:	
50	TTATCATCAC AAGTGATTTT GAAAATAAAA AAATCGAAGA TGATGACAAT GATTCAGGTA	60
	GTGTGCCGAT ATTGCCGTTT ATTAAACGAG ACAAAGCATA TCAAATTATC CAGAATTTAG	120
	TACCAGATTT ATCTTATCAA CAAGTTAATG AAGGTATGCC TTTGTCAGGN TTCCACAGAC	180
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AACCATTATT ATTGTTATTA CCGATATAAC CATAGTCATA TGGTTATTGT GATCCAAGGT	300
ACCTTATGTC AACAGCGGGT TAAAGCAGAG ACAATACATC AGATTCGGCA TGAACGAAAT	360
TATATTTAAn GCTnCTAAG	379
(2) INFORMATION FOR SEQ ID NO: 1044:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 399 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1044:	
ATATTGAACT TGAAGACCAT GCAGATATAA ATGAAATAAC ATATCGATTA TCAAAAATTT	60
TCGGTATTAA ATCTATTAGT CCAGTATTAA AAGTAGAAAA AACAATAGAG GCAATAAGTG	120
CAGGGACAAT TAAATTTGCG CCATTNTGAA GAAAACAGCA CATTTAAAAT TGATGTGAAG	180
CGTGCCGATA AAAATTTCCC AATGGATACG TATGAATTAC AGCGTGAATT GGGTGGTGCA	240
GTATTGAAGC ACTTCGACAA TATTTCAGTG aATGTCaAAC GTCCAGATCA TGGAAATTCg	300
AGTGGGMAGT TLAGGMTTAG ATGCCAATTT TATATGGTAT ĢŅAAGAAGTT GGTTCCGGGG	360
TTCCAGGTGG GATTTACCNG TTGGGTACTG GTGGGTNAA	399
(2) INFORMATION FOR SEQ ID NO: 1045:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1045:	
ANGATAAACA GAGGAGCACA AAAATGAATN NAAATATAAT CATCAAAAGT ATTGCGGCAT	60
TGACGATTTT AACATCAATA ACTGGTGTCG GCACAACAGT GGTTGATGGT ATTCAACAAA	120
CAGCCAAAGC AGAAAATAGT GTGAAATTAA TTACCAACAC GAATGTTGCA CCATACAGTG	180
GTGTTACATG GATGGGCGCT GGAACAGGAT TTGTAGTTGG GAATCATACA ATCATTACCA	240
ATAAACATGT TACTTATCAC A'IGAAAGTCG GTGATGAAAT CAAAGCACAT CCTAATGGTT	300
TTTATAATAA CGGTGGTGGA CTTTATAAAG TTACTAAGAT TGTAGATTAT CCTGGTAAAG	360
AAGATATTGC GGTCGTACAA GTTGAAGAAA AATCAACGCA	400

(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 626 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1046:	
	ATAAACTTCT ACACCATCAT CTTTACCTAC AACATTTGTA GCTTTAACTT TTAGTCCAAA	60
	GTTATCTTTA AAGAATTGTT CACCTACTTT TTCAAATTCT TTACGATGCT TCTTCACAAA	120
15	TTCAATCGCA TCTTTTCTG CAGGTGGTTG AAAGCCTTGT CCTACATATT TTGAAGCTTC	180
	CATTICTICT GGTACTGATT TTGTTTCTGT ATTTGTTTCT GTATTTGTTT CTGTATTTGT	. 240
	GTCTTTTTT GATTCATTAT TCATCGCTGA ACATCCTGAT AACAGTAGCG TTGCTATTAA	300
20	GATTAATTTC GCCTTTTTAA ACATAGCTCA TCACCCATTT ATGTGKTTAT ATAGAATATT	360
	AAAAAGCATT TTAAAAAAAA TTTATTCATC TTTACGATAC ACTCCATATT CTATTGGATC	420
	ATTATCATCA TAAAAGGCTT TTTTAGTATT AATAGTAGGC TTTCCTATTT GAATTGTAAT	480
25	TGTAGATTTT TCTGGCTTAT TTTTAAAATT ATATAGTTTA TCACTCAGTT CAATTACATC	540
	ATCAACTGTA TTGTCTTTAG TAAAATTTTC CTTTGTACTA AACAATGTTG TTACTGTATC	600
30	TGTATTAGCA GCGnAATTCA CTTCTT	626
	(2) INFORMATION FOR SEQ ID NO: 1047:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 317 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	ed to the	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1047:	
	GACGGCGTTC AAAATGCAAC GGTCAATTTA ACAACAGAGC AAGCTAAAGT TGACTATTAT	60
45	CCTGAAGAAA CAGATGCTGA TAAACTTGTC ACTCGCATTC AAAAATTAGG TATGACGCGT	12
	CTATTAAAGA TAACAATAAA GTCAACGTCA CGCAACTGAA GCGTACAACA TAAATTGATA	18
	GNTATCATAT CAGCAGTATA TCTTACCACT ATAATGTAAT GTTGACACTT TCATATGCAT	24
50	ATACAGACTA TTACGATCA'I GTCCATTAIT TAGCCCACTG TCATTATATG GTGGCATTAT	30
	GAGGGTATAA ACTTAGn	31
<i>55</i>	(2) INFORMATION FOR SEQ ID NO: 1048:	

5	(A) LENGTH: 223 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1048:	
10	ATACGNATTA TGCAAAAAAT AAAGTGAGAT TGGCATATGT GTAAATCTAA AATACTGTTG	60
	AAAAATATTT TTAGTGAAGT AATCAGAAGT TAAAGATTTA ACTGAAGTAA AAATATAATC	120
	AAGATTACGA GTCATTAACA TTTAGCTTTA AAGAGGGAAA CATATCAAAG TAGGTTAGCT	180
15	AAGNAAAACA CCGACTAAAT CGGGGATATT TCGTGACATG TTG	223
	(2) INFORMATION FOR SEQ ID NO: 1049:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 608 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1049:	
	AAATATGAAT AATGCAATTG ACCAACGTTC GATAACGTTG CCATACCCAT ATTAAATTTT	60
30	GTATAACCTT GTTCTTTACT CCAAAGTAAC ATATGCAAGT ATAGACCATC CATTAATGGT	120
	AAATCTAACT CTGGCAACCA TCTAATTAAA TCGACTGAAA TGGCATCATT AAAGTATGTT	180
	GGCATTAAAC TACAAAATGC AATTACTTCA TTTTCTTCAT TTCGCATTAC ACCAATTGGC	240
35	GCTTTAGATA AGTATTCTTC ATTAAATnCA CCAACAGAGA AATGCATTTC CYGACGATTA	300
	TCTAGCCATA AATCACTTAC ATGTTGAAGE TCATTTAEAA ATTCAGTTGT AAACGGEGGE	360
40	TCAATAATTT CGAACGAAAT ATTAAGTTCA TCGAATTNAT TTAAAGTCGC TCTAAATCCC	420
	ACGGCGTTTT TTACCTGAAG TTGAAAATTG CGTTAAATCA ATAATTGCTT CTTCACCTAA	480
	TTTGAAAAAT TGGTTACCGG nATTATGATA TAAAGGCATG TGTTGATCTG TAACTTGATA	540
45	GAATATAACA TCATAGCCTA AATACTCAGC GTAATTATAG AATGCTTCTA ACAATTCATC	600
	AAAGGCAT	608
	(2) INFORMATION FOR SEQ ID NO: 1050:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
<i>5</i> 5		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1050:	
	TGTTTTCTA CGCTAAACTA TATGATAAAT TGCCTATGTA TTTACTGGTG TTTATGGCCT	60
5	TTACAGCTGT AATTTTGATT ATGATGTACA TACAAGAGAA AAATGAAAAT TACAAAGTTG	120
	AAAAAAGATA TGTGGTTAGA TATCTCACAC TTAACGTTAT TGTGGGATAT ACTTTGCCAT	180
	TGCTTTTGT ATCTATTTAC GTTTTTGGTG TAGTCGGTTT TGGATTTGAT GTTTTCAATT	240
0	ATTGTCTAGG TAKTATCTTG ATGTYATWTA TTTCTTGGTT TAGGTnTATT nT	292
	(2) INFORMATION FOR SEQ ID NO: 1051:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 734 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1051:	
	TARATCHTCA AAGATTTCTT CTARAACATT ATAATCTTCA ACGATACTCG AATAATAATA	60
25	CAGCTCATCA TTTCTGGGCT TGGTATAATA AAATATAACT TGCCCACCTC CATCGTCCAC	120
	ATATGCAATT ACATATACCT TTTCCCACTC TACTGGTATC ATTTCATTGA TCTCATTTGC	180
30	AATTTATTG TACATTTCAC TTAATTTTTC TTCGAAATTC ATGTTATCGC CTCTATTGTT	240
	CAGCTTCTTC TTGCTCTTTA ACATATTGCT CGATTTCTTT AACTTTATTA ATTTCATATT	300
	CCGTTTCTGG TAAAATTCCA AATTTTCTAT ACTTATAGTA ATTTTGTCGA CCTACTTGAC	360
35	CAAATTCTGA ATTTATCCAA TCAATATAAT CAAATGAAAC TTTTAATTCA CCTTCTCTTG	420
	TAAAGTCAAA TTCGCATGAT GTCCATGGTT CATGTCCTTC TTCTTTAAAT AAATTCCTTA	480
	AATTTTGAAA TTGTTTATAC AACTCATACA CTGAATCCAT AAATTCCGAT TCCGATATAT	540
40	CATATTTATT TAATACACTA GTATAGTAGT ATAATTCATT ACTTCCAGGT TCTGTGTAAT	600
	AGTAGAACAC TTCTCCTCCT CCGTCATCTA TATATGCCAT TGCATATACC TTTTCCCACT	660 720
45	CTACCGGTAT CATGCTGCTA ATCTTATTCG CAATCTCGCT ATACATTTCA CTTAATTTTT	720
	CTTCGAAAGT CATG	734
	(2) INFORMATION FOR SEQ ID NO: 1052:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 775 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1052:	
	ATTTTTAACC AAAATTGCTT TTTTATCTGA AAAGAAAGGC AATGTTAATG TTTCTTCAAC	60
5	AATTGGTGCA ATCTCTGTTT CGTATAAATT ATATTTCACA AAGTTAAAGT CATCTCTATC	120
	ACTTTTCAAA AATTGTGATA TGATTTCTGC ACTTTGTTTT TCAACCAATT CAGGCACATC	180
	TCCATAAATA GCTACAATAT TGTCGCTCAT TCATTACACC CTTTCATTCG TTTGACACAT	240
0	CAATAGATTA TATCATGTTT CTGTATCTAT AAACCACTTG CATTTCCATA AGAGCTTGAA	300
	TCAACTTTTA AATTATCATC TAAGTCAATT GTAACTTGAC CGTTTtGTTG ACTATTGTAA	360
15	ATGCGLACTG CGAATCCTTT GCAATCGTTL AACAACTTCT ATATTAGGAA GWTGATACAT	420
	ATTGTTCTTC CCAGAAGAAA TCAAACTTAT TTTAGGCTTA ATCATCTCTA TAAATTCTTT	480
	AGAACTACTT GTCTTGCTCC CATGATGTCC TACTTTTAAA ATATCAATCT CCGGCAAGTT	540
20	ATATTTTTT AGTAGTAAAG ATTCATTATT TTTACTAGCA TCGCCCATTA ATAAAACTTT	600
	TTTATTTTGA TATGTAATCA TAGTAATAAT CGAATACTCA TTTTTATCTC GGCTATTTGG	660
	ARTAAAACTA TCAAAAAAAT AGAAAACTAC TATCTCCAAG TTTAAAACTA CTAACTTGTC	720
25	TTACATCCAT AAGTTTAATG GTTGTACTTA TGGGCTTAAT TTCCGATAAT AACCA	775
	(2) INFORMATION FOR SEQ ID NO: 1053:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 234 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1053:	
	GAGACCAATC ATCATAATGA ACGACAATCA TGTATTTAAT ATTTAATAAA ATACTGAATA	60
40	ATGCTATAAC TGCCATTAAT TGAAGACCAA TCGCATCTAA TGCGACAACA CGATCGGCAA	12
	GTGATGGGCC TAGCACACG CGAATGAGCA TAGCTAACAT AGGANGTGAC AACTATGATT	18
	AATGCAATAA CGATGAATAA CCTTGATGAn TCATTATAAT TCGCCCACCT CTCT	23
45	(2) INFORMATION FOR SEQ ID NO: 1054:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

	CTACTGGTAT CATCCACTGA TTTCATTTGC AATTTCATTG TACATTTGAC TTAGCTTTTC	60
	TTCGAAAGTC ATGTTATCGC CCCTATAGTT CAGCTTCATC TTGCTCTTTA ATATATTGCT	120
5	CGATTTCTTT AACTTCTTCC ATTTCGTATT CCATTTCTGG TAAAACACCA AACTTTTTAT	180
	ACATATAATA GTTTTCACGG CCTAATTGAT CAAACTCTGT ATTTATCCAA TCAATATAAT	240
	CAAATGAAAC TTTTAATTTA CCTTCGCTTG TAAAGTCAAA TTCACTTGAT GTCCATGGTT	300
0	CAAGCCCTTC TTCTTTAGAA AGTTTCTCTT AACTTCTTAA ACAATCTATA TAAATCCGTC	360
	CACAAATCAT AAAATACTTT TTCAGAGACA TTATACTCTC	400
15	(2) INFORMATION FOR SEQ ID NO: 1055:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1055:	
25	GNGGCATATA TAGCGTTGGC GGTATAACAA AGAAAAATGT GAGATCAGTG TTTGGATTTG	60
	TAAGTAATCC AAGTCTACAA GTTAAAAAAG TTGATGCTAA AAATGGCTTT TCGATAAACG	120
	AGTTGTTTTT TATTCAAAAG GAAGAAGTAT CATTGAAGGA ACTGNACTTT AAAATAAGAA	180
30	AACTCTTAAT CGAAAAATAT AGATTGTATA AAGGAACGTC TGATAAAGGT AGAATTGTTA	240
	TCAATATGAA AGACGAAAAG AAGCATGAAA TTGATTTAAG TGAAAAATTA AGTTTTGAAC	300
35	GTATGTTTGa TGTAATGGaT AGTAAGCAAA TTA	333
	(2) INFORMATION FOR SEQ ID NO: 1056:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 347 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1056:	
	TGGGCAGTTA CATTTATGAT TATCAGCACA TGTTTAGCTT ATAAATTTTT ACGAAAGTTT	60
	AGCCGTTTAT AAAGCACATG CATAATGAAA CGAGTATITG CCACTTGATT AGTACTICAT	120
50	TATTATGTCG AAAATAAAAA TAAGTGGTAT TTTTAATATA TTAAGAAGCA CTCATAATCG	180
	GCTGTTAATT AATAATATTT TTCATAAGTA TTGATTCATC ATTTTCTTTA TGTTAAATAT	240
55		

	TAATACAGAT ATCAATATGG CMAAAGIGIT MAAIGAATCA GAGGIAA	34/
	(2) INFORMATION FOR SEQ ID NO: 1057:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 312 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1057:	
	TCCAAAACGG AGAGCCAAGA GTTAACTCTA CTTATATAGG ATACGCGCCA ATTGATGATC	60
15	CAAAATTAGC GTTTTCAATT GTATATACAA ATCAGCCTGT ACCACCACCA TGGTTAACAG	120
	GTGGAGACTT AGGTAGAGAT GTAATTAACT ACTACTTTAA GCAGTTAGGT AAAGATGATA	180
20	AAAATAAAGA CAAAGACAAA TAAAATTTAA CCTGACGATT GTGTAGCGCA TGGTTGTAAA	. 240
20	ATTTTAACTT TGCMAATATT ATAGATGTTG GTATAATAAT AAAGTCGTAT TLAGAAATGA	300
	TwAGGaGGGA AT	312
25	(2) INFORMATION FOR SEQ ID NO: 1058:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 404 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	·
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1058:	
35	GCCATTTTGC GATGCTAAAT CCATTGAAAA TGCAATACCT GAAAGTCCAC CAAACAAAGA	60
	ATTGTTATAT TGACCACTCT GTAAATATGG TGCTAATTTC ATGATGTACT TATGCACAAT	120
40	TTGCTCAGTA TTAATATCGA AAACTTTTEG ALAAGCATCT AAAAACAAAA TGATACCTGG	180
40	TATACCATGT GATAAAGTTG AAGGTTCAAA ATAATCGGTT TCAGTAGATG CTTTTGAAAT	240
	GAAATCATCT ACTTCTGAAA TCTCTTGAAA CTTCTTCTTC AATATTAGAT TCATATCAAT	300
45	CATTITEGIC ACCACCAA IGCITITGAG TITTAACAAI ITCITITACA ATAGATAAAA	360
	CAAATGTTTC TTGATCCTTA TCAATGCCAA ATATTCGATT GNAG	404
	(2) INFORMATION FOR SEQ ID NO: 1059:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 233 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1059:	
5	ATGTACATAG GNATGACATA AGTGTGCCTT CTTTTTCAAG ACCCTCCATA GAAATAATAC	60
	ATGGATGTGC ACCACGNTAC TACCTCTTTA ACGTTACCAG AATTGATAAA TTAACTTTCT	120
	CTTGTGTTGC TAAACCTACA ACTGGTGTAC CTTCTTCGAT TAAGGCAATT GTACCATGTT	180
10	TAAGTTCTCC ACCAGCAAAA CCTCGCTGAA TGTAGAAATT CTTAAGTTTA AGT	233
	(2) INFORMATION FOR SEQ ID NO: 1060:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 295 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1060:	
	GCACCACTAC TGTTAATAAC ACACCTAAAA AAGTCGAAAT ATAAGGGTTA ATCGCTGTTT	60
25	TAAATGTATA TCCTAGTGCG ATTGCCATTA ATTATCCGAT AGCTTTTTCT GCTGCTTCCA	120
	TAGTCATCTC ACCTAATGTT GGATGTGCAT GGATTGTTAA TGCGATATCT TCAGCATTCA	180
	TACCAGCTTC AATTGCTAAA CCTAATTCAG AGATAATATC TGATGCACCA GTACCAACTA	240
30	CTTGAGCACC GATTAAAGTA TCATCTTCTT TAGTGTAATA AGTTTAACAA ATCCG	295
	(2) INFORMATION FOR SEQ ID NO: 1061:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 413 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1061:	
	CAATGCCTCT CGTGTTGCAG CTTCTTCCGG TGAAAAACCA ATATTTTCAA GTGCAATAAT	60
45	TTGATCTAAG TCCTGCATGA TTACTTTTCT TAATACCATA AAAACACTTC CTTAGCCCTA	120
	TATATCAAAA GTAATACCTT CATCTTTATA TTCATTATTT TCAAACTACC TTCACTATAA	180
	AAAACGAGTC TTTTTATTGA AAGCCATTCG CCTTAATCAA TTAGACAAGT TGTATKATAC	240
50	GAATTAGTAA ATAATCATGA TTATAATTCA TTTTAAGCAT ACTCAAAAAG ACTGGTACAT	300
	GTATACCAGT CTAATTCGAA AAAATATATT TAGTTAAAAC CATTTCAAAA ACGACTTCAC	360

(2) INFORMATION FOR SEQ ID NO: 1062:

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear					
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1062:					
	AAGCTGCATA CTCTCCAAAC TTAGAACCAC CGAAGCGATT CACAAAATAT TTATTAGCTA	60				
	AAAAGTCGGC ACATAAAATT AATATTGTTA GCAATGCCAT AGATACATAA AACACCCATG	120				
15	ATAAATGCTG ATTATGAAAG CCAAATTGAT AGATTAAAAA GCCAACCCAT AATACTAAAA	180				
	CAGAAGGAAT AATCGGCTTA ATCAACCCAA CAAATGCTAA CATGAAGGCA GCGATGATAA	240				
20	GTAGCCATAA AATAATTGTC ATGTTGATAT CACATCCTCT TTTGTATTTT TTGATTTTTA	300				
	GTAAAGAATA TAAGTATCAT ACCTAACATG GTTGATGCTG CTGGATACCA AAANATACAT	360				
	TTTCCCAAAC CTTACCCAGT GGACTCCTAG GCACCACCTT	400				
25	(2) INFORMATION FOR SEQ ID NO: 1063:					
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 					
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1063:					
35	TGGATCAGAA GGAATCTGGA TGCCTATTGA TGACAAAGGA TACTTTAATT TTGACTTCAA	60 ,				
	AACGAAACGT TTCGATGATT TAGAGTTAAA GAAAAATGAT GAGATCTCAT TAACATTTGC	120				
40	ACCTGATGAC GAAGATGAGG CATTGAAGTC ATTAATTTTC AAAACTAAGG TAACGAGTTT	180				
	AGAAGATATT GATAAAGCAG AAACTAAATA TGACCATACT AAAGTGGAAA AAGTAAAAGT	240				
	ATTGAAAGAT GTTAAAGAAG ATTTACATGT AGATGAAATT TACGGAAGCT TATATCATAC	300				
45	AGAAAAAGGT AAAGGTATTC TTGATAAAGA AGGTACTAAA GTAATTAAAG GTAAGACTAA	360				
	ATTCGCAAAT GCAGTTGTGA AGGTAGACTC TGAACTAGGT	400				
50	(2) INFORMATION FOR SEQ ID NO: 1064:					
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 434 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double					

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1064:	
5	GTGGTCGTGA AGCAACTGAT TTCAAAGAAG AAGATATCGA GCTTTTCAAA GACATTGCCG	60
	ACAAAGTAAA ACAAACAAAT AGTTATGATC TAGCGTTTGA TGAATTAGAA AAAGAAAAAG	120
	ACTTCCTGCA AGTCATTGTC AAAAACGATG ACAAAAACTT ACCTACTAAT CAAAATGTCG	180
10	CTCAACTAGT AGAAGATTTA CGCCTAGAAA TCCAGAAAAT GCGCGAAGAA CGTCACCTAC	240
	TTGGTCAAAT GATGAATCAA GTACATCAGC AACAACAAGA ATTAAAAGAA CTTCAAAATC	300
	AACTTACATC TAAAATCGAT TCAAATAGCG AATCCTTAAA AGCCATCCAA ACATCACAAG	360
15	AGGCTATCCA AGAAGCGCAA GCCTCTCAAG CAAAAGCATT AGCTGAATCC ACCAATAAAG	420
	TTGGAAAGAA TGCT	434
00	(2) INFORMATION FOR SEQ ID NO: 1065:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 239 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1065:	
30	TAAAACATAT GGCTTGATAT TGCAGAAGAA TTGAAGTTAT CGTACCAGAA ACGGTACATA	60
	ATCATGATTA TATGGAAACG AAAAAAATAA AAATGGGTCA TTTAATATAG GAGGATTTAA	120
	CATTGAATTT TGAAGGTAAn TAATTGGAAA AGATTTGAAG TTGCATCGTT ATTATCGTTT	180
35	AATGATTTTA TCACTGGAAG ATTACTTGAA GGTGCAAAAG ATACNTTGAT TCGACATGA	239
	(2) INFORMATION FOR SEQ ID NO: 1066:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 202 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
45	(with grouping programmers and to No. 1066)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1066:	6.0
	AAATATCTAT AGACCTTTAT TCGGAAATGG TTCGTCTCCA GAATGGAAGG ATGAAGTACC	120
50	GAGTATTGAA AGGTAGAAGG TCTCCAAACT TTACCTGNAC GTGCACGANA TCTAACTGAA GATGATTTAG CAATTGAATT GAAACAGCCA ATTGTCGGTT GTAATAACTT AGGAGAGTTA	180
	GAIGAIIIAG CAAIIGAAII GAAACAGCCA AIIGICGGII GIAAIAACII AGGAGAGIIA	180

(2) INFORMATION FOR SEQ ID NO: 1067:

5	(A) LENGTH: 749 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear							
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1067:							
	CTACAATTCG ATCAACGCCG AAGTTAGATA CACCGATTGC TTTAATTTTA CCATTTTCTT	60						
	TTAACTCTTC TAATGCACGC CATGAGCCAT ATACGTCATT GTAAGGTTGG TGAATAAGCA	120						
15	CTAGATCAAG ATAGTCCAAA TTTAATCGTT GTAATGATCG TTCGATTGAT TTGATAGTAT	180						
	CTTCATAGTT AACATTTTCA ATCCATACTT TAGTCGTAAT GAATAGTTCA CTTCTATCAA	240						
20	TACCTGAAGC TTCAATACCT TGACCTACTT CAGTTTCATT TAAATAACTT TGTGCTGTAT	300						
	CAATATGTCT ATAACCCGCT TTAATTGCTT CTTTAACCGC TTCTGCnGTT TGTTCTTGAG	360						
	GAATTTGAAA TACTCCGAAA CCTAATACTG GTATCTTTAC ATCTTTACTT ATTTCAATAT	420						
25	GATTCATAAA ATGAACCTCC TTTATCTtGT ATGTCCACTA TAAACCATGG AGCGAACTCT	480						
	ATAGCAAGCC ATAGGTTTAC TTTCTCCCC AAAGACGTTC AACATTGTCA TCATAATTAT	540						
	CACTAGCATT GATTTTAGCA ATATGATTAT CATAATTATC AATTTTATAT TGTAGTAAAT	600						
30	CTCTCGCATC ATGAATTGTC TTTAAGTTTT CATTTAATTC TTCGAGTTGC TTATTTAAAA	660						
	TTTGCTTTTG CTGTGCTTGA ATATTTTCAT TTTTAGGCAA nTGCGCTAAC CTGCAAAATT	720						
	CGATAAGCGA TTCAATACTG ACGCCTGCA	749						
35	(2) INFORMATION FOR SEQ ID NO: 1068:							
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 436 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear							
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068:							
	TCCTCGAGAT AGACAAGAAT GGTGGTACAA TGTTTTTTAT GACGATGGCA AATATnATAA	60						
	GAANATAA'I' AAGAATGACA TGTCAAAAAT TAGGCGTAAT TTTTAGATTT ATCTATATAT	120						
50	TTATGCCACC GCTCAAACTT TTATMAAAAG TAAAAAGACA ATATTTATAT TGAACTTGTG	180						
	ACGTGAATTT CTAAAACACA ACCAACAATC CACAAGGAAA CTAGTAAATA AGTTTAAATA	240						

	TACTGACTAA AAAGATTTTG AAAGTGATTA AGTATTTAAA ACACGCCAAT CTTAAACCGC	360				
	TATTGACAAA TATGAAGCGG AACCACCGTT GTnTTTCTTT TnCAGGTCCA ATTGAATAAA	420				
5	TGTTGATGAA TAGAAT	436				
	(2) INFORMATION FOR SEQ ID NO: 1069:					
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 					
15						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1069:					
	TTCTCAAGTA ACAGGTATTA TTGTTACTGG TACAATCAAT AGAGAAAAAT ATGGCATTAA	60				
20	CTTTAACCAA GCACTTGAAA CTGGTGGCGT AATGCTAGGC AAAGATGTTA AATTCGAAGC	120				
	ATCAGCTGAA TTCTCAATCT CAGAATAATC TCATTACACA ATCCTCATTG TTTTAATATA	180				
	TATACGAAAT GCCAACTATA TCATCCCTAG GTATAGTTGG CATTTTTCGT TTAACTCATG	240				
25	TGTAACAAGC ACTAACTGTT CACCCTAATT TTAGACGCCT TTCATTCAGG TAGGTCTTAT	300				
	TGAAACTGAA AACTTTGaTG ACCTTTTGCA AAGCCATTAA CTGTATAAAG CATAGATCCT	360				
	CCGCCCATTT CTATATCATT GGAACAAATG ATGAGTTGAT TTGTTCCAGG TATAAATTGC	420				
30	GGATGAGTAG AACGTAACAT ATGCCCTTCA TCTCGGCCTG GTATCAATAT TTGTCCTATT	480				
	GGATAACCCC TTTTATTAAA AACTAACACT CGACCTTGGA CCATACATTG CTACGGATAA	540				
0.5	ATTATCGGCA C	551				
3 5	(2) INFORMATION FOR SEQ ID NO: 1070:					
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 325 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear					
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1070:					
	TATNATGGTA ACGCATGANC CTGTTGCAGC ACGCTATGCA AATCGAGTAG TGATGCTANA	60				
	AGATGGTCAA ATTTTCACTG AATTATACCA AGGGGATGAC GATAAACATA CCTTTTTCAA	120				
50	AGAAATAATA CGTGTACAAA GTGTTTTAGG TGGCGTTAAT TATGACCTTT AACGAGATAA	180				
	TATTTAAAAA TTTCCGTCAA AATTTATCAC ATTATGCCAT CTATCTTTTT TCGTTAATTA	240				

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	CAGAGTCATA TCCAATTATA CnGGC	325
	(2) INFORMATION FOR SEQ ID NO: 1071:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 771 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1071:	
15	TAAATGCCGC AATTGGATAG CTTTAATATA ATTAATAGTC AAGGTATTnC CAACAAnAAT	60
	ATATTATCCA CCCGAAGGAA GCGGGGTATn TTTGTTACTG ACGTCCCACA AGAAGCACAn	120
	ATATTAGATA GTGCTTACTC TGAAATTAAA AAATTAAGAG ATTATGATGA AAAACTAATT	180
20	ATCCCAGGAT TTTTTGGCGT ATCTCATGAA GGATATATAG TTACATTTCC ACGTGGCGGA	240
	TCAGATATAA CTGGCGCCAT CATATCAAGT GGTGTTAGAG CCACAATTTA TGAAAATTTC	300
	ACCGATGTGT CTGGTATTTA TAAAGCTAAT CCAAATATCA TCAAAGATCC TGAATTAATC	360
25	GAAGAAATCA CTTATCGAGA AATGCGTGAA TTATCTTATG CTGGTTTTAG TGTTTTCCAT	420
	GATGAAGCCT TACAACCACT TTATAAAGAT CGCATCCCTG TGGTGATTAA AAATACGAAC	480
	CGCCCTCAAG ATAAGGGTAC ATTTATAGTG CATGATAGAG AAATAAATGC GAAAAATGTG	540
30	ATTAGCGGTA TAAGTTGTGA TAAAGATTTT ACCGTTATTA ATATCAAAAA GTATTTAATG	600
	AATAGACAAG TCGGCTTTAC TAGAAAGATA TTAGGTGTCT TAGAGGATAA TAATATTTCA	660
0.5	TTTGATCATA TGCCTTCAGG TATTGATACT ATCAGTATCG TTATGCGTTC AAAACAAATT	720
35	CAAAATAAAG AAACAAAAGT ATTAAATGAA ATTCGTCAAA AATGTGATGT T	771
	(2) INFORMATION FOR SEQ ID NO: 1072:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 237 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1072:	
	COGTOGATOC STTTGATOTT GAGTGAGGIG CCAATGAAAG TTATGAGCCA CGTTGTCGCG	60
50	CGCACCATAT CGTAGCACCT AGTGATAATA ATAAGGAGGA ATTATAAGTG TTTGATCAAT	120
	TAGATATTGT AGAAGAAAGA TACGAACAGT TAAATGAACT GTTAATGACC CAGATGTTGn	180
55		

(2) INFORMATION FOR SEQ ID NO: 1073:

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 733 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1073:	
	CTTCTTGTGA GGGCGTTACA TCACCGGATG GATGATTATG AACTGCGATG ATTGCATTGG	60
15	CATTTTCTCT CACCGCAATA CTAAAAATTT CACGTGGATG TACAATCGAA CTATTTAATG	120
	TACCTTTAAA AACACAGGTT TCTTTAATCA CTACATTTTT TGAATTTAAC AATAAAATGA	180
	CAAAATGTTC TTGTGTTAAA TCTTTCATTG TTGGAATCAT ATAATCAGCA ACATCACTTG	240
20	GTTGCGTTAT TTKTATACGA TTATTTTCAG CTCTTCTCCC CATCCTTTCC CCTAACTCAA	300
	ATGCTGCTTT TAAAGTAATT GCTTTTTGTA ATCCAATCCC TTTAACTTTT ATCAAATCGT	360
	TAATTGAAGA TTTTTCAAT TCATTCAGAT TCGAAGCAGA TTTAAGCAGT TCATTACTAA	420
25	TGTCTATGCT CGAGAATCCT TTTCTTCCGG TGTTAATTAA TATAGCTAAT AATTCTGTAT	480
	TCGAAAGACT TTTTGCACCA TGGCTTAACA AACGTTCTCT TGGCATTTCT GAAGTTACCA	540
22	TTTCTTTAAT TTTCAAAAAT ATACGCCTCC TAAAAATTGA TGGATATCAT TATAAAAAAG	600
30	TGAATTGATA AAAAAGGArA TAAATATAAA TGGAACAAGG GGTAATAGTT TAATCGGCTT	660
	AAATATCATG GTAATTAAAG CAACTAAACC AGCAATGACA AATGTAAATA AnATGACATA	720
35	AATAGTGAAT TGG	733
	(2) INFORMATION FOR SEQ ID NO: 1074:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 768 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1074:	
	ATGGTTATTT TTTATGCTCT AAATCGTATG TGTTTATAAG GTTCAATTTC TTGCCATTAT	60
50	TAATTTTGCC GAGCAGTAAT GGGTTGTTAA AGTATCCATC AATTATGCTT AGCAATATTG	12
	AAAAATTTAA ATGAAAAAGC GGTTCAATTC TTGAAAAATA GTGTATATTT ACATTTTGGT	18
	AATAACTAAC TATAATTTAC ATAAGGAGGT TGTCATTTGG TAGTATTGTT ATCTTATAGT	24
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	TATTTACATA GAAGATCGAA ATGTGATTAT TGTAATTCGT CACTCAAAWG GTATGAATTA	360
	ATGCCGATTA TTAGTTTTTT ATTATTAAAA GGGCGATGTC GAAACTGTCG AAAGCGTATT	420
5	TCCCTAACAC ATTTCTTAGG GGAAACCTTT GCTTTAATAC CTATCGTCTT TATTAAGTAT	480
	GATTTCACAT ACGTAAATGE ACGCTATTTA TAACTACATA TGTTETTCTG CTTATTTTTA	540
	CTATGACCGA TATCACTTCT TTAATGTTAG ATTGTCGCTT AATTATAATT TATTGTATCG	600
10	TTTCTCTCTC GTTAAGTATG ATTTATCCAG TAGCTTTTAT CATTATTAGT ATGACCACGC	660
	ATATATTCTA CTTTTATTT CGGGCATATA TTGGTTATGG TGACGTTTTA CTAATATCTG	720
15	CACTTTCTTT GTTTTTCCCC TCTCCAATTC ACTATTTATG TCATTTTA	768
	(2) INFORMATION FOR SEQ ID NO: 1075:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1075:	
	TCATATTCAT TTAAAATACC ATTCATCTCA GCTTTTCTCA TTTTCTCTTT ATAAAGTTGT	60
	ATTTCGTGTC TTAATTCTGG CTCAGACATC TCACTCAATT TCTTCTGTTC CATCGGCAAT	120
30	ACCACTTTCT TCTAATTTAG CTTTAATTTT ATCATATTTA TATCCTTTTC TCATAAGGCC	180
,	TTCGATAGTT TTTGAAATTA ATTTCTGTTG CGTGTACTTC TTTCGATTTT TATTATAAAT	240
35	TTTTCTAAA TCTCGTTGTA ATAAATCGTC TAAAACCGCT TCATCTTGTG TAAAATCCAT	300
	TTCATTCAAT ACAGCATGAA TGGTTTCCAT TTCAAACCCT TTTTGAATTA AAGATTGCAT	360
	TACTTTTGCn TnAACTnTAT TTTGTGGCCC nTTTTTTGTT	400
40	(2) INFORMATION FOR SEQ ID NO: 1076:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 753 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	(xi) SEQUENCE DESCRIPTION: SEQ 10 NO: 1076:	
	TTAGGTCAAA ATATGTTTTA TCCAAAAGGC ATTTTATCTC AATCTGCTGA AGCAAAGAGT	60
	ACAACATATA ATCCAACTAT ACGTATGGCG ACAAACAAG ACGGAAAAAT GTTTGCATCA	120

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	CAAGGCATCG AAGAATTACG TGATTTATGG CAACAAAAAA TGTTGCGTGA CAATCCAGAG	240
	CTATCAATCG ACAACATGTC ACTACCAATT GTTACGAATG CATTAACACA TGGTTTATCT	300
5	TTAGTTGGCG ATTTATTTGT AAATCAAGGT GACACTATCT TGTTACCAGA GCATAATTGG	360
	GGTAATTACA AACTTGTTTT CAATACGAGA AATGGTGCAA ACCTTCAAAC ATATCCTATC	420
,	TTTGATAAAG ACGGGCATTA TACTACTGAT TCACTTGTAG AAGCTTTACA ATCATACAAT	480
10	AAAGATAAAG TCATTATGAT TTTAAATTAT CCTAATAATC CGACAGGTTA CACACCTACG	540
	CATAAAGAAG TGACTACCAT CGTCGATGCA ATTAAAGCAT TAGCTGATAA AGGTACAAAA	600
15	GTTATAGCTG TTGTGGATGA CGCATACTAT GGTTTATTCT ATGAAGATGT GTATACTCAA	660
	TCATTATTTA CTGCATTATC TAATTTAAAT TCAAATGCAA TATTACCTGT TCGTTTAGAT	720
	GGTGCAACAA AAGAATTTTT CGCATGGGGA TTC	753
20	(2) INFORMATION FOR SEQ ID NO: 1077:	
25	(A) LENGTH: 405 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1077:	
	AGAAGCGATT TGACZATAAA ACAATTGAAA AACTTTTGGA AAGCAAGTGG TGGGAGAAAA	60
	CGCCTGACAA ACTAAAAGGA TTTTCGGTTG AATATTTAAA TAAAAAGGAT ACTTAATGAT	120
35	ATGAGAATTT TAAATATTGT ATCGAGTAAT ATTGTTCAAG ACCCAAGGGT ACTTAAACAA	180
	ATAGAAACAA TTAAAGGCGT TACGGATGAT TATAAAATTG TTGGAATGAA TAATTCACAA	240
	rctactaata agcgattgga aaatttagat tgtaattatc gtttgttagg tagcaaggta	300
40	GATCCAAÄÄA ATATTCTTTC TAAATTAATT AAGCGTATAA GATTTGCAAC AGGTGETATC	360
	CGAGAAATTA AAGCTTATAA ACCTGACGTG ALTCATGCAA ATGAT	405
45	(2) INFORMATION FOR SEQ ID NO: 1078:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 504 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1078:	

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	CATATTCACA CCTCAATATT CCATAACTTT TACTTTAATA TCAATCCACT TAAATCCATT	120				
	CACATCATTG AGTATAAAAT AATATGGTGA TATACGTTGA AGTTGATTAT CTTATATATA	180				
5	AGTATACTTC ACAGAATTTA TAAAATTGTT TAGTCATCAT CTTCAGTGTT TAATTCAAAA	240				
	ATATAGAATC TACTGTATTG CATMATAAAT TGAAATGCCA CAAATTGTGC TCCAGCGATA	300				
	ACCAACATGC TCACAATAAT TATAAACTTA GATTCTACGA CATTAGGMAC CALATATATT	360				
10	CGATAATTTT TTCAATATAT ATAAATGAGC TCAACGCAGT TAATAATAAA CCGAAATGTG	420				
	TTTTAGTTTT ACCACCCAA CGTTTTGTTA CTTTAGGTAA TTTTAATAAC GTGAACATTC	480				
15	CGCCAATTAC TAATAACAAA TAAC	504				
	(2) INFORMATION FOR SEQ ID NO: 1079:					
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 645 base pairs (B) TYPE: nucleic acid					
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear					

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1079:

CATTCTTAAT	CAACTTCTTC	ATAATGGGAA	TTTGGCATGG	TAnCGAAGTG	TATTACATTG	60
TTTATGGTTT	ATACCATGCA	GCATTGTTTA	TAGGTTATGG	CTATTATGAA	CGTTGGCGTA	120
AGAMACATCC	GCCACGTTGG	CAAAATGGTT	TCACAACAGC	ACTTAGCATT	GTGATTACAT	180
TCCACTTTGT	AACATTTGGC	TTTTTAATCT	TCTCAGGTAA	ACTTATATAA	TAAAGGAGAA	240
TTTAATTATG	GAATTTAGAG	AACAAGTATT	ATTTTTAAA	GCAGAAGTAG	CAGAAAATGA	300
TATTGTAAAA	GAAAATCCAG	ACGTAGAAAT	TTTTGAAGAA	GGTATTATTG	ATTCTTTCCa	360
AACAGTTGGA	TTATTATTAG	AGATTCAAAA	TAAACTTGaT	ATCGAAGTAT	CTATTATGGa	420
CTTTGaTAGA	GATGAGTGGG	CAACACCAAA	TAAAATCGTT	GAAGCATTAG	AAGAGTTACG	480
ATGAAATTAA	AACCTTTTTT	ACCCATTTTA	ATTAGTGGAG	CGGTATTCAT	TGTCTTTCTA	540
TTATTACCTG	CTAGTTGGTT	TACAGGATTA	GTAAATGAAA	AGACTGTAGA	AGATAATAGA	600
ACTTCATTGA	CAGATCAAGT	ACTAAAAGGC	ACACTCATTC	AAGAT		645

(2) INFORMATION FOR SEQ ID NO: 1080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1080:	
5	AGATGCCAAA ATCAAAACCA ATAATTTGGC AACAACATAT AAGTCCACTT TACCGGACCT	60
	NTAAACTTAT CGTACTGTTA AGAACCAAAC GACTGCCATT ATTTGGTCCT AAAGCCACGA	120
	TGGTGGTAGC CNTTGTAATA ATGCTGGCGT AGAAATTAAC CGCCACCCCT AACACCGAAC	180
10	TATAACGCGG ATAAACCAAT AAAATTATGA TATAATCATC CGTTAAGTCA ATCCATAGTT	240
	TAACATCCCT TATGTTTAAT TTACTCT	267
	(2) INFORMATION FOR SEQ ID NO: 1081:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 441 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1081:	
	ATATTTGTCC ACTATTAGAA GATTGTAGAG AAGGACAAAA ACGTTATAAA GCTAGTTTGA	60
25	AAGAAGCGTG ATAACATGAC AAATATTACA AAAGAGGTAT TTGATAATTT AGAACAAGAG	120
	ATTGATTTAT TTGCCAAAAA TAAGACATTA GGTTCTAGTG AAGCAAAGCC CTACTTGGAT	180
30	GAATACCATA GTAAAATTAT TGATTATTTT AAGCAGGTTA ATGACATAAC TGGCAATATT	240
	GATTTTGATA AATTAAATCA ATATCCTGTT GTGCCAATGA ATTTTAAAGA AAGATATGAT	300
	TATATGATTG AACGTAAATA TCATTTTATG GGCTATCGAC AAATGAAGAC CTTTAAAACT	360
35	GAATTGATTA AAATGNATGC TAGTTATCAA ACAAGGTTAA AGAATAAGCA GGTATNGACA	420
	AGATTGATCA TTTCCTAGTG T	441
	(2) INFORMATION FOR SEQ ID NO: 1082:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 410 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1082:	
50	AAAATTTCTT AGLTGATGGT TATTGTTGTT GATTTGAATA ATTTGTAGCG AATATTTTGT	60
50	AACAGGGCTA CTAAGAATTT TTATAACAAG AAGTGATTTC AATCGTACTA ATTTTCAGCG	120
	TTTGATGACA AAAGTGTATG TCCAAACTTA AATAATGGCG ATAAAATTTA AGTCATGGGT	180

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GTTGAATATC AATAAAAGAT TAGCAAGTTA GTTCAAAATG GCTATGTATT GTTTTTTGAA	300
ATACATAGGT TTGAAATCTA TATTAATTAT GCACCAAATA ATTTAATTAG ACTCTATCGA	360
AAATTTCCAA ATTTTGCTTA CTATCTTTCT AATTTTACTT TTATATTGTG	410
(2) INFORMATION FOR SEQ ID NO: 1083:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 586 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1083:	
CAGATATTCC CTTCTATTTA CAAGTTGGTA ACCCATATTT ATCAGACAGC GTAGATAATC	60
ATACCGAAAA GTTGTTAGAA CGCTACGAGC AGTTGGTGGA TTTAGTTATG YAAAGTAATG	120
ATATGAATCA CGTTTATGTG TTACCACAAC TTCATACATT ACTTTGGAGC AATAAAAAAG	180
GTGTATAAAG GATAACTTAT TTTACTTTTT GCAAGTCATA TCTAATGAAT AACAATATAT	240
TAATTGATAT AATAGTTGAT TGAAGTATAA CGAACAGGAG TCCATCATGA TTGTATATAT	300
ATTAATTAAT ATTGCTATCG TCGTACTTAT AACTGGATTC AATTTATATA GGCATCAAAT	360
GCAACATTTA TCATTAAGTG CAATGTTGTL ATCTATTACG ATaAACGCCT TTATAAATAC	420
ATTCATAATT GATAAATATA ACTTTATTAC TCTGTGTACT ATAACGATGT TTATCATTTG	480
GACGATACTA CAGTTTTACA TTGATAAAAA ATTAAAACCT GTATACATTA CAGACCAAAA	540
ATTTATTGCT ATCATATTAA CGATTGTTGT CAGTTTAACG CAACGT	586
(2) INFORMATION FOR SEQ ID NO: 1084:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 638 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1084:	
AACACAAGGT AGCGTCATTA GCATTTAGAT TTTATTGCCA AATTATATAA CGATTTATAC	60
ATCANTAGA AAACAATAGA TGATGTATCT GCAGTTTCTG AAGTGAAATA TGATATTAAA	120
TCACAAATGA GTGATGATGA GATTAAGCGT TTAGAGGAAC AAGGACTTCA AGCTATTAAA	180
GAAGGACAAT TTGCAGTACT TTTGATGGCA GGTGGTCAAG GAACAAGACT TGGTTACAAG	240

	TIMAAAACAT TGAATCATCA ATCTGGACAT ACGATTCAAT GGTATATTAT GACAAGTGAT	360
	ATCAATCATG AAGAAACTTT AGCTTATTTC GAAGCACATA GTTATTTTGG ATATGATCAA	420
5	GAAGCAATCC ATTTCTTTAA ACAAGATAAT ATTGTGGCGC TTAGTGAAGA AGGGAAGTTA	480
	ATTTTAAATC AACAGGGTCG TATTATGGAA ACGCCGAATG GTAATGGTGG CGTGTTTAAA	540
	TCTTTAGACA AGGCAGGATA CTTAGAAGAA ATGTCTAATA ATGGCGTTAA GTCATATTTT	600
10	CTTGAATAAT CATCGACAAT GTTTTCAGTA ACATGTTG	638
	(2) INFORMATION FOR SEQ ID NO: 1085:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 618 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1085:	
	ATTGCAATAT TATCCGCTTG GTTCAACACG TCATCTTTAT tAATACCATT TATTGGAAAT	60
25	tCcACCcATT TCCcGGgCTt CTtACTTCCc TTTATAAAAC TGcCCATTTA ATGAATACTG	120
	TTTAGCTTCA TCTATTCGTA CTTCCACTAG TTTACCAATC ATTTCTTTAG GCGCTTTGAA	180
	ATTAACTAGC TTATTTTTAT CAGTGTAGCC AGCAAGAACC TGATCATCTT TTTTACTACT	240
30	TCCTTCACAA AGTACTGTTA CAGTTTGTCC TTCGTACTTA CTCATAGCTA TTTGTGAATA	300
	ATGACCAACT TTTTTATTCA AACGTTGCAA TCGTTCCTTT TTGACATTTA AAGGTACATT	360
35	ATCTTTCATT TTAGCAGCAG GCGTACCATC ACGTTGTGAA TACAAGTACG TATATGCATG	420
	TTCAAAACCA ACTTCATCAT ACAGAGTTAA AGTTTCTTCA AATTGTTCCT CTGATTCATT	480
	TGGATACCCT ACAATAATAT CTGTAGTTAA TGCTACATTA GGAATTCTAT CTTTGATTCG	5.4
40	TTTTACTAAA TCCAAATAAC TTTCTCGTGT ATATTTTCTA CCCATTATnT TTAATACTGC	60
	ATTATTTCCA GATTGAAC	61
	(2) INFORMATION FOR SEQ ID NO: 1086:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 502 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1086:	

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	CAGCAATATC ATGATCAGTT TAATTCATCA AGAAAGTCTA TCTATACTTT TACAGAAACA	120			
	GTTCAACCAA ATCGTGTTAT TTATGATTTT TATGATTATG ATCCGTATCA ATTAGCAGCA	180			
5	AATAATGCGA AAGCATTAAA GGATCATATT GAACAAAACT TTAACTTTAA AGTCCAAAGT	240			
	ACCGGTGTTA KTTACTTTAG TGATGGTACA GTTAATATCA TTCAAGGTTC TGAAGAAAGA	300			
	GATAAATATG TTGATACAGT TTCAACAAAA TCTTCGTTAC GACGTATTAT TAGCGAACCA	360			
10	NAGAGCTATC TAAACACCCT TTAAATAAAG AACAGGTTGA NCAAATCACA GCTATATTCA	420			
	AGTAAAATCA AAGGCATAAT AATCCATTAC GCTCGATACG CACTATGGTT ATTATGCCTT	480			
	TAAATTATTT CTATATAA nT	502			
15	(2) INFORMATION FOR SEQ ID NO: 1087:				
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 429 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 				
2 5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1087:				
	TTGCCTGATG GACGATGGCC ATCACAGACT GAGTTTAGAT TGTCTTTAAT GCAACAACTT	60			
	GCTGTAAACC AAATTACGAG TGGTAATGAA AGAATAAGTT CAGTTAATGG GCCACCAGGT	120			
30	ACAGGTAAGA CTACTTTATT AAAAGATATA TTTGCTCATC TAGTAGTTGA mAGAGGTAAA	180			
	GAGTTAGCTA AACTAAATAA TCCTAAAGAT GCATTTGTCA ArACAAAAAT TCATGAAACG	240			
	GATGATAAAT ACGTATACTT ACTAAAGGAn nTATTGCCAA ATATAAGATG GTAGTCGCAT	300			
35	CTAGTAATAA TGGAGCTGTT GAAAATATAT CTAAAGATTT ACCGAAAATT GAAGAAATTA	360			
	TAAGANATCC CGAAAAATGT AAATTCCCTA AATATGAACA GAATTATGCA AATTTAGCAC	420			
40	ATGAATTAA	429			
40	(2) INFORMATION FOR SEQ ID NO: 1088:				
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 611 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear				
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1088:				
	TAAGACCTAA TATTTTGGnC CAATACTATG GTGCAGGTNA TTTATATATG ACACCAACAG	60			

	ATCCATTATT ACATGAGTTT GGTACGAAAA AGTATCCAGA TGAATATCGA TATGGTTTCT	180
	ATGCTAAGCC AACATTGAAT AGACTTAACG GGGGATTCTT TGGACAAGTC TTTACTGTTT	240
5	ACTATAATGA TAAGTATGTA GTTGTACTTG CATTAAATGT AAAAGGAAAC AATGAAGTTC	300
	GAATCAAACA TATTTATAAT GATATTTTAA AACAAAATAA ACCTTACAAT ACGAAGGGTG	360
	TTATTGTTCA ATAATTAATA TAGAAGATAT AACATGTATA TGGCATTAAG GCATCGACCT	420
0	TATCTGACCA GTATACGAGT TATATCTTCT TTTTTATAGT GGTAAAAAGT TTAAAGTATA	480
	AGGTTGAAGA AGGATGAGTT TAAAAATATG TGTTAACTGA TAAAAGGGGA NATCATTTGG	540
5	TGAGTTGGCA TCAGnCTAAA nTGAATGAAG ACGAATACGT TGGTCCATGC GTGGTGTGAN	600
•	TGTTTCTAA A	611
	(2) INFORMATION FOR SEQ ID NO: 1089:	
?0	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 644 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1089:	
	CTGGATAATC GCTTTAATAT GATCAATTTG CTTTTCACTC ATATTAAGCT TATCTAGCCC	60
30	TTTCATTTTA TTCATACCTG GAATCATTTT CATAATATCA TCCAGTGGTC CTAGATTTTT	120
	CACCYGWTCA AGTTGTTCTA AAAAATCATC TAAAGTAAAC GATGACTCAC GCATCTTTTT	180
35	CTCTAAATCT TTTGCTTTTT CTTGATCCAC ATCTTGTTGC GCTTTTTCAA TTAAACTTAA	240
33	CACATCACCC ATACCTAAAA TACGTGATGC CATACGTTCA GGATGGAATA GCTCTAAACC	300
	ATCTAACTTT TCACTCATAC CAACAAATTT AATTGGTTTT TGTGTCACCG AACGAATAGA	360
40	TAAAGCTGCA CCACCACGTG LATCACCATC TAATTTAGTT AAGGLAACAC CTGTGACATC	420
	AAGTTGATCG TCAAAAGATT CTGCAACATT GACAGCATCT TGACCCGTCA TTGAATCGAC	480
	AACTAACATA ATTTCGTTTG GTTTAGCAAT GTCTTTTACT TCTTTTAATT CGTTCATCAA	540
45	TGCTTCATCG ATGTGTAATC GACCTGCTGG TATCAATGGA TTACAAAGTC TAAATGTTCT	60
	TCTTTAGCAN GTTTTAATGC ATTAGTTACA ATTTGGTGTG GGCC	64
	(2) INFORMATION FOR SEQ ID NO: 1090:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 207 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	·

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1090:	
_	GATCCTATCG TTTTAGTGCA TGGTTTCAAT GGGTTTACAG ATGATATTAA TCCTTCAGTG	60
5	TTAACTCATT ATTAGGGCGG TAATAAAATG AACATTCGCC AAGATTTAGA AAAAATGGTT	120
	ACAAAGCTAT GAAGCAAGTA TAAGTGCTTT TGGAAGTAAC TATGACCGCG CATTGAACTT	180
10	TATTATTATA TCAAAGGCnG TCGnGTA	207
	(2) INFORMATION FOR SEQ ID NO: 1091:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 212 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1091:	
	GACTCTAGAG GATCCCCGCT CAAATGCCAT TTGGTGATAT TCGTGAAGCT GCTGGCGAAA	60
	AAACATTTAA TCCAGTGGAA GATCGTTTCG TAATAAAAAA ATAATCAATA TATTGTTAGG	120
25	AATGGGACAG AAATGATAAA GATTCATTAG TTATTCATTA TGTTGTAGTT CTTACACATT	180
	AGCCGCTGCT AATnGCAACT TAAGAnTAGG TT	212
30	(2) INFORMATION FOR SEQ ID NO: 1092:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 208 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
<i>35</i>	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1092:	
40	TGGACCTGCA ATTGGTTGCC AGCAGCAACT TTAGCTTCAT AGCTAGCTTT GTGAGCAAGT	60
	GGTAAACCTG GAACGATATC ACCAATTGCA TAGATATTGC TGATAGACGT ACGGCTTTGT	120
	TTATCAACnn CTAATAATCC ACGTCAGCGA ATTTAACACC TAATTCTTCT AGGCCTAATT	180
45	CGTCGTGTTT GGACGACGAC CTACATTA	208
	(2) INFORMATION FOR SEQ ID NO: 1093:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 902 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1093:	
	CTTAAAAGTT GTnTCAATAA TGATTGTATT AGTTGCATGC TTATTATATA TGAATCATAG	60
5	TATTGATITA CCTACCCTTA TTATGATTTC AATTTTTTCA TTTGTGATAT TTGATAGTGT	120
	TGAAAATATT AATAGTGCTG CACACGTACT TGAAATGATA GATATGACGA TAGATGATAT	180
o	TGMAAAGATA AAAAATGCTC CAGAACTGGA TGAGAATGGA AAAAATTTGA CGATTAAAAA	240
υ	TGAAAATATC GCTTTTCAAA ACGTGAACTT TTCATATGAT GATAAACAAG TGATAAAGAA	300
	TGTGAATTTT GAGATACCTA CACAAACATC AACAGCAATA ATTGGACCTT CAGGAAGTGG	360
5	GAAATCTACA TTATGTCACT TACTCTTGCG CTTTTATGAT ATCGATGATG GAAATATTCG	420
	CATCGATGGT GTTGATATTA AAGATATGAC ATTAAGTACG TTAATGTCGA AAATTAGTGC	480
	AGTATTTCAA AAGGTGTATT TATTTAATGA TACGATTGAA AATAACATAT TGTTTGGCAA	540
20	TCCAGGTGCA ACGAAAGAAG AAATTATTCG TGCCGCGAAG CAAGCATGTT GCCACGACTT	600
	CATCATGTCA TTACCTGAGG GATATCAAAC AATGCTAAAT GAAAAAGGTA GTAATTTATC	660
	TGGCGGAGAA AAGCAAAGGA TTTCTATTGC TAGGGCGATA TTAAAAGATG CACCAATAAT	720
25	TATTTTAGAT GAAGCAACTG CAAGTATTGA CCCTGAAAAT GAACAGCTGA TTCAAACGGC	780
	AATTAATGAA TTAAGTAAAG GCAAAACAGT AATTACAATT GCACATAAAC TTGAAACTAT	840
	TAAANATGCA GATCAGATTA TAGTGCTCAA TGNAGGTGAA ATAATTCAAA AAGGTAGTCC	900
30	TG	902
	(2) INFORMATION FOR SEQ ID NO: 1094:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 632 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1094:	
	ACGCAAGGGA TATGATTAAA CACCATAATA TACAATCACC TTTTTTATAC ATGAAAGCAC	60
45	TAATAGAATC GATTCATTTA AACATAAAAC ATGATTTTAA CCAGCAAGAT TTGATTGAAA	120
	TACCAATTGT GTATGGTTCG AAATATGGTC CGGATTTAGA ATCACTTTTA AAACATTACA	180
50	AAATCAAGCT AGAAACTTTT ATTGAATTAC ATTCTAAGGC GCAATATTTT GTTTCGATGA	24
50	TGGGATATTC ACCTGGGTTL CCTTATTTAA CTGGATTAAA TAAGAAATTG TATATTAATC	30

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	GCGGTATTGT AACTACGGAT ACAATTAATG ATTGGTTAGT TATTGGTTAT ACACCATTAT	420					
	CACTITITAA TCCGAAAGAA TCAGATTTCG CACGCTTAAA GTTAGGCGAT AATATTAAAT	480					
5	TTAGACCTAT CAATGAAAAT GAATTAGAAG TAGGAGCGTT TAAAGATGTC AATCATAATT	540					
	GAAAAAAGTG GCTTATTCAG TAGCTTTCAG ACTTTGGCAG AAGGGGATAT GAACATGATG	600					
10	GTGTAATTCC ATGTGGTGCA CTTGATACTT TA	632					
	(2) INFORMATION FOR SEQ ID NO: 1095:						
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 212 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear						
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1095:						
	GCAACACGAT TGCTAAAAAA TGATATACTT ATTAATTGTT GCAACACTTG TTTATGTGAT	60					
	ATACTGATCA TGGCATTGTG GCGGATTGAT GACCATACAC ATGACGTGAC AATGATAAAT	120					
25	CATTGCCACT ACTTGTTAAA ACAGCAATTT CTCAAGTGGA AGCTGGTGCN ATATATTnCG	180					
	CCAATAATAT GATGGATGGT TTGTTGCTGA AA	212					
•	(2) INFORMATION FOR SEQ ID NO: 1096:	•					
30 35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 466 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1096:						
40	AATGAACTGG GTATTnCTTT TGCCATGCTT GCCCACTGCC ATGCATTTGC TGAAGAATGT	60					
	TTTTGTAGAA CCGGCTTAAG AATTTGAAGT TTGTAGTAGT ATCTAAAAAG ATTACTTGGT	120					
	GATACTCAGG ATGAATTCCT TGTTCATTAT TTTCAGCTCC TTTGCCCTGA ACCATCTGGA	180					
45	ACAGAGTTAT TTGTGAGTTT TTACCCAATA CTGTGTAATT ATAAAGGTAA TTAATTCAAA	240					
	ACGCAAGCCC CTATATAATG TTTATTAAAT TATAGGTCGA CCCGTTTTAG TACTTTCTTC	300					
	TGCAGACTTT TGTAGCTGCT TGAAGAAATC TECATTATTC TTAGACCTTT TAAGTTTGCG	360					
50	AATAAATCTT TCAGTAAAGT CAGTTGAGTC AGTGAATAGA TTTCTTAATT GCCATAATGT	420					
	GTCTAATTCA GATTTACTTA TCAACAATNC TNCTTTACGC GTTGAA	460					

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(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 208 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1097:	
10	TTTTGATTCA ATAGGCGGTT CCGTGTTATC ACTGACAACT TTAGTTGTAG CTTCATCTTT	60
	ATGTATTTCT TCGTTAAATC CTTCAAGTTT TTAGTCGTGG GATTTTAACC TCAGGATGTT	120
15	CCATCATGTC TTGACTATCA AGTCCTTnTA CACGTGTCTT TATGTGATGC TTGATTGCGT	180
15	nCCCTTACTT TTTGAATAGG GGTAGTAA	208
	(2) INFORMATION FOR SEQ ID NO: 1098:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 571 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1098:	
	CCTTCAACGA AAATAGCATA TTGACCATAA ATATTATGAA TTGTTTGTTC AACATCTTCA	60
30	GTTATTGGAT CTTGACTCAA AAATACATTA AATACTTCAA TACCAAATTT ACGTGACATT	120
	TCTACAGCTT CATACGTATC AATAATACCA TCTTGACTAT AATTAAATGC AGACGGTTCG	180
35	CCGTCTGAAA ATANGATTAA AAATCGTTGA TGTTGATTTC GACGCATTAA TCGTTCACTT	240
	GCAACTCTAA TAGCAACACC ATCACGATTA TCATCTTGAG GTTCAAGTGC CATAATACGT	300
	GGGCCATCTT TTTCAAAGGT TGAGTAATCA TAGTTAATAA TTTCATTAAT GATATTTGGT	360
40	TGTGCATGCT CGTCTGAATC AAAGGCATCC TCACTGAATG ATAAAATTTC ATGTTTAATG	420
	TTCAATGCTT TTAACGTCTC GTGGAATAAC, ACTACACCTT TCTTCGTTTC AGCCATTTTA	480
	TCATGCATAC TTGCTGGACG CATCAATTAA CAATGTAAAT GTnCGCATCA AATGATTnAC	540
45	TTAAATCTTG TTTTTTGTAA AACAATTTAT A	571
	(2) INFORMATION FOR SEQ ID NO: 1099:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 214 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1099:					
	TGCAAGTGAA CAAGTCATTA ACTTGTTTAA TACACGTGGG GCACAAGTCG AAGAAGTTTG	60				
5	GGTGAAGGGC CATGAAATTA CAGAAACTGG ATTAACGGCT GGTCAACAAA TACTTGGGAA	120				
	ATAACAGTTC TATTAAGAAG CGGACAGATG GAAAAGATTT TACCTTTCAT CTGCCGCTTT	180				
	TTGATTTGAA GGCCGGACCn AATTTACCAn GGAA	214				
10	(2) INFORMATION FOR SEQ ID NO: 1100:					
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1158 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 					
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1100:					
	CACCGTATTG TACAAAGAAT TTAAAGTTTT CGATTTCTTn TCTTAATTTA TCATCAGCTA	60				
	TCGGTTTGGT TGGGATAATT TTATTATGTT CCATTTTTAC TGGATATTCT TTTTCTTTAC	120				
25	TACGTGAGTA TCCTnTTTTA TCTTCCCATA ATTCCCTCAC AATAAATTCA CCTTTTGTCG	180				
	TTCTGGTATT GCGGTCTACA TACAGGACCA ATCCTCTGGA TTCCATATTC TTTCCATTTG	240				
30	TTTCTATTGT CATTTTAGAG TGAATTATCC AAGTGCCTTT GTCGCCCTTT TCAAACTCTT	300				
50	GATCTCGAAA GCCTTCCTTA TCATAAAAGT CTTCAAGATT TTTAGTTGGA TACAGGCTCA	360				
	ACGTTTTGTT GAAGTTTTCT TTAATTTGTT TATCTTTACT GCTTTCTTCC TTTTTCATTC	420				
35	CGCAAGCCCC TATAAAAACA GCTAATAATA CTAAATACAG CCAGAGCCTC AACCTTTTTG	480				
	AGTGAATCAT CATTTCACAT CCCCATTTTT ATTTTTGATG CAAAGTTAAG TECAAATTCC	540				
	AATATTAATA ATATTAGAGG AAALTTLATG ATTAAATCCT CGTGGATTLT AATTGTTAGT	600				
40	TGTATTTTC ACATATCAAC ATCACAAATT ATTTAAAAAG CGCAAATATC TTTATAATTT	660				
	TTATTGGCCT AACCAACTAA TTAATTAAGA TAAATTGCGC TTATATTTAA AATAATAACA	720				
	CTGAAACTCA ATGTATTTAC TTATTAAAAT TGATGTTTAA ATACAACTTT ACTAACATTC	780				
45	ATTTTTCGGT TTACATTAAT TKGTTAGATA ACGATATATA TCALCTCTTA CAGCTTTATC	840				
	CAGTGCTAAA TCCATCGTTA CTACGTTTGA ACCATTCGGC ATTTTATCTT GCTTTTCTGA	900				
50	ACCTTCTATA TATCCAGCAG TTCCTAAATA ATAAAAATAT ATACCATCAT CATCTTTTTT	960				
	CTGTACAAAA ATATACATTT TAATTCCTTT TGCTCTATGG GACAAAATTT TCTGAACTTC	1020				
	TTTTGATTCT AGCGTTCTAT TAGATTTAGT AAACCATTTT AATTCATCTT GACTTAAAAA	1080				

	TGGCATTTCT TGGCTTTT	1158
	(2) INFORMATION FOR SEQ ID NO: 1101:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 353 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1101:	
15	CCAAATGCTA TAAATGCAAA AATnGCTAAT GCGATATTTT TATAGAAAAT ATCTGGTCCT	60
	AAATTTTGTA AATACGTGGT AAACGTTGCG TATGACAATA AGCCAATCAC TACAGCGTAA	120
	ATATGTGAAA TAATTAAACC GAACCGTCTC GCTCTTTCAA AAACAAGTGT TGCTAAAATA	180
20	ATAATCAGTA ATCCAAATGA CAAGGGTTGT CGCCAACTTA ATGGTAAAAA CTGACCTAGA	240
	TAGCATCCTA TGCCAAATAT AATCCAATAA TACATAAAAT AAAGCCACAC TTTACTTALT	300
	GATTGAGCAT GCTGGTTTTG ATGATAATAT GAATGATTTG TATTTTGCGA CAA	353
25	(2) INFORMATION FOR SEQ ID NO: 1102:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 194 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
3 5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1102:	
	CCCACACGTC TTCCACCGGA TAGGTTTCGA GCTCGGGCGA ACCGGGCAGG GCGGTGACCA	60
	CCCCGTGCGG TGTCTTCTTG GCCAGCTTGT TTGCGAGCTT GGCCAGCGTC TTCGTGGGGC	120
40	CAATGCCCAC GCAACACGGG ATGCCCACCC ATTGGAGGAT CTGGGCACGG ACCTGGCGGG	180
	CCATCGCTTC GnTG	194
	(2) INFORMATION FOR SEQ ID NO: 1103:	
<i>45 50</i>	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 220 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1103:	
	INT. OPENIOR PROPERTY PAR IN THE PROPERTY OF T	

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	TCGCTTTTGC TTTTGCATCA GGTATTGCTG CTATTTCAGC ATACTTTTTG ACTTTCAAAT	120
	CTGGTGATCA TGTCATCTTA CCCGATGGAT GTATATGGGC GGTTACTTTT CGTCTCACTG	180
5	TGGCAAATTT TGGATCGATT TAATATTGAA TTTTACAACC	220
	(2) INFORMATION FOR SEQ ID NO: 1104:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 235 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1104:	
	GGACATTGTA TCGACATTTC AAAGATAAAA GCGATTTATG CTACTACGTC ATACAAAGAG	60
20	ACCTTGATAT TTTTATCACT CATTTTAAGC AAATTAAAGA TGACTATCAT TCTAATTATG	120
	AGGTTATGCA AGTGTCGTCA TCGCTTTTAA ATAAGTCATA ATAAAAATCA AATAATTCTT	180
	GATAAAATGC GCTTTGGTAA AAACGTAATT TATTGTTGCC TGCTTCAATA CATTG	235
25	(2) INFORMATION FOR SEQ ID NO: 1105:	
30 -	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 229 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	·
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1105:	
35	GCGGGGGCAG GTAAATCCAC TTTGACACAT CTTATTGCAG GTGTTTATCA GCCAACAATA	60
	GGTACTATAA GTACAAACCA GCGTGATTTT AATATTGGGA TACTTAGTCC ANAGCCCTAT	120
40	ATTTCAGGCT CTATAAAAGA GGATATTACG ATGTTTAAAG NTATAGAAAA TAATACTAAT	180
	GAAGAAGTGC TAGACGAAGT AGGGTTTATT AGACCAAGTG CCATCCTTC	229
	(2) INFORMATION FOR SEQ ID NO: 1106:	
45 50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 596 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1106:	

rA	TAAAAT	CAAAATTTGA	TGAAGTAAAT	GTAATCGCGT	CAACAAACGG	TAGAAAGTTT	120
ΑT	TAATGGTG	AAATATTAAA	GCAATTTTGC	GATAACTATT	ATGACGAATT	TGaAGACCCT	180
TT	TTTAAATC	ATGTAGATAT	AGCAAATAAA	CATGACAAGA	TTATTATTTT	ACCTGCGACT	240
TC	TAATACGA	TTAATAAAAT	TGCmAATGGT	ATATGTGaCA	ATTTATTATT	AACTATTTGT	300
CA	TACAGCTT	TTGrAAAACT	TTCTATATTT	CCAAATATGA	ATTTACGAAT	GTGGGAAAAT	360
CC	AGTTACTC	TATAATAAA	TCGATTATTA	AAAGATTATG	GTGTATCAAT	ATATCCAGCA	420
AA	TATTTCAG	AAAGTTATGA	ATTAGCGTCA	AAAACATTTA	AAAAGAATGT	TGTCGCACCT	480
GG	AACCATAT	AAAGTTCTGG	gAATTCATTT	Gagattagaa	TATGGAAAAT	CaTAAAGCGC	540
GC	KATTGATT	AGTTTAATGA	ATGATTGGAG	TCnTTTGAAG	ATnCGATTTA	CAATGG	596

(2) INFORMATION FOR SEQ ID NO: 1107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1107:

ACTAGCTAAA	AATAATATTC	TATTCTTTTT	AACATGGGCA	GTTCCAGCGG	CAATTAGTGG	60
TATTTATATT	AAATATATAA	ACAAGGCTAC	GGTAGAAAGA	TTTTTTTAAAT	TAGTATTTTT	120
CATATTTTCT	GTTTCATTTA	TTTTTGTAAT	TTTAATACCA	AAACTTACAG	GTGAGATACC	180
TAGCTATATC	AATTTTGGAC	TTATGAACTA	TCAAAACGCT	TCGTACCTTT	CAGCATTTAC	240
TGCCGGATTA	GGCATTTATT	TCATTATGAA	AGGTTCAGTT	AAACATAAGT	GGATATATGT	300
TCTATTTACA	ATAATTGATA	TCCCTATTGT	GTTTATACCA	GGAGGGCGTG	GAGGTGCTAT	360
TTTATTAATT	CTTTACGGCT	TATTTGCATT	TATACTTATT	ACGTTTAAAA	GAGGAATACC	420
TATCGCAGTA	AAAAGCATTA	TGTATATTTT	TGCATTAAGC	ATATCTAGTG	TATTGATTTA	480
CTTTCTTTTT	ACAAAAGGTT	CGAATACTAG	AACATTTTCA	TATCTACAAG	GTGGAACACT	540
TAATTTAGAA	GGTACTTCTG	GgAAGAGGAC	CGATTTATGA	AAAAGGTATT	TACTTEATTC	600
AACAAAGTTC	GTTATTAGGC	TATGGGCCAT	TTAACTATtA	TAAACTAATC	GGAAATATAC	660
CACATAACAG	CAT					673

(2) INFORMATION FOR SEQ ID NO: 1108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 506 base pairs

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	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	•
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1108:	٠
	TCACAGTGGC GGCACAAAAA GTAAGTGGAG ATTATTTTAA TTTAATTGAC CATAACGATG	60
	GCACAATGAG CTTTGCTGTT GCAGATGTCA TTGGAAAAGG TATACCAGCT GCTTTAGCAA	120
10	TGAGTATGAT AAAGTTTGGC ATGGATTCTT ATGGACACTC ACAATTACCG AGTGATGGTT	180
	TAAAACGTTT AAATCGTGTT GTTGAAAAGA ATATTAATCA AAATATGTTC GTCACAATGT	240
15	TTTATGGTTT ATATGAAGAA ATGAACCATT TATTGTATTG	300
	CTGGATATAT TTATCGCGCT GAAAAAGAAG AATTTGAAGA AATTTCAGTT AGAGGTAGAG	360
	TGTTAGGAAT CAGTTCACAA ACACGATATC AACAACAAGA AATTCCAATA TACCTTGATG	420
20	ATTTAATTAT CATTTTAACG GATGGTGTGA CTGAAGCTAG AAAAGTGAAG GTACCTTTAT	480
	AGATAAACAA AAACTTTTAG AATATA	506
	(2) INFORMATION FOR SEQ ID NO: 1109:	
25 30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 552 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	·
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1109:	
35	TGATATTGAA AAAGATGTCA TTGTTAAAGC ACAAGAAAGT AAAATTGCTC AAGTTATCAC	60
	GAATTTGTTA ACGAATGCAA TTAACTATTC TTATGAAGAT GGAGATATTA ACGTTCGTGT	120
	GTATCGAGAT GACTTTCGTG TCATTTTCGA AGTACAAGAT TTTGGTATAG GTATTAAATT	180
40	AGAAGACCAA CAACGTATTT TTGAAAGATT TTATAGAGTA GATAAAGCAC GAAGTAGNAG	240
	ATTCTGGTGG GACAGGTCTT GGATTATCAA TTACAAAGCA TATAGTAGAS GCCCACCAAG	300
	GCAATATTGA AGTGAATAGT CAAGTTGGCA AAGGCTCAAC GTTCAAAGTT ATTCTAAAAG	360
45	ATTATAAAGA ATAANAATTA AAGTGGTAAC AGCGCGTGTA TTTTTCACGA AGTTGTTGCT	420
	GCTTTTTTAT TTCGTTCAAA TCTCTATTGG TATTAAATTA GAGTTAATGA AGTGGAATAA	480
50	ATTCGGTTGT CAATTTTGTC ATTTGTATAT GTCGATTTGT AAGTTATAAG TAATAGATTG	540
	TTGTGAATCA nG	553
	(2) INFORMATION FOR SEQ ID NO: 1110:	

(A) LENGTH: 244 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1110:	
10	AACAGATCAA CAATTGCAGA TCAATTACTC GTCATATTGA TCAATTATCT CTGACAACGA	60
	GTGATGATTT ATTACGTCAT TGATTGATCA TCACAAGATA AGTCGCTATT GATTTCTCAA	120
	TTTTACAACG ANATTAGGAA AGCTGNAGCA GATAATTGGC TAAGTTGGAC GATAAAGGTT	180
15	ATCAATCGCC AATCGTTGCC ATTGAAGAAC TTTTGCTCAC TGGCGCACGC TTCAGATGAT	240
	ATTT	244
	(2) INFORMATION FOR SEQ ID NO: 1111:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 825 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1111:	
30	AGTATTGAGT GTTTTGATTT AAGAGACTTG GAAAGTGAGT CAATAATCAA AATCTTACTC	60
	AATACTTTTA TTTTGGTACT CGCAATTTAG ATTTGTTAAC TAATTTTTTC GCTTATTATA	120
	AAACGAAACA ATCAAGTAAA CGATAAAGCC TACAAAGATA CCCAATAAAA TAGATAGTAC	180
35	TGCCGTCACT ATTAATGGTA ATTTGAAAAA TATTTGTAGG AAAATmCCAA TGATAATTGC	240
	GATAATTACT GCAALTAATG TGACTGTATT TTCATTTGAA ATGTTCATLT ATLLTCACTC	300
	CTEAACAATA ACATTATATC ATGCTATAGC TTTCCAAAAT ATTGAAATAT GTAGATATGG	360
40	CTATTGACGA TATTTCTTAA CTTTTATATG ATTAATCGGA ATGAAAAAAG AGAAGTAGGT	420
	GGCAATATGA AGTCAAATAA ATCGCTTGCT ATGATTGTGG TAGCCATCAT TATTGTAGGT	480
	GTATTAGCAT TTCAATTTAT GAATCATACG GGTCCTTTCA AAAAGGGGAC GAATCATGAA	540
45	ACTGTACAAG ATTTAAATGG TAAAGATAAA GTACATGTTC AAAGAGTTGT GGATGGTGAT	600
	ACATTTATTG CAAATCAAAA TGGTAAAGAA ATTAAAGTTA GGCTTATAGG GGTTGATACG	660
50	CCAGAAACGG TGAAACCGAA TACGCCTGTA CAACCATTTG GCAAAGAAGC ATCAAATTAT	720
	AGTAAGAAGA CATTAACAAA TCAAGATGTT TATTTAGAAT ATGATAAAGA AAACCAAnTC	78
	GCTATGGTAG ACCATTGGCG TATGTATGGA TAAGTAAAGA TCGTA	82

(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 621 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1112:	
10	TCCCTATAAA TCCCCACAAA AAAAGGGTAA ATCCGAACGT CAAATTTCAT CTCTTTATGC	60
	CAATCAACGA TCGATTTACC TTTTAAAATT TAAAATGTAT CTGTAATACT CTTAGCAATA	120
15	TTTGTATATG CTGCATCTTC CATAGGTGGA TTGTGTAATC CTGCACGCAT GTCACGATAG	180
	TAACGTTGTA ATGGTCGATT CATTTCTAAG CTTTTAGCAC CAACTATTCT CATCGCTAAA	240
	TCAATCACTT CAAGCCCTTG ATTCATTACC ATCACTTTAC TCGCACTTGT TGGATTTCTT	300
20	ATCTGACTGT CATCTTTATA TTGTTGATAC CCTTTTGCTG TACTCCATAA AAATTGTCTC	360
	GCACATAACA ATAGCGTTTC CATTTTCCCT AAATTTTGTT GCACAGTTGG CAATGTTGCA	420
	ATCGTTCCTT CAATACTATT AGGGCTATGT TGGATTGCAA AGTCTACAGC ATAATTTCTA	480
25	GCAGCTTGTG CTATACCTAA ATAACAGCTT GGTATATGCA ATATCCAACC ATTTGGCGCT	540
	TTACTTTTCT CTGTTTCCAC TAAATGTTTT AATGGTACTT TTACATCATT TAATATTAAA	600
	TCATGACTTT CTGTCGCTCG C	621
30	(2) INFORMATION FOR SEQ ID NO: 1113:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 619 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1113:	
	GTACCTTGTT TTTCAGTGTT AATTTCCCAA ATATAACCTG GTGTAATACC GTATTGTTTT	60
	GAGAAGTACT TGAAGGCACC TTCACTTGTA ATCATGGCAC GTTGTTCTTC TGGAATGTCA	120
45	TTAAATTTGT CTTTACTGTC TTTACTGTCA TTATTTAATT TTTCCAATTG AGCAATGTAT	180
	TIGTTACCTT GCTTTCATA ATCTGCTTTA TGTTTTTTGT CGTTATCGAT AAATGTTTGT	240
	TGAATIGTTT TTACGIATIT AATACCGTTA TCTAAACTTA ACCATGCGTG TGGATCTTGT	300
50	TTATCTTTGT TGCCTTCTTC ACCGTTTAAA TAGATAGGTT TAACATCTTT TGATACTGCG	360
	ATAACTTTTT TATCTTTTAA TGATTTACCA GCCTGTTCTA AGGCTTTTTC AAACCAACCG	420

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	ATATCYTTAG GTTLAACYTC aTAWTCATGA GGATCTKGAC CAACAGGTAC AATACNATGA	540
	ATATCGACGT TGTCTCCACC AACATTTTTA GCCATATCAG ATAGAATTGA ATTCGTCGnT	600
5	ACTACTTTNA ATTTGCCAT	619
	(2) INFORMATION FOR SEQ ID NO: 1114:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 549 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1114:	
	GAAAACCGCA CGACAATGAA AAAAGATATC CGGTTAAAAT GGTCGATAAT AAAATCATTC	60
20	CAACAAAAGA AATTAAAGAT GAAAAAATAA AAAAAGAAAT CGAAAACTTT AAGTTCTTTG	120
	TTCAATATGG TGACTTTAAA AATTTGAAAA ATTATAAAGA CGGAGATATT TCATATAATC	180
	CAGAGGTGCC GAGTTATTCG GCTAAATATC AATTAACTAA TGATGATTAT AATGTAAAAC	240
25	AATTACGCAA AAGATATGAT ATACCGACGA GTAAAGCTCC AAAGTTATTG TTAAAAGGTT	300
	CAGGGAATTT AAAAGGCTCA TCAGTTGGAT ATAAAGATAT TGAATTTACG TTTGTAGAGA	360
	AAAAAGAGGA AAATATATAC TTTAGTGATA GCTTAGATTA TAAAAAAAGC GGAGATGTAT	420
30	AATCATGGCT CAATCAGAAT ATGAAATCAA TCCCGGAAAA AGAGAGTGAT GAAATGATAA	480
	AACGTGTAAA TAAATTAGTG CTTGGTATTA GTCTTCTGTT TTTAGTCATT AGTATGCACT	540
35	GCTGGTTGT	549
33	(2) INFORMATION FOR SEQ ID NO: 1115:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 317 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45		
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1115:	60
	TGTTATTGCA ACTATTAAAA ATATNAAAAA CAAAGACTTA ATTGATTATT CTTTATATAT	
50	TAAAAAAGGT TTAGTGGAGC CATTTATTGT ATTCTATAAT CAAGAAAATA TATTCTACAT	120
	TAGCAATGCT GTTATAGATA TCATCAGTGT ATCCAAAGAT ACTCTTGATT ATATAAAGTC	180
	AGAATTCAAT GATCACTGTG LTCGCCATAC TGATTTTATA GCACAGAGAA AAGCCGTAGT	240
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	TTATCATCIT CGATGAA	317
	(2) INFORMATION FOR SEQ ID NO: 1116:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1116:	
15	ACTATGACTG CAATGCCAAC AATGAATGTT ATTGCATAAA GCATATGCAT TTAATCAAGC	60
	TTATGTTATT TAGCAAGGGC AAGCCACTTC TCGATTCATG GCTTGCCTTA TTTTATTGTA	120
	TATTTTTAAT TATCGTTGCT GGGCCCTTGA TTGACAATCG TATTAAAATG GCCTTATTAA	180
20	GTCAACTTTG TCTATACGGT TTGGAATCTT CTACCCAATG TCTTATAAAA GACAATCCCG	240
	CACCTGAAAC ATAACTCATG AAnATAAGAA nATGGTATAC CATTAATnTG AATCCATTTC	300
	CANTITATAA CGTTGTAAAT GACACATAAT TAGAATCATA AAGTTTTTCG TGGGATATTG	360
25	AAACTTTACC CATACGAGAC ATCATGGATA AAAGCGAGGC	400
	(2) INFORMATION FOR SEQ ID NO: 1117:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 696 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	•
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1117:	
	TGCATATAAT GTTCAAACGG CAATGATTCC ACTGTATAAA CCTCTTGTCG TGGATGATCT	60
40	TTAATTTGTT GTTTTAATAA CTGAACTCTT TTTTCATGTT CATAATGAAC ATAAATAAAT	120
	GCACTAAGAT ATATCACAGC TAAAACTAGT GATGCACCTT TAATAAAATT AACATTGATT	180
	GACTTATATT TCCGAAATTC TTTTAATAAA ATAATTAAAA TGATTACATG TATCGTATAA	240
45	ACAATCAAAA AATTACCTGG TTCTATTGGA GTAACAATGA CTAGTGTCGA CGCCGAAACA	300
	CATATTGCAA TAAGTAAGGA ATATAAAGTG ATTTGTGTTT TACGATCATT AATAGACAAA	360
	TAAATACCTA CAAATATCGA AAACGCAAAG TAACCACATA CAATTACGTT CACAAAACCA	420
50	ACCAATCCAA TATCTGTATT TTTATTTAAT AAAAACTGAT TGTAAAATAG TAAATAATAA	480
	AGCGGTAAAG TGATAAATCC TATCATAATG ATACGACGCT TTAATATTGT TAAATGTACA	540

	ATCTGACTGA AAATGACACC ATATGGAAGT GACGTTGATA TCATTTCTGC AAATTTTGAA	660
	AAGATACCTT GATTATTTGA AACTTGTTGA TATTCT	696
5	(2) INFORMATION FOR SEQ ID NO: 1118:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 223 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	. •
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1118:	
	GCAGTGACAA TCAATAATTT GTAACTAGAA GATAATAAAG AGAACGCTCT ATAGAGACGA	60
	ATTGAAGGTT TGATTTTAAT GTCTGTTAGT AAGAATCATA TCAATGAGAT GCCTATAGTA	120
20	CTCAGANTAT ATTAAATTAA AACCGTCATT AATTGTTTTT CCGAAAACCA TTTGTAACCA	180
	TTTNAATGTA GTTGGACCTA CCTACGTTCT CCAATAATCC ATT	223
	(2) INFORMATION FOR SEQ ID NO: 1119:	
<i>25 30</i>	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 265 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	·
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1119:	
<i>35</i>	CTGCTTTACC TTTTCCAACT TTAGAAATTG CTACATAGGG GCCTTCTGCT TTACCGCCCC	60
	AATTCCAATT CCACATTTTC AAGAAATAAG GAGGCAAAAA TGTTCATATA TGAATTGGAA	120
	TTATTTGTTT TCTTATTAGG CCGAGATGCG CCGCGTGCGG CTGCTGGAGA TGGCGGACGC	180
40	GATGGATATG TTCTGCCAAG GGTTGGTTTG CGCATTCACA GTTCTCCGCA AGAATTGATT	240
	GGCTCCAATT CTTGGAGTGG TGAAT	265
45	(2) INFORMATION FOR SEQ ID NO: 1120:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 329 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(wi) CROWENCE DESCRIPTION, SEC ID NO: 1120:	

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	CATGACATTA CATGCTTATT TAGGTAGAGC GGGAACAGGT AAGTCTACGA AAATGTTGAC	120
	CGAAATAAAA CAAAAAATGA AAGCAGATCC GCTTGGAGAT CCAATCATTT ȚAATTGCGCa	180
5	ACTCAAAGTA CATTTCAATT AGAACAAGCC TTTGTCAATG ATCCGGAATT AAATGGTAGT	240
	TTAAGAACAG AAGTGTTGCA TTTTGAACGA TTAAGTCATC GTATTTT-CA AGAAGTTGGT	300
	AGTTATAGCG AACAAAAGTn ATCTAAAGC	329
10	(2) INFORMATION FOR SEQ ID NO: 1121:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 252 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1121:	
	ACACCTCTTT TTTAATATAT GTGAACTATA TATAGTGTAT AGAGAGGTTA CTTGTTACTC	60
	AATATAAACA AAAATCAACT TTGTCAAAAT AAATGTGACA AAATTAAATA AAGTGTCATC	120
25	AATGTGACAG TATAGATCAT TTTGCAAAAA GTCAAAACAA AAAAATTGTT TTAGGGATTT	180
	TTCAAAATTT TCATTGTGGA AAATGATTTG nCAAAACAAA ACAACACnTT GTGAGCAATG	240
	AAGCTTCAAT GG	252
30	(2) INFORMATION FOR SEQ ID NO: 1122:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1122:	
	NAATAATAGG CGCCACCTAA TAAACCAGCT GGAATGCCTA TCATTGGTGT TGTGAATGAG	60
	CTTAATACAA TAACAAGTAT TGTTAAAGCA ATGACGTTAT ACCAAGTTAC AGTCAAATTT	120
45	TTCAAATCCT CATATGATTG TTTTACTAAT TCTCTAAATT TCATGATTCA ATCTCTCCTT	180
	TTCTTAAATC AATTAATAGT TATACTGCAT TGCTTAAAAT CAANATATCT AATGAAGCAT	240
50	CTTTTAATCG TAAGTGTTAA AIGGTTTTCT TAATCAATTT GTTIGAATGT ATAANAGCAA	300
	TTAAAGCAAA AGTAATGTAA ATGAGGGTGT ATACAACAAT TACTACAATA ACCGGCATGA	360
	AGGAAATATT ACCCATCAAT TTCATAAATG CGATTGCGGC	400

(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 270 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1123:	
10	AATACAACCT TTTATCATAG TGTAAATGTA TTCTACCAGT ATTGAGAAGT TTTCATATTA	60
	TTCAATACCT GAAATCGCCA TAGTAATATT ACTAAATGCA CACTGCATAT GTTGTTTAAC	120
15	AACACAACTT TAAAAATATA TTCTAACTCT ATCTACGAAT GTACTTAAAT ATCATAACAA	180
	TCTATTCCAA ATCHAATTAC ATTATTAGCT ACCTTAAAAA CCAAACCGAG GCCTTAGGCC	240
	TCGGTTTAAA TATATATAAC GnGCGACATG	270
20	(2) INFORMATION FOR SEQ ID NO: 1124:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1124:	
	GGTCTTCTGT ATCAAATTAT ATTATGAGAG TTAGACTCAG TATTAATGAA ATCGTTGATA	60
	AAGATCAAGT GCTTGCATCA CAAATAGGTG GATTACTATG ATGTTTAATC AAATTAATAA	120
<i>35</i>	TAAAAATGAA TTAGAAGAAT CATATGAATC TGAGAAAAAA CGTATAGAGA ATGAACTGCA	180
	AAATTTAAAT GAACTTAGGC ATAGAACTCG AAAAGAAAAT GAACGTAGTT ATGATGTTTT	240
	TCAATATTTG AAGCACGAAA TGAATTATAG TGAAGATGCC CAAAGGAAAA TGACGAGAAA	300
40	TATAGAAGCG TATGAGCAAG AAATCAATGA GATAATTAGA AAGCAAGAAT GGAAATTAGG	360
	AAGAATATAA AGAAGACTTA AAAAAGTCTT ATGAAAAGCA	400
45	(2) INFORMATION FOR SEQ ID NO: 1125:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 377 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1125:	

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	AAATATAYTC GATCATTGAT AATATGTGCT TTACTATTCC AAATAACTTT CAAATTTTGA	120
	TANTATTCAT CANTACTCTC ANTATAACTA ACCAGTTTAT ACAACCATTC. GCCATCGACT	180
5	TTCACATATT TTTGAATACT ATTTCCAAYT TLAAGACGTG TTGGTTCATT TACAAAATGC	240
	CCCAAATTAA TACCACTTAA TAATCCAAAT GGAGTTGGAC GTGTTGACAT TCTAATTAAA	300
	TATTITAATA AACTITCITT AGCATCTCTA ACCTTCTTGT TATCGCCATC AAAATTTATT	360
10	nCnTGTAAAG TACAATA	377
	(2) INFORMATION FOR SEQ ID NO: 1126:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 227 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1126:	
	GTTACATTAC TGTTCATGTC CACAACGTTT GTCAGCGATT ATCATCATTG TGTTATATCT	60
25	TATTTATAGC AAGTGCATGG TCTGGATAAG TAAAGGTATT CATACTTAAG TAACTTGAAC	120
	ATTGGTTTAG GACTATTTTA ATGGTnCTGC TTNAATTGTT GGCCAACTGG TTCTTATTTT	180
30	AAATATGTAA CTAGCTCTAC GGGTAGTTAC TAAACACATC CTGGTTT	227
	(2) INFORMATION FOR SEQ ID NO: 1127:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 717 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	•
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1127:	
	CCAATGATAC CGTTATAGCA TGTTAATGTT TTTGTACGAA TATAATCTAA AACTTCGAGT	60
45	TCATCACTTA ATTTCCACGT TTCTGCTTTG TTTAACCACA TTAAAGGAGT ATGAATGnCA	120
45	AAATCTTTGT CCATAGCTAG GCTTAATGTT ACGTTCATTG ATTTTATAAA ACTATCGCGA	180
	CAGTCTGGGT AGCCTGAAAA GTCTGTtTCA CATACGCCTG TAATAATATG CTTAGCCCCA	240
50	ATTTGATAAG CIAGAGCGCC TGCAAACGAC AAGAAAAGTA AATTTCTAGC TGGAACAAAT	300
	GTATTAGGTA TACCATCTTC ATTATTAGTA ATTTCCATAT CATGTTGTGT TAATGCGTTT	360
	GGAGTAAGTT GTGATAATAA TGACATATCT AAAACGTGAT GTTTCATTCC TTGATCTTGT	420

	AGTTCAACTT CTTTGAAATG TTTTTTTGCA TAAAAGAGAC ATGTTGTACT GTCTTGACCA	540
	CCACTAAAGA CAACGATGGC TTTTCATTA TTTAATACAC TTTCCATTTT GTAATTGCTC	600
5	CTATCATTAA TAATATTAAT AAAGAGGTTA ATGGCATTGA TAAGCCCGTT TTTAATTTAT	660
	AAAATAAAAA AAGCCnATCT CCATAAAAGA TAGACGANAG AAATGGGTTG CTCCTAT	717
	(2) INFORMATION FOR SEQ ID NO: 1128:	
0	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 595 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1128:	
20	GATTATTGCA TTGACAACTT ATATCTATCT AACGTTAGTA GCATTTAATT TCATTTCCGG	60
	GGTTCTAACT TTACCAGGAT TAGCGGCGTT GGTATTAGGT GTAGGTATGG CTGTAGATGC	120
	CAATATTATC ATGTATGAGC GTATTAAGGA TGAACTTCGA ATAGGTAGAA CGATAAAGCA	180
25	AGCCTTTTCT AAAGCAAACA AAAGTTCATT CCTAACAATT TTTGATTCTA ACTTAACAAC	240
	AGTTATCGCC GCAGCAGTAT TATTCTTCTT CGGTGAAAGT TCAGTTAAAG GTTTCGCGAC	300
30	AATGTTATTA TTAGGTATTC TAATGATCTT TGTTACAGCC GTGTTCTTAT CAAGATTCTT	360
50	ATTATCATTA CTTGTTTCAT CAAATATATT CAAAAATCAA TTTTGGTTAT nTGGTGTTAA	420
	AAAGAATAAA CGACATGATA TTAATGAAGG TGTAGATGTT CATGACCTTA AAACTTCATT	480
35	CGAGAAATGG AATTTTGTTA AATTAGCTAA GCCATTAATT GGAGTAAGTA TTTTAATTGT	540
	AGTGTCGGTT AGTTATTCnT TATATCTCAA GTAAACTTAG GANTGANTCT CAAGT	595
	(2) INFORMATION FOR SEQ ID NO: 1129:	٠.
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 371 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1129:	
50	ATTITAACTT TCTAAGAACA AGTTGTCAAG ATTTTTTCTT AACATATCAT GTTCTGTTAC	60
	AATATTAATA ATGAATACCG AAAGGACGAA TTGCAAATGA AAAGCGTTGG CTTAATCACA	120
	GAATATAATC CCTTTCATAA TGGGCATCAA TATCATATTA ATCAATCTAA AAAACTTACA	180
55		

	ATCIATAATA AGITACTOOT GCAAAATGGC TTTCCACCGC TGTTTAGTTT CGGACTACCA	300
	GCAACTGCAG TTATCACTGG CGNCATTTGC GACTGCCGTT AAGCGCGGTT TTGGTGCGTA	360
5	CATGCnTGGn G	371
	(2) INFORMATION FOR SEQ ID NO: 1130:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 200 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1130:	
	ATGATGATGA GATTATGACT TTGCGAAAGA TATCGGTGCG CCTTATGAAT TTAAAACAna	60
20	nTAAAGACCA TGGTCGTTAC CGGTAGTTAA CTTTGCAGCT GGTGGCGTTG CGACTCCTCC	120
	AAGATGCTGC TTTAATGATG GAATTAGGTG CTGACGGTGT ATCCGTTGGA TCCGGGAATT	180
	TTAAAACCAG AAGATCCCGG	200
25	(2) INFORMATION FOR SEQ ID NO: 1131:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 203 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	٠.
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1131:	
	ATGAGCTAGT CGATTAAAGT TAATATTTGA AAATGAAGCA GGGCATTAAA TGCAATAAAT	60
	TAAATAAGTT GTCATTAAAG CATTAATAAT AGAAATGATT TTAACAGGAA AAAAGTGATG	120
40	AATATTTGGA AAAGATATAT ATCGTGCACT GTCCTGAGAG ATTAGATTTG GGAAACCAAT	180
	TTATCCnTGA ATCGAGATGT nGC	203
	(2) INFORMATION FOR SEQ ID NO: 1132:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 182 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1132:	

	ATCTAACAGT ATTGAAATCT TTGTTAGCGT CAATCGACCA TGTATTTTTA AGTATTGTCT	120
	CTAACAACTT AGCACGACGT CTTAACCCTT TAGTAAACAA TCCTTCTTTA GnTTTAGTAC	180
5	GT	182
	(2) INFORMATION FOR SEQ ID NO: 1133:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 485 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1133:	
	CAAATTTAGC CAGGNATACA AATACATATA ATAAAACTGT TTGTAAGCTT ACGTTGACAA	60
20	TCTGGCGTAA TTGGAAAACT AATGAATTTT CTCCAAGTAG GTTTTACCCT GTAAACMAAA	120
	TAACAATTCM AATAATATGr AATCACAAAg CGACTAGAAA TCCGGTAATA TGACTAATCA	180
	TATATTCAAT GTGTAATAAT TTTAACAGCA ATAAATAGAC AACATAATAA TTTAACGTAT	240
25	TAATGCCGCC AACAATGATA AATTTTAAAA TTTCAGCATG CGTTTGTGTT AGTTTCATAT	300
	GTGTACTCCT CAACATCANA ATATATGCAT AACTACGTTC TCGAACATAC TCGAATATGC	360
	GAGCCAATCC GCTTCACTTC AAATATGCTT ATTTCAATCT TTATACCCTT TCACAGCAAT	420
30	TTAGTCTCTT TnCCCTCATC CTTATAGGCC nTATATGTAA CCGATTATCG GGTGGACTCA	480
	TTGGC	485
35	(2) INFORMATION FOR SEQ ID NO: 1134:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 213 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1134:	
45	CTTGTTTTAT CGACAGATGC TGAACACGCA GTCAAAATAA ATAAATTACA TAATAAAATT	60
	CCAATTAATC TTTTCATAAT ATCATCCTTT TGTTTTTCAA TTGATATTCA TTTTCAATTA	120
50	TAAAATATTA rAAGAATTAG TCAACGCCTG TGAGTAATAC ACATCAGTAA CATTICTATI	180
	TTCATTTATG ATATTATCTA ATTATTAATT TAT	213
	(2) INFORMATION FOR SEQ ID NO: 1135:	
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5	(A) LENGTH: 526 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1135:	
10	TGTGACTCCA TGTATTCATG TATCATTGTA CATTTGTGAA TTGGTTGAAA ACTGATAGTG	60
10	CCCGTTTAAT TACAGGTACT GAGGATGCTT TCAGGACATG GATTTGTTCG AAAATATGAC	120
	AATATTTCAC TATGGCTCTT CACTTCTCTA GGGAAATTGC TATCTTGATT AATCCAATCA	180
15	ACCAATTCAC CTAATGGTGT GTCATCACCA AGAAAACTTT GCATAAATTC GTAAAAGCTC	240
	AATACCTCAC CTCGATTAAT ATACTTGAGC CATTAATATA ATACCATAAA AGAATGTGTA	300
	TTTTaCATAA AACTTTTTAT AAAGCAATTT TATAAATCTA AATTTATTGA ATGTTTAAGA	360
20	AGTTGTGTAT AATGAAATAA ACGTGTTGAA ATAGTTAGGA TGATGTTAGT GGATATCAAA	420
	CATATGAAAT ATTNTATTGA AGTCGTTAAG CANGGAGGCA TGACTAATGC TTCCAAATCA	480
	TTATATATTG CACAACCTAC AATTAGGAAA GCNATTAAAG ATATTG	526
25	(2) INFORMATION FOR SEQ ID NO: 1136:	
<i>30</i>	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 321 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1136:	
	AGCAAAAGCA ATGATGACAA AAGAACAAGC TATGTTAGCA GATGGAAGTA TTAAACAAGA	60
	TCAATATGAT AAACAACTGT TATCGANAAT CGGAAAATCA CAATTAGATG AATTGTCTTC	120
40	TAAAGATTTA CAAGTTTTAG CTATTTTTCC GAGAGATGAA TGCAGGAACA GTTTTAGATC	180
	CACAAATGAT AAAAnATGGA AGATGTTCAG TGCAAAAAGA GTATGGCAGC AGTTTTCTCC	240
45	AGCAACTTTT CCAMATTTAC CCAGGTGTTT AACACGTCCT ATTGGATTTG GGCTTAGGAC	300
43	AATTATTCCA TATGGGCGGA T	32
	(2) INFORMATION FOR SEQ ID NO: 1137:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 330 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
55		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1137:	
	ATAAATCCTT ATAAAATCAT GAGTTGGACG ACTTATCCAC ACAATTATAC TTTTTCAGTT	60
5	CTCTATATGT CAAATACCTG TGAATATGTT GCTAAAAATA GTATAACTTT GTGTGTAATT	120
	TCTAATTATC CACAATTCTG AAAACTATAA ATGTGCATAA GTGGATAMCT TTCCTTCTAT	180
	AGAGTATCTG TTAGTGAGTG TATCAAAACA GTTTGGGAAA TAATTTATAA AGTnTGTATA	240
0	AGANCTGTAT AAGGTGTTCG AACATTGTAA ACACTCATGC TTCGGACCAA ACTCATGGTG	300
	ATGTTATGAA ATTTGATTGC TCGCATCGnG	330
15	(2) INFORMATION FOR SEQ ID NO: 1138:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 459 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1138:	
25	CTTGATAAGG GAAGATTTGC CAGCACCATT CGGGCCCATG ATACCAATTA TTTCGCCGCG	60
	TACTGGTATC GATAAGGAAA TGTTTTTAAG TACATGCTTA TTACCTAAAA ACAGATTTAA	120
	ATCTTTTGTT TCTAACAAAC GTTTATACCT CCTAATTAAA AGTTTAGGCT AACCTAATTA	180
30	ATTGTATAAT AAACTGAGAA TATTTATCAT GTCAAGTAAA TTCGTGATAT AATATAGACA	240
	ATGTATGTGA GGTGAAAGTA TGTTAACTGA AGAAAAAGAG GACTATTTAA AGGCAATCCT	300
	TACGAATAAT GGCGATAAAA ACTTTGTGAC AAATAAAATC TTATCTCAAT TTTTAAATAT	360
35	TAAGCCTCCA TCTGTAAGTG AAATGGTAGG ACGTCTTGAA AAAGCAGGCT aTGTTGAAAC	420
	AAAACCATAC AAAGGTGTTA GATTAACAGA GGATGGTTT	459
40 .	(2) INFORMATION FOR SEQ ID NO: 1139:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 165 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1139: TARATACTCT CGCCGGTTAT TTCGCTTCCT CTATACGGAT TGGCGAAAGA TACGGTGCAT	60
	CGGTTTCAAC TAGCAAACGC TCCATTGACA CATGCTTAGC AACTTCTTTA GGCTGTTTAG	120

	(2) INFORMATION FOR SEQ ID NO: 1140:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 214 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1140:	
	ACCTGAATGC CCATCAATGA CAGACTGGAT AAAGAAAATA TGGTACATAT aCACTATGGA	60
15	ATACTATGCA GCCAGAAAAA AATGAGGTCA TATCTTTTGT GGGACATAGA TGCAGCTGGA	120
	GGCCATTATA TTTAGTAAAC TAATGCAGGA ACAGAAAAAC AAATACTGCA TGTTCTCACA	180
	GCAGGAGCTG AATGATGACA ATTCATGAAC ATAA	214
20	(2) INFORMATION FOR SEQ ID NO: 1141:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 229 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1141:	
30	GTTTCTAGTT GTTTATAGTT ATCGCATCTC TTGATGTAAA ATCTAAGATG TTTATGCATT	60
	TCTAGATGTT AATTCTTCGC TGCTTAAGAA TTATCTTGAT GGTAAATCTA GTTGTGCCAT	120
<i>35</i>	GCATTTTCTC ATGATGAATC TAAGGTGTTA ATTCATTGAT GTGTGCTGTT TCTTGnnGCT	180
	TCATTATCTT GATGGTGAAT TTCGTTGTCT AATGCACTTT TTCAAATGA	229
	(2) INFORMATION FOR SEQ ID NO: 1142:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 311 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1142:	
50	TTATGAATCG TAAACACTAT TATGAAATTG CGAGAGTAGT ATGGACAATT AGAATGATGG	60
	TTTGAGATNA ATGAGTGTTA TTAACCAGTG CGTCATTTTC AAAATTAGAT GCCATTTGCT	120
	GTTTATAATA AGAAGATTTG ATAATTAACT ATGATAAGAA AAAATAATAA TCCCCTAAAT	180

	GGTAAATGTG TGAATAGGAA TATCGTTAAA CTAGTTGTGT TCATGCTAAT TTTAGTTGTA	300
	GCAGTAGCGG G	311
5	(2) INFORMATION FOR SEQ ID NO: 1143:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 403 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1143:	
	GATCATGCTG CTTATGAATT ATTAAAAGAG CAATTAGAAG ATGTGCTTGA TACATTAACT	60
	GATAGAGRAG AAAATGTATT ACGATTAAGA TTTGGTCTTG ATGACGGCAG AACAAGAACA	120
20	CTTGAAGAAG TTGGTAAAGT TTTCGGTGTT ACACGTGAAC GTATTCGACA AATTGAAGCA	180
	AAAGCACTTA GAAAATTAAG ACATCCAAGT CGTAGTAAAC GTTTGAAAGA CTTTATGGAT	240
	TAATTTATAT CAATTTTAAT GATTGATACC AAGACATGAA TAAGCGCTTA TTTATTTTTA	300
25	GATTAAGATT TAACTTGAGT GAGGTTGGTA CATTGAATAA TGTTCAACCT CTTTTTTCAT	360
	AAAGGAGAAT AAAATGATTT CGTTAAATAA CCGATTAACG ACn	403
<i>30</i>	(2) INFORMATION FOR SEQ ID NO: 1144: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 612 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1144:	
40	nTTTTTATTG ACGAATnGAT TTGGATGCCA GTGGTTTGGT CCTAAATCTT GAATGGTAAT	60
	CGGTATTTEG AAGTTGTCAT GTGCTACACG GTAACCGATA CCNATAAGTA CGAGTGCGAT	120
45	GACAATGGTT GTTACGAGCA AGATGTATTG TAACCATTGC TTGAACACAA CAAGTTGTAT	180
45	ATAAGGCTTC ATTGACGATA CCTCCAAACC AATACAGCTA AATTAATTAT CAAAAGTGCG	240
	ATGAASCTAA GATAGAAACT AGGGTGCAGT TCTAAAATGT AGTTGTTTAA AATAATTTCT	300
50	AACAATTGAT TTGTTACAAC TGCGAACGGT TGAATATTGA AAACACCATT TGCTATATGT	360
	TGTAAAAAA TCGTAGGTAT TGTTAAACCA GATAACACCA GGATGACAAT AGCTAATATG	420
	ACTITACTAA TACTATTCAA CAAGCCTGTT GTTAAAAGTT CGATGAGTAA TAACCACAGT	480

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	AAGATATICG GAATACIGAA CACAATCCAA ACTACACCAA CGATACICCA TAACATAGTA	600
	TAAAACCATG Tn .	612
5	(2) INFORMATION FOR SEQ ID NO: 1145:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 223 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1145:	
	GAATTAATTA CGCAATATCC GCATCTTAAA TCAGTAATCG AAAAATATGC TTTAAAATAA	60
	AAGTGATCAA TGAAGTGGTT TGAAGGTTGT NAATAAACCT TTGAGTCACT TCCATTTTTA	120
20	AANGTATCCT GGATGGAACC AGAATAGATT TGAAGCTTCA GCGGTTTTTA ATGAAAATAG	180
	CCATTAAATG ATTTGGAAAC GGTAAGAGGG GGTATTTAAA ATG	223
	(2) INFORMATION FOR SEQ ID NO: 1146:	
25 30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 598 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1146:	
35	CGCTACGGTT GTCACGTAGA GATTAAAGAC ATTCGTTTTA GCAGTCTTTT TTATTGAAGT	60
	AGACAATGCA AGATTAAATG GTAGTGTCAT TTCATTTTAT TCAACTGCTA GTAATACAAT	120
	ACTCAGTGTT ATTTCTGAAG ACTGGTTGAT AATGAGACAT GCATATTTAC AAAACTGTGT	180
40	ATATTGTGTA TATTGTATAT ATACAGAAGT TGATAGGGGG ACGTTGATGA AAATAATTTT	240
	AAAAAACAAT AGTGATTTTC CGATTTATGA ACAGATTAAG CAACAAGTAA AACAAAATAT	300
	TTTAAAGGGA CATGTTGCTC CTGGAGAGCA TTTGCCGTCA ATGAGAGAAC TTGCCAAAGA	360
45	TCTTCAAGTA AGTTTGATTA CTACCAAACG TGCTTATGAA GATTTAGAGA AAGACGGTTT	420
	TGTTACAACA ATTAGAGGAA AAGGGACCTT TGTTAAGGAG CAAGATAGTT CTATTTTAAA	480
50	AGAGAAACAA TTTTTTACCA TGAAAA11TG GGTTAAAGGA ATTGGGTTAA TTAAGCNCAA	540
	GCCCATCCGA ATTGCCACTT GAGGGANTTC CAGGATATTT NACCGTCATT TATTGAGG (2) INFORMATION FOR SEQ ID NO: 1147:	598

5	(A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1147:	
10	CAAATCCAAG TGCAACAGCT TTATCAACCG CTAAAGCTAA ATCCGTATCA GCTTTTTCAG	60
	CTTGAACTGG TTTGATTTGT AACTGTTCTG TTAGAAGTTG GCGTTCTTCT TTACTGACTG	120
	AATCAAAGTC TCCCACTGAG AAAAAAGGGA TAATTTGATG CTTCAATAAA ATCAAAGCAC	180
15	CTCTATCAAC GCCGCCCCAT TTACCTTCAT TACTTTTGGC CCAAATATCT TGCGGCAAGT	240
	GTCGATCAGA ACATAATAAA TTTATATGCA TATACACTCA ACCTTTCAAT GCTTGTGTGA	300
	CTTTTTAAAA TCCCCTGGTT AAAGGAAAAT GAACNGGTTA CCAGCATTGT AGGCACCATT	360
20	TCAACACCAA CTTCGGCGGA TCnGGATTAC GCCTCCATCC	400
	(2) INFORMATION FOR SEQ ID NO: 1148:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 352 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1148:	
	TTTTATGGGT CGTATTTTTT AAAGAACAGT CATCTCAATC AAAAGAATAG AATTATGATT	60
3 5	AAAATTGATG TrGTGTAATT AAAGTAAGAA ATrrkAAATT TCCTAGATAC TAGATAAATC	120
	GTTCAATATT TTATTAATAA GGAGGCCAAT GAYTGTGAAT TATCTTAAAC ATAAGTTTTA	180
	TAACTTGTTA ACTACAATGA TTGTTCTCTT TATTTTTGTA CTTTCTGGTG CGATTTTTT	240
40	AACATTTCTA GGGTTTGGTT TATATGGATT AAGTAGAATA CTTATTTATT TTAGGTTGGG	300
	TGACTTTACA TATAATAGAA GTATGTACGA TAACCTATHA TATTATGGCA GT	352
	(2) INFORMATION FOR SEQ ID NO: 1149:	
45 50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 916 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1149:	

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	GGCAAGTGTC	GATCAGAACA	TTTAAATTT	ATATGCATAT	ACACTCAACC	TTTCAATGCT	120
	TGTGTGACTT	TTTTATAATC	CTCTTGTTTA	AAGAAAAATG	AACCTGTTAC	TAGCATTGTA	180
5	GCACCATTTT	CAACACAAAC	TTTCGCTGTA	TCGGTATTTA	CGCCTCCATC	AACTTCAATA	240
	TCAAAGTTTA	ATTGACGTTC	CATTTTAATA	GCATTAAGAC	CCGCTATTTT	TTCTACGCAT	300
	TGATCAATAA	ATGATTGACC	ACCAAACCCT	GGGKTAACTG	TCATCACTAG	TACATAATCA	360
10	ACAATGTCTA	AAATAGGKTC	AATTTGTGAT	ATKGGKGTAC	CAGGATTAAT	TACTACACCA	420
	GCTTTTTTAT	CTAAATGTTT	AATCATTTGA	ATAGCACGAT	GAATATGAGG	CGTTGATTCG	480
15	ACATGAATTG	AAATCATATC	GGCACCATGT	TCTGCAAATG	ATGCAATATA	CTTTTCTGGA	540
	TTTTCAATCA	TCAAATGTAC	GTCTATAGGT	AATGTTGTGC	CTTTTCTTAC	TGCATCTAAT	600
	ATTGGTAAAC	CAATAGATAT	ATTAGGCACA	AATTGACCAT	CCATAACATC	AAAATGAACT	660
20	CCGTCGACGC	CTGCTTCTTC	AAGTCGTTTT	AATTCATGTT	GTAAATCCAA	AAAATCAACA	720
	GATAATAATG	ATGGATATAG	TTTTGTCATT	TAATATCTAA	CCTTTCTATT	TGAAATTTCA	780
	TTAAATAGTT	GTAAATAATG	GTCGTATCTA	AATTGCGCAA	TATTCCCTAT	CTCTAATTGA	840
25	TGCnTAACCA	TTACCATTAG	GGTCCTTGGn	AAGGnTACCA	ATCCCAAACC	TTACCATGGT	900
	TCCCCCATAA	CGGTTT					916

(2) INFORMATION FOR SEQ ID NO: 1150:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1150:

RA T	TGGTTGT	GGCTTCATAA	TGTGCAGTTG	CTAGACTGAC	AACAACATCG	TTTTCTAAGC	60
CTA	CGATAAA	GACATAATCG	TTTTCGGTTT	TGTTGTTTTC	TAATGAGCGT	TTGATGATAC	120
GT1	TATCTTC	AGTTAAAGAT	ÄAATTTAACT	TAGTATCGTA	AAGTTTAAGT	GCTTCGTTGT	180
CAA	rgtggatc	TTTGACAGAT	TGAATGGTTT	TAAATTCCAT	AAGAACACCT	CCCCAATTTA	240
AAT	ATTATA	TAGCATAATC	GCCTGCTGTA	AAAGACTGTT	CATAAACTTT	TAAATGGTAT	300
AA	AAACTGT	ACTATCTTAA	ATTAGACAGT	ACAGTAATCT	CATTTTGAAT	TCAGTGTGAT	360
AA	CTAAGCLT	TGGGACCTTT	AGATGCnTTC	ACAAAATGTG			400

(2) INFORMATION FOR SEQ ID NO: 1151:

	(A) LENGTH: 156 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	(5) 10:02001. 12:1001	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1151:	
10	CACCGTAGTT GCTACCGAAT ACCACCATGT CGCCAGGTTG TGCTAAGAAG TCCGGTGTAT	60
	TITGGTATAC AGTTAGCTAA TCCGTCGAAG TTGTTAGCGA CGGnATATCT TTTGACCTAA	120
	ACCTTTTAGA GTAATCCAAA CAAAACTTTC CAACCA	156
15	(2) INFORMATION FOR SEQ ID NO: 1152:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 233 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1152:	
25	TCAATATATT TATTTTCTAA TGTTAGCATT AGACTGTCAA TTAACTTGCT AAGTTGTTCT	60
	TTTTTAGTAA TTAAATAACG CATATAATCA TCTAAATTTT TCATTTTTTC ATCTAGCATT	120
30	AAAAGGTAGT GCTTGATATT ATTTCTACTG TTGCTCCAAA AACTGnTCAA ATATACGTCA	180
	CATAGTCATA CTACACCTTT ATATAGTTTA AATACCAATn GCATGACCTC GTG	233
	(2) INFORMATION FOR SEQ ID NO: 1153:	
<i>35</i> <i>40</i>	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 339 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	A CONTRACT PROGRESSION CON TRACT.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1153:	60
45	TATATTANCT ATCGTTTAGT GAATCGTTTT TTTAAAGTAA AGAGAATTTC ATATATTACT	120
	GGTACAACTA CAAGTGTTAA TAAAGTTGAT GAAATTMAAC CACCAATAAC TGTAGCAGCT	180
	AATCCTTTCG AAATAAGAAT CGNGCTATCT TGACCAAATA ACANAGGAAC TAATGCACCA	240
50	ATTGTTGCAA TCGCCGTCAT TAATATCGGT CTAATTCTAG TACCGCCTGC TTCGATTAAT GCTTCTTTCA TCTCCATGCC CTGTTGCTCA TTATTAATAA CACGGTCTAT TAACACAATG	300
		339
55	GCATTTGTTA CTACGATnCC AATTCAACAT TAGCATACC	

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(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 817 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1154:	
10	GTCACCCGAG GAGATATnCA ACTATTACCA TCAAGATGNG AAAAATGGTG CCTTGGGCAA	60
	TTGGTTTTT CATTTAATC TTAATTATTA TATTGTTCTT TTTACTAAGA AACTTCAATT	120
15	CACCTGAAGC GCAAACTAAA ATATTAGTGA ATGCGATTGA GAATAATGAT AAACAAAAAG	180
	TAGCAACATT ATTAAGTACT AAAGATAATA AAGTAGATTC TGAAGAAGCA AAAGTATACA	240
	TTAACTATAT CAAAGATGAA GTTGGGCTTA AGCAATTTGT CAGCGACCTT AAAAATACGG	300
20	TACATAAATT GAATAAGAGT AAGACCAGCG TAGCTTCTTA TATTCAAACC AGATCTGGTC	360
	AAAATATATT ACGTGTAAGT AAAAATGGCA CACGTTATAT CTTTTTCGAT AATATGAGCT	420
	TTACTGCACC TACCAAGCAA CCAATTGTTA AACCGAAAGA AAAAACAAAA TATGAGTTTA	480
25	AATCTGGTGG TAAGAAAAG ATGGTTATAG CTGAAGCAAA TAAAGTGACG CCAATAGGTA	540
	ATTTTATACC GGGGACATAT AGAATTCCAG CTATGAAATC AACTGAGAAC GGTGATTTTG	600
30	CAGGCCATTT AAAATTTGAT TTTAGACAAA GTAATTCTGA AACGGTAGAT GTTACTGAAG	660
30	ATTTTGAAGA AGCAAATATA TCTGTAACTT TAAAAGGCGA TACAAAATTA AATGATAGTT	720
	CTAAAAAGT AACTATAAAT GACCATGAAA TGGCATTTTC AAGTTCCAAA ACGTATGGTC	780
35	CATATCCACA AAATAAAGAT ATTACCATTT CCAGCTT	817
	(2) INFORMATION FOR SEQ ID NO: 1155:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 322 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1155:	
	ANAGAAAATC TACTCTTTA TTTCACCGGT CCTTTCNTAT CTCTCATTTG GCATACTCCT	60
	TITTCCATAT TITCCACTIT CANTACAGTG AATTTACATG TAATTTTACA AATACAATAG	120
50	GAGTGCACAA TGGAATATAA CACTTATCTT TATAAAATTA TTTTATATAT TGaCGCACTT	180
	AAAACAATCT ACAAATAAAA TTATTATTT TAGTTTTCAA TGAATAATTC ATTCTTATCT	240
	NUMBERS OF STREET	

	ATTTAAAAAT ACATTTAACT GC	322
	(2) INFORMATION FOR SEQ ID NO: 1156:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 777 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1156:	
	GTTTCCAANG GAANGNGAAA AGCGTCAACC AATGTAACTA TTTAAAGTCA AAGTGTTTGA	60
15	CCAAATTTGA CTTAATATGT AAAATAATGA GTAACAGTTA TTACAAGGAG GAAATATAGA	120
	TGAATTTAAT TCCTACAGTT ATTGAAACAA CAAACCGCGG TGAACGTGCA TATGATATAT	180
20	ACTCACGTTT ATTAAAAGAC CGTATTATTA TGTTAGGTTC ACAAATTGAT GACAACGTAG	240
	CAAATTCAAT CGTATCACAG TTATTATTCT TACAAGCGCA AGACTCAGAG AAAGATATTT	300
	ATTTATACAT TAATTCACCA GGTGGAAGTG TAACAGCTGG TTTTGCGATT TATGATACAA	360
25	TTCAACACAT TAAACCTGAT GTTCAAACAA TTTGTATCGG TATGGCTGCA TCAATGGGAT	420
	CATTCTTATT AGCAGCTGGT GCAAAAGGTA AACGTTTCGC GTTACCAAAT GCAGAAGTAA	480
	TGATTCACCA ACCATTAGGT GGTGCTCAAG GACAAGCAAC TGAAATCGAA ATTGCTGCAA	540
30	ATCACATTTT AAAAACACGT GAAAAATTAA ACCGCATTTT ATCAGAGCGT ACTGGTCAAA	600
	GTATTGAAAA AATACAAAAA GACACAGATC GTGATAACTT CTTAACTGCA GAAGAAGCTA	660
0.5	AAGAATATGG CTTAATTGAT GAAGTGATGG TACCTGAAAC AAAATAATTC AAAGTAAAGA	720
35	GTAGACTAAG CNGTCTGCNC TTTTTGTATG AGTAAACCAA GGTGTCAATA ATTTGTN	777
	(2) INFORMATION FOR SEQ ID NO: 1157:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 155 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1157:	
	TAATGTTGGT AAATGGGTTA AGGCTCAAGG TCGTATTGAA GAAGATACAT TTATTAGAGA	60
50	TTTAGTTATG ATGATGTCTG ATATTGAAGA GATTAAAAAA GCGACAAAAA AAGATNAGGC	120
	TGAAGAAAGC GTGTAGAATT CCACTTGCAT ACTGC	155
5 5		

(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 400 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1158:	
10	GACTGGTAAA ATTTACTTGC AAGTAAAGCT AAAAGGTCAA ATAGÀTAAAG AACAACTTGT	60
•	TTTTCAAAAT GACAAAAATG AAGAATTTCC TTTTGTTATA AAAGATGAAA AGGATGACAC	120
15	AATAGTAAGA ATTTTAATTG AACAGCATAT GGATAAAATC AATATGCATG TTAAAACGTT	180
	GGCTGAAAAG AAAAATCTAG ATAACAAAGA AATGGTGTAT TCTATTCATT TTAAAGAGAA	240
	AAAAGTACAA CATGATGATG CAAAAGAAGT GCCTTCAAAA CATCAAAATC AAGAAAATAA	300
20	TCAAGATCAG CTTAAAANAG ATATTGATGA CAAANAAGAT AGTCAAAAAT CAGATACTAA	360
	GGGAAAGACG TACTAGCCTT TTTACTGGAA AAAGGGTTTA	400
	(2) INFORMATION FOR SEQ ID NO: 1159:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 347 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1159:	
35	GTTGGTACAG TGTTGAGTGG CTTTGAATAT CGAACACAAA AAGAAAAGTA TGACAATTTA	60
	TATAAATTTT TCAAAGATAA TGAAGAGAAA TACCAATATA CAGGCTTTAC AAAAGAAGCA	120
	ATAAACAAGA CGCAAAATGT CGSATATAAA AATGAATATT TTTATATCAC TTACTCGTCA	180
40	AGAAGCTTAA AAGAATATCG TAAGTATTAC GAACCATTSA TTCATAAAAA TGATAAAGAA	240
	TTTAAAGAGG ATGGACCAGC CAGAAAGAGT GATTACGCGC TATCAGTCAG TACACATGTT	300
	AGTCCAGGAA TTTCTAGCAT CNGTGTGTGA ATGANGGGTA CTTTATN	34
45	(2) INFORMATION FOR SEQ ID NO: 1160:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 203 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

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	ATAGTTATTA ATTAGTAGAA TGAGGATATT TAAATATAAA GGATAGTGTT GAACTTATGG	60
5	ACATGAATTT CGATTATACA TGAACGGTGT TGTAGAACAA GCAAGGAATG AAATTGAATC	120
	TGCGGGATAT GAGCAATTAA CTACTGCAGA AGATGTTGNA AAGTCCAAGA TGGNCACCTA	180
	GTTATGATCA TCTGTATGTG GTG	203
10	(2) INFORMATION FOR SEQ ID NO: 1161:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 203 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1161:	
20	AATTTTCCnT TTCCATTGAC ATAACAATAT TTAATGGGGC CCAGTTACAG GAAATATCAG	60
	TTTAATTTCG TCTTCAATAC CATAGTCATA ATATTGAGTT TCTTGTGTTG GAAAATTTCC	120
25	TACATAGTTA CTCATTTTAA TTTGTnCAAT GTTTGAATTC GGAGGCACTC TGTTAGCATA	180
	TCTTTAAACA TTAAATATGG ATA	203
	(2) INFORMATION FOR SEQ ID NO: 1162:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 220 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1162:	
40	GCCATTTTGT TGATAAAGGT ATACTAAAGG TTATCGTTTT GAAATTTTTA GTAACTAGGA	60
	TATGTTTCGT GTTATAGGAC CGGAATTTGT GGTATACGGT AAAATTTTAA TGCTATTGGA	120
	ATTITIAAAA ATGGAAAAAC ATGGACATTN AAATTGGAAT TTCATAATAT GTCCTAATTG	180
45	GACTTAACTT GTTGGGAGTT CATTTTACTA TTTnTATGGT	220
	(2) INFORMATION FOR SEQ ID NO: 1163:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 409 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	TTCACGTGCT TTGCCATCTT TTAAGAAAAA CACAGAAGGC TTTTGCATTT GATTGTAATT	60
	GGATGCCATA GAGTAATGAT ATGCACCAGT TGATAATATA GCAAGATAGT CTCCACGTTT	120
5	GACTGGATGA AGGTAATTTA GCGTCTTTAA TAATGATATC ACCAGACTCA CATAATTTTC	180
	CAGCTATAGT TACACTGECA TCTGCTTCTT CATTTCTATT AACAAGCAAT GCTTGATACT	240
	TTGCGTCATA AAGTGCAGTT CTGATATGAT CACTCATACC GCCATCGATT GAAACATATT	300
10	TATTALTCTC TGGAATTTCT TTAATGGLTC CAACTTCATA TAAAGTAACG CCAGCLTCAC	360
	CTACAATTGA TCGTCCCGGT TCAATACCTA TTTCTGGTGC ATCTATACC	409
15	(2) INFORMATION FOR SEQ ID NO: 1164:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1164:	
25	CTAAATAATT GTTTAAATTT TTCTTTACTA TTTAGACTCT TTCGTTTGCC ATGACTTTGT	60
	TGACTTGCAA TGATATGAAC TTAATTTTTG CGAAAAAAGG AATCTAGATT CATATATTCG	120
30	GTAAATCTAC CTTCTTCATC TTTTTGAACT TGTAATTCTA GCAATTCACG TTGTATCAAA	180
	TTTTGAATAA CCATTGTAAT ATCACGTGGT TGCATAGTTG AGCCCTTCTG AAGCAATTCA	240
	ATTGAAGGCG TTTATTTGAG TTTCGAAGCA TAAATCAATT TAAGCAAAAG ACTAAATCTG	300
35	CTCATCTAAA CCTAAGTCAC GTAAGGTCTA ATAATCNCTC GTATCACTAC GGTCTGCTTT	360
	AATGATATTA nCCAGTnCGT GCCCCTTTAA ATTAACCANA	400
	(2) INFORMATION FOR SEQ ID NO: 1165:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 327 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1165:	
50	TCGTGATTAT TATTAACATT TTTTAGTAAT TGATAAAAAT CTTTTCTCGC TTCTGTAGGG	60
	CTAGTGATAA TCATATAAAC CCTCCTTTGT TTTCTGTTAC GCTAATTATA GCGTACGCAC	120
	TTGAGTACGT CATATTACCA ACGAGTTCAT CGTATNCTTA ATACCTATAT GCTATCGTTC	180
55		

	GGACACACTA CCGTnCCCTA CCGCTTAACC ATTTTCGGGC TTAAATATTT TnAAAATTTT	300
	GTGAGGATCC GCTTAAAAAA CCCCATA	327
5	(2) INFORMATION FOR SEQ ID NO: 1166:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 148 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1166:	
	TTAGGATTTC AAAAATATGT CAGGTTTTCT AACATAAAGC TTAAAACATT GATATAACTG	60
	CGATTTCGAC TTCTAAAACG aCATTAAACA ATCTACAGCT AAAATATTTT TTCAATTTTT	120
20	AAAAATAATC nGATAAATCT CCGCAAAA	148
	(2) INFORMATION FOR SEQ ID NO: 1167:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 243 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1167:	
	NAAGGTTATC GCTCGTAAAG ATGTTGTTGA AGAAGTATTT GACGACAGAG ATGAAGTGGA	60
35	TTTAAGTACA GCGCTTGTTA AAACCCTGCA TATGAAATTG GTGTATTACG AGAAGAGTAC	120
	ACTAAAGTTT TGGTCGTGTA GGTCTCAGCA GCGAACAGCA GTATGCACGT CTnCGTGTGC	180
	TGACGTGAAT TTTATTTGAG GATTATAGAC AAGAGAGACA ACTTACTGGA TTTTGCCCTG	240
40	TTG	243
	(2) INFORMATION FOR SEQ ID NO: 1168:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 321 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1168:	
	TTATATACTA CTATAAAGTA ATCCAACTCT CAAGAAGGTA AATGGGCAAT CAAAAGCTAA	60

	CTACGATATG ACGCACAAAT GTTTAGGGTA GGTGTTGACA TGTGTACAAA AACCAGCAGA	180
	AAATGGTTGT ATTCTTAGGG AAGCATTCAT CCTGTTTGTT TATGGATTCA TGTTACGTTA	240
5	CGCAATATGT TTTTATGTAG CACAGCGAAG TTACAAGTTT ATACGCTATA TATCCHTTGA	300
	ThATAAGCAG ATGAAAnCGG C	321
	(2) INFORMATION FOR SEQ ID NO: 1169:	
10 15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 191 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1169:	
20	TCTACATATA AAATTACTCT AAAAATATGT ATAGTCATAA ATTGTTGGTT GATTTAATTA	60
	AAAGTATGGA AATTAAGGGG CTCTTATGTA TATAAAAAAA TGAATTATGA TAAAAATGTAA	120
	GANAATATTT AGGGTCGATT GGAGAGATAC CAGTGGTACC AATTAGAAGA CGACAGTTTA	180
25	ATGTTACCAT A	191
	(2) INFORMATION FOR SEQ ID NO: 1170:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 303 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1170:	
	AATGTGGCAA GGATGTGTGA TATGACTACA CATTTAATAT CATCCTACAT AATAATTTTG	60
40	CGCGCCAAAT TATCACACAT ACCACACCTA CGATAACAAC CAGCAAATAA GGAGATAGCT	120
	ACACGTATTT ATCGTCCAAC GCACTACTAT ATGTTGTTGn ATGGGCACAA GTTACAAGTG	180
	CTGCGCGATA nCAAAAGGTA TACCCCTAAA ACGTCCCAAA ANAATCGGTT GCCCTCTAAA	240
45	TIGTITGTGT GCCATGATTA GTAAGCTCCT ATGTTAGAAA CAAATTTTTA ATATGTATAT	300
	TAG	303
50	(2) INFORMATION FOR SEQ ID NO: 1171:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 299 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
<i>55</i>		

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1171:	
5	AAAAAGGTGA GAAGACAATA ACGNACGCCA ACACTAAAAA ATCCATTAAC TGGAGAAATT	60
	ATTAGTAAAG GTGAATCGAA AGAAGAWATC ACAAAAGATC CAGTTAATGA ATTAACAGAA	120
10	TTCGGTGGCG AGAAAATACC GCAAGECATA AAGATATCTT TGATCCAAAC TTACCAACAG	180
	ATCAAACGGA AAAAGTACCA GGTAAACCAG GAATCAAGAA TCCAGACACA GGAAAAGTGA	240
	TCGAAGAGCC AGTGGATGAT GTGATTAAAC ACGGACCAAA AACGGGTACA CCAGAAACA	299
15	(2) INFORMATION FOR SEQ ID NO: 1172:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 821 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1172:	60
	CCATAGCACC ATACCCATAA CCAACCCGGA TCCACTAACA AATAAGTAAT AATTNACACG	60
	TAAAGAAGTA AATAGTTTGT TTAGTTTTTT ATCAACATTA TCAATGTTTT CCTCGACAGA	120
30	CACTGGAATT TTAACGATAG CTGTACCATT TGTAATTGAG TAGTTCGTTA TTTCACCCAT	180
	ACTACTATTT GGTAAAATTG TTAATTCTCC TGAAATTGTA TTGATTCGTG TTGAACGAAG	240
	TCCAATTGAT TTAACTGTTC CCTCTGCTAC AGTTGTACCA CCGTTATTTA TCTTAACATA	300
3 5	ATCACCTACA TCAAATTGGC TTTCAAATAT AATAAAGAAT CCTGTAALTA CGTCTTTAAC	360
	TATAGTTTGA GCACCAAAAC CTACTGCTAA GCCTACGACA CCAGCACTGG CAATTACCCC	420
	TTCAACACTA ATGCCAAATT TACTTAAAAT CGTCGTAATA ACTATAAACC AAACGATATA	480
40	CTTCACTACA TTTTGAACAA GAGATATTAA AGTTTTAGAG CGCTTTTTGT TACTCTTTTT	540
	ACTITIATIT TGAATCITAA ATCCCTGTTC AATCATTTTA TTCAGTATTT TAATAACTAT	600
45	GAGGGCTACG ATAATATAAA TAACAATCAT AGCGATTTTA GTTGCAATGT TTTCATATGT	660
	TTCTATTTTT GTTAATGGCT CAAATAGAGA TGAAATAATA TTCATGACTT GATTCATGAT	720
	AAGCGTTACT CCCTTCTATA TGATATATCA ATATTGLATT CATATTTLGA TATACTTCCC	780
50	AACCTACGAA AGTCTCAATA TATCTAGAAT CAAATGGTCA C	821
	(2) INFORMATION FOR SEQ ID NO: 1173:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs	

(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1173:	
	CCCGAAATTA AAATAATAAT GTATGAATTT TTAAATATGA TTTAAACGTT TTCAGTTTTT	60
10	ATGAAAACGC ATGCATTTTA CAAATAAAAA TGGTACGATG GCACTGGTTA AAACGTTTTA	120
	CTAAAAACAA ATCATGAGGT GTATAACATG GCTGTCTCTT GATCAGATCT TGATCCCCTG	180
	CGCCATCAGA TCCTTGGCGG CAAGAAAGCC ATCCAGTTTA CTTTGCAGGG CTTCCCAACC	240
15	TTCCCAGAGG nCGCCCCAGC TGGnCAATTC CGGTTCGCTT GCTGTCCATA AAACCGCCCA	300
	GTCTAGCTAT CGCCATGT	318
	(2) INFORMATION FOR SEQ ID NO: 1174:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 206 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25 '		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1174:	
30	GTTTTAAAGC GGTTATAAAG GTAAATATGC AATATTATAA ATATCTTCTT CAGAACTAAC	60
	CGAATCTCTT AAACTCATCT GTTTAGATAG CGTTTCAAAT TGATAAGTTT TAATTTTAAC	120
	CGTTACAGTT TTAGCTGACT GCTGTAATTT ATTTGACGTG CAGCTGTTTT CCTGACAATn	180
35	CCATACTGTC TTAAAnCTCT GCATCA	206
	(2) INFORMATION FOR SEQ ID NO: 1175:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 653 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1175:	
	TCTGCATCAT GATATTTTAC ATCATCACTT ATAAGAACGT CACCTACATT TAAACTTTCA	60
50	TCTAAAGCTC CAGCAGAACC TGTATTAATA ATGACGTCCG GTTTAAACTT ATTAATTAAT	120
	AATGTCGTAG AAATTGCAGC ATTAACTTTT CCAATGCCAC TTTGGGTAAT CACTACTTCT	180
	CTATCTTTTA AAATGCCAGT ATAAAATTTA ACATGTGCAA CTGAAATTTC GCTTAATTGT	240
55		

	TTTTGATTCA CCTCTTTTAA AAAATCCTAG CATTTGTTAT TTTATCACAT TTTAATCACT	360
	ACAACGACAA GTATCATGAT TTTCATTACT GTATAAAACT TTTGCTTTAT TTTTTATAAAA	420
	AGCTCTTTCA ATAACTTGGT ATCATAAATA ATTATTTTTG AACTCATAAC AGTGAATTCG	480
	ATGCTTCTAA TITGTCTATT TTTCAAAAAC TAATCATATC AATTACATCA ACCAATCGTG	540
	TCAAGAAACT TTATTAAATA ACAGGAAAAT GATATGTTTA AAATAATAAT GATGAAATAA	600
	GAGGATTTTA CAATGGCTGA AAATAATCAA AATAGTCTCG TAACAAAGAT AGC	653
	(2) INFORMATION FOR SEQ ID NO: 1176:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 410 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1176:	
	ACATGGCCGT TnGnATCAAG ATCGTCAACG ATTGATTGGT ACAATTGAAG TGCCTATGAC	60
	ATTGGCAACC GTTGGCGGTG GTACAAAAGT ATTACCAATT TGCTAAAGCT TCATTAGAGC	120
	TACTAAATGT AGAGTCAGCA CAAGAATTAG GTCATGTAGT TGCTGCCGTT GGTTTAGCGC	180
	AAAACTTTGC AGCATGTCGC GCGCTTGTGT CAGAAGGTAT TCAACAAGGT CATATGAGTT	240
	TACAATATAA ATCATTAGCT ATCGTTGTAG GGGCAAAAGG TGATGAAATT GCTAAAGLAG	300
	tGAAGCTTGA AAAAAGAACC CCGTGCAAAT ACACAAGCAG CGGAACATAT TTTACAAGAA	360
	ATTAGACACA ATAGTAAAGG CGALAGCGAT TAAAGAAAGT TAAGTCAGTC	410
	(2) INFORMATION FOR SEQ ID NO: 1177:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 146 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1177:	
	CATCAAGATA ACTACGGTTA TAATCCAAAC GACCCAACAT CATATAACTA TACTTACACT	60
,	ATTGATGGCA CAAGGTAACT ACCATTACAC ATGGGAAAGG TAACTAGCAT CCAAGTCAAT	120
	TAAACCAAGA TAATGGCTAC TACAGC	146
	(2) INFORMATION FOR SEQ ID NO: 1178:	

s	(A) LENGTH: 225 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	-
	(xi) SEQUENCE DESCRIPTION: SEO ID NO: 1178:	
	TGTTCCTGGT GGAACTTTGG TTTCTTAATG TCATTCCAAA TTGCTGTATA TTCATTCATT	60
10		60
	GGTATTGAAC TTATAGGTGT ACTGCTGGTG AACGAAAGAT CTGAAAAAAC CTTACCGAAG	120
	CAATTAATAA TGTACTATCC GTATTTATAT CTATATCGTG GTMATATAAT ATGTCATCAA	180
15	CTGGATnTAC GTCAATAGAC CTTCGTAACC TTAATATCGC GACAT	225
	(2) INFORMATION FOR SEQ ID NO: 1179:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 319 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1179:	
	TGTACGCATA TGGTATCACT TGATGACCAA TTCACTTTGT CGAGAATAAC GTTATTTAAA	60
30	GACATTGATT TAAAGAATTG GTATTnCGTT AATTGTATTA GACTTTTCAC AGAAGTAGCG	120
	ACAACAATGA TTTCATCGTA ACACGTGCGC ATATNAAGCA TGGGAAAAGA CATGGNCTAT	180
	TGACCTGGCC TTTTGTGCAC TCGTACGATT GGTCAAACGT GGCTATATTG AAAGTTTGAA	240
35	ACAAGATGCG ACGGACACAC ATGCACGGGT GGGGATAGAT CTTGAGTCTT ATTGAGACGC	300
	TGTGACTGTG GCTGACATC	319
	(2) INFORMATION FOR SEQ ID NO: 1180:	
40 45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 654 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1180:	
50	TTTTATCTTG GTTTTGAACT AGATATGTGT AGTCAGGTAT AACATAATCA ATCCCTAATA	60
	AGTTATCATC AGGGAATTTG ATACCTGCAT CGATAATGAC AATTTCGTCT TTATACTCAA	120
	CTGCATAAGT ATTTTTACCG ATTTCACCTA GACCTCCAAG TGCATATACA CCTACTTCAT	180

TTCGTAATCT AAATGTGCGC CCTCTAATTT AGTGATAAAT TCGATATTAA AATTACGATC	300
TTTCAAGTAA CGACGTACTT GTTCTTCTGT TTGAGCTTCA ACATAAAGTG ATTGTGTATT	360
TTCACGCACA ATTACCTCGT CTCTGTTATG TTGATAAAAA ACTTTAAATA CTGCCATGTT	420
AAAAATTCCT CCTAAGAATG TTTGTYTAAT TTATTGTTAA CCCTAGLAAA ATCGTATTGG	480
AGTATATATC GATAAATTCA TTCCAATCAT CTCTATAATG TAACTTAATA ACGATTTGGT	540
TAATAACTAG GTTCATCATG TCGTTCATTT TAAAAAATTA GTGAAATAAC ACTAAAATTT	600
CAGTTAAATC TTATTTTACA TGATGAATGA TAATAAATAA AGCAGTTTAT CTCA	654
(2) INFORMATION FOR SEQ ID NO: 1181:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 231 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1181:	
CGGGTATATT ATAGACAACG TTTAAGGACT TCTTTTTAAC TAACTTGTTA AATGTTGCTG	60
TATTTTGTA TTCAACACTG TAATATAGTT CTTCTGACGC TGATGCATTA CTCATTGTAA	120
TAGATATTAA AAGACTCAAT ATTATTAAAC TAATAATAGC GCGCTTTATG ATTTTCATAT	180
TCTAATCTCA AATGAATTCC AGAACTTTAT ATGGTTCAGG TGCGACAACA T	231
(2) INFORMATION FOR SEQ ID NO: 1182:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 245 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	, ·
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1182:	
TAAGTTTATT AAGCTCTTGT CCGTTAGCAA TCACGCTACC GCTAGAAATT TGGTCAATTG	60
AACTTAGTAC ATTTAATAAG GTTGTCTTAC CTGATCCAGA AGGCCCCATA ATCGCACGAA	120
TTCGCCTTTT TGTATGTCAA GTAATATCTT AGGCTGAATG GTGCTTTACG AGTTTGAACA	180
GTGCCGAAAA CGCAAGCCCC TTGATATCTT AAATGTGGAG ACTACAACnC ATCAGTGnCA	240
CGGGA	245
(2) INFORMATION FOR SEQ ID NO: 1183:	

5	(A) LENGTH: 490 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	-
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1183:	
10	AGGTAAAGAT GATGGTGTAG AAGTTTATGT GCATTGCGAA GATCATGGCA TTGTATTTAA	60
	TGCAAGTCTA CCTTTGTACA AAGATGCCAT CCATCAAAAA GGATCAATGC GTAGTAATGA	120
	CAACGGTGAT GATATGAGTA TGATGGTGGG TACAGTGCTG AGTGGCTTTG AATATCGAGC	180
15	GCAAAAAGAA AAGTATGATA ATTTATATAA ATTTTTAAAA GAAAATGAAA AGCAATATCA	240
	ATATACAGGT TTTACTAAAG AAGCAATTAA CAAGACGCAA AACGTCGGGT ATCAAAATGA	300
	ATATTTTAT ATTACATATT TATCAAGAAA TTTAAAAGAA TATAGAAAAT ATTACGAACC	360
20	ATTGATACAT AArcAATGAT AAAGAGTTLA AAGAAGGTAT GCAACGAGCT AGAANAGAGC	420
	TAAACTATnC TGCTAATACA AATACTGTAG CAACGTTGTT TAGTACGAAT GATGAAAGGA	480
25	ATAGAAAAGA	490
	(2) INFORMATION FOR SEQ ID NO: 1184:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 153 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1184:	
	CTCGCATTIT AATAAATCAT ACTCTTCTTT TCTTGCATAC GAATTAGAAT AACTCGCGAG	60
40	ACCTATAAGT CTCTTTCCTC ACTAGATAGT TTATACTTTT GGTCnGTTGA AGTCAATAAT	120
	TTTATCTAAA GCTATAAAAA ATCTTTTGAT AGC	153
	(2) INFORMATION FOR SEQ ID NO: 1185:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 164 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1185:	
	TCATTTATAT ACTGTATCAC GCTATCTTTA GTATGTGTGC ATNATCATTC GTTAGTGCGT	6
55		

	AATGAACGTT ATATTTTAAT TCATGATTTA CTAAGACCAA CAAT	164
	(2) INFORMATION FOR SEQ ID NO: 1186:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 143 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1186:	
15	CACAAGTGAC GTCATATTAT AAAAGTCACT CGGTTTGCGA TACGTTCTGT CTAAGAAATA	60
15	GCGACGTGCA ATTTCATATT TTnTATAAAC ATCCGTTGAA AAAGGACATA AAACCATGCG	120
	TTGAACCAGG GTCTATACTT TCT	143
20	(2) INFORMATION FOR SEQ ID NO: 1187:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 209 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1187:	
30	CGTACAAGTT AAAACGTTTA TACGATTACG AAAAACCACC GAAGAGTGAG AAAGATCCAA	60
	TGGTTGTATA TGCAGTAAGT GCAGGATACA AATGGTTCTT TGCTTATCCA GATGAACATA	120
25	TAGAGACTGT TAATACATTA nCAATCCCTA AAGATGTCTG TTTATTAGCT CAGCATGAnC	180
35	ATACAGTTCG GTCACATAGT GTCAATTCA	209
	(2) INFORMATION FOR SEQ ID NO: 1188:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 243 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1188:	
	TTGGAATCGC TGTCGACGGA TAGCAACCTG GATTGTAAAA ATAATGTTGG CTTTAAAAAT	60
50	ACCGTGGCAA TATTAAATGA ATAATCGCTG CTGAATATAC ACCCAATGCA CATTGAACTA	120
	ACATAAnCCC ATTTGACTCA TCTACGCCCA CTATTGGCTT TATAGTCACT GAACTAAGCT	180

	IAI	243
	(2) INFORMATION FOR SEQ ID NO: 1189:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 527 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1189:	
15	CACCAGGCAT TACCATACCA GCACTCATAC CACCAATCAC KCTCGATAAC ATCAATACCG	60
15	AAAAATTGTG GCCAACTGCA AACATAAATT CTGACACTGA AAACAAAATT AATCCTATAC	120
	ATATAATTAA TTTCTTCCCT AATTTGTCAG CTAGCGTACC ACCAAACGGC GATATAATCA	180
20	TTTGAGATAA CGCAAAAGCA GCAACTAGTA ATCCTAAATC ACTACCAGTT AATCCCAAAT	240
	CTTTTAAATA AACAGGCAAG ACTGGTATTA CTAAACCGaT ACCTAAAAAA ATCAAGAAAA	300
	TATTAAAATA TAAGACAAAA ATCTGTTTAT TCATATGCTC ACCTCTTTTT TCTCCATGTC	360
25	ATGCTTAAAG CTGTTATTCT TCTTTTCCAC GACAGATTGC AATTCATGCT AAATATTCGT	420
	AAAAAGTTTC TATATTGTAT TACAACATTG CTACATTTGA CAATATTTTt TCTTTGTAAT	480
	TATCACTATN TTCCATTTAA TTGTATAATT AATGACATAT TNNAATA	527
30	(2) INFORMATION FOR SEQ ID NO: 1190:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 889 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1190:	
	AAAACGTGGC AGTAATTCAG TGTATGTTCA ATATGATGAT ATTATGTTTT TTGAATCATC	60
	AACAAAATCT CACAGACTCA TTGCCCATTT AGATAACCGT CAAATTGAAT TTTATGGTAA	120
45	TTTAAAAGAA CTGAGTCAAT TAGATGATCG TTTCTTTAGA TGTCATAATA GCTTTGTCGT	180
	CAATCGCCAT AATATTGAAT CTATAGATTC GAAAGAGCGA ATTGTCTATT TTAAAAATAA	240
	AGAACACTGC TATGCATCGG TGAGAAACGT TAAAAAAATA TAATAAGATA ATAAAGTCAG	300
50	TTAACGGCGT ATTCAATTGT AAATCTTGTT GGATTTTAAC AAGATAACTA GCAAATGCAC	360
	TGTATAGCTG GCTTTTTAAT TTTATTAACA AAATTAAATA TGACGCGTGA ATTAAAAAAT	420
55		

	CTCTACAATC CTATGGCGCA ATTTTTAACA AAATATACTA AATETGAAAT TGACAGTTTC	540
	CATAAATAAA ATGCTATAAT TTCCTACTCC GTGAATCTTA TTTTGTTTTA AAAAACAGTG	600
5	TAGCACAAGm TTCAACTIGT TTCCTACACT GTTTTATAAA TGAATTATTT AAAATGCTTG	660
	TTCAACCTCT TGTAATGTTG GCAAACTATT AATAGCACCA TACTTCGTTG TCACTATTGC	720
10	AGCAACGCGA TTGCTAAACG CTAAAATTTC CTCACCTTCA TTTTCAAATA ACTGAGTTAA	780
10	ATTTAACACA TCGGTTGCTA AAATCCTGCT AATAACTGCA CCAATAAATG CATCCCCTGC	840
	CCCAGTTGTA TCAACAGGTT TTACCTTATA GCCACTATGA TAATGATTA	889
15	(2) INFORMATION FOR SEQ ID NO: 1191:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 254 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1191:	
25	AGTTAAAGGC GTTGAATTAA TGGCCTTCCC ACACATGACA TATAAACAAG CGTGCGCCTA	60
•	TGGTCTGATA ACCAGATACA CGTTTGAATG GATTAATTGC GTTCTCAATT AGGCGTGATA	120
	TGGCTTTAAA GATTTnAGTC TGTTGAAATG ATGGTGAATT AAAGCATTGC GCTAAAGGTG	180
30	CACTGACAAT ATCTCGTAAA GATATGGTGC TTTAACAGAT TTGTAACATC TATGGTCTAA	240
	nGATACGGGG TTAA	254
35	(2) INFORMATION FOR SEQ ID NO: 1192:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 189 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1192:	
45	GGCTCATAAG TTACACCTAA TGCATCTTCA TCTGGAAGCT GTGGTTTATC ATCTTCTAAA	60
	TCAGCAGTTG GCGTTTTTTC ATATAATTCC TTTGGCGCAC CAAGATACGC TAATAATTGA	120
	GCTGTGTATn CTAGGCATCC ATACCGTATT CGTTAAACCA GTATATTTCA GCTGAATGAT	180
50	CTGTCCTAC	189
	(2) INFORMATION FOR SEQ ID NO: 1193:	

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5	(A) LENGTH: 215 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1193:	
10	TTGATATTGA TCGATGACCG GTGATGTGAA ACTGAAACTG ACCAATGAAT GAAAAAATGG	60
	GCAATGTTTT TGACAACAAT GGTCATTTAC CAAATAAAAA TATTGnCACC ATTAATACCT	120
	GNCAAACGTG TTTGTTCCTA AACCTAAAAT GATAAATCCT ATTGAGATTA TGGACTTGGT	180
15	AAGCTGCAAT CTTTTAATA TCTTTATAAG CAATG	215
	(2) INFORMATION FOR SEQ ID NO: 1194:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 158 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1194:	
	AGAATTTGCn ACTGGTTTAC CAACGCATCT ATGTTCGGTC GCTATACCGC ATACAGATGT	60
30	CGAACATATT AACCATAGAA CGTAGGTGTG GTGTTCTAGA AAAAGAAGTG CCGTTATTGA	120
	AATGGGACAC TTGATCAACA GCCGAGTGAA ATCGTTTT	158
	(2) INFORMATION FOR SEQ ID NO: 1195:	
35	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 180 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1195:	
45	ACTGATTGCC GTGTCTGTGG TTGATCATTG ACTAATTGTT GGCCATCATT GGnTTCTTGG	60
	TCTAATAGTC CTCTTGCTCC TGCGTCGTAA CATTGATGCC AATCATGCAC CACAGCCTTT	120
	CGGTTCATCA TAACATTTCT GCCAATGTCT CTACATGACA CGGGCTCATA TTTCTTTCTG	180
50	(2) INFORMATION FOR SEQ ID NO: 1196:	
<i>55</i>	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 274 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1196:	
_	GTTAAAGCGA ATTATTCACA ATATAAAAAA TCATCTGATC AAGTCGTATT AGAATTAGGT	60
5	ACAAATGGCG ACTTTACTGT CAAACAGCTC GACGATTTAC TTAATCAATT TGGAAAAGCC	120
	AAGATTTATT TAGTTAATAC ACGTGTTCCA AGAATTTmTG AGGGCAAATG TAAATCGATT	180
10	ATTAGCTGAC GCGGGCGAAA CGGAAGTCCC AATGGTCACA TTAATTGGAT TGGGTATTAG	240
	GCGCTTCACA AGGGACCTTG GTGGAATATT TTTG	274
	(2) INFORMATION FOR SEQ ID NO: 1197:	
15 20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 154 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1197:	
25	ACGTAACCTA TATTCATCTC TGTTCCCAAT AATAATAACA ATACATAACT GATATTAGCT	60
	GTCTTTCATC TCTAATTAAT ATGCGTCATG AGCTAATATC GGTTATTTTT TTGTGTCAAA	120
	NAATTTTAT TTTATCTCTC CATCGCATTA ATTG	154
30	(2) INFORMATION FOR SEQ ID NO: 1198:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 249 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1198:	
40	AATCCTCACC CGTAATAAAC TCGTTTTGAA TGCGTTGTTC GAACTCACGG TATATTAAAG	60
	CAATATCCTC TAACTTATTT TTAGTTCGAG TTTGCATATT TTTATCAGCA ATAAAGTGTT	120
45	CTAAATGTTC AGGCGTTACT GCATATTTTT TAAAATCTTG AATTTGTTCT GTTAATTTTT	180
	CACTAAACCC ATAATATTTT GCTTGTGATT GATAAAGTTT TAAATACTTT TGTTGTTCnT	240
	GAACAATGn	249
50	(2) INFORMATION FOR SEQ ID NO: 1199:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 165 base pairs	

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1199:	
	TIGGTAAAAA TCGACATCAA ATACTAAATC TGATCCATCT GAATCCCATG TITAAAACCG	60
	AACTTGTGCA TTAATTGTAA AGTTCAAACT CTTCATCTTC ATAGATCGCG ATGCGTCTTT	120
10	TAATTCTTTA GGTGATACTT TGTAGATCTA TAACAAAATT AnCTA	165
	(2) INFORMATION FOR SEQ ID NO: 1200:	103
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 236 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
20	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1200:	
25	TTATTAGCGA TTAAAAATAT GTCCTTTTTT AATAAAGGAG ATATATGTTT AATTGGATGT	60
	CAACATCGGA GTCATTGGCG AAAAATAGGG CTGCGGTCGA TGGAGTTCAA AACTATTTTA	120
	ATGCATTACA TGTTGTGAGT NAAGAGCAGG CGTACTTTTC TTTTCAAGGA TGTGACATAT	180
30	CACAGAGCGT ACAATAGAAA CTCAGATACC ATTACATGGA nAGTCCGCGT CCAATG	236
	(2) INFORMATION FOR SEQ ID NO: 1201:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 146 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1201:	
	TAATGCTAAA CAGTATTATG GAGATAATGG CTTAGTTCAA ATTTCTGATG NAAGTCAACA	60
45	CTTCTAAAAT TTGTAAATGA AGCATTAGAC AATAACGAAC AATCAGTTGA AGATTACAAA	120
	AATGGTAAAG GCAAAGCTAT GGGCTT	146
	(2) INFORMATION FOR SEQ ID NO: 1202:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 385 base pairs´ (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
55		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1202:	
	ATTGATGATA GTATTGATGG TAATACCATA AACATACAGC ATTATCACAA GTAAAAGTAA	60
5	GCCTAAATGT CCATAAAATC TACTTGTCAC AATATATGTC GGTATTATCG TAACGGGAAG	120
	TCATTTCGTA CTTGATTAAA CTTTTGTGTA ATTGCTTTAG TACCTTCTAA ATACCTGGTT	180
	GATGAGACCA CATACTGATA CCACCATAAC CATAAACAAA AGGTACACCA GAATTGGGCA	240
10	TACTTCTTAT TCCATCCAAA CCTCCGTAAC CTAATTGCTA CGGGTAATAT TCCAGCACAC	300
	TAATAGTATT GATGTAATTA ACTGAACGGC CGCTnGATAA TAAGTCTTAC AGTCTTAAAC	360
15	GTCCATGCGC ATCnTnACCC ATTCA	385
,,,	(2) INFORMATION FOR SEQ ID NO: 1203:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 580 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1203:	
	ACATTGAACG AGTACAGAAA ACTTATTGNA AATAAAGGCT GTTAAAGATA AAGAAGAAGA	60
30	TACTTACAGA GGTAAGTATT TTGCGGAAGA AAGAAAAAAC GAAAAATTGG AAAAAGAAAA	120
30	TATAAAACTA AAAAACAAAA TTTATGAATT ACAAAACGAA GAAGATAACG AGGAGGACGA	180
	AGAAGACAAG GAGGACGAGA ACGATGTATT ACAAAATTGG TGAGATAAAA AACAAAATTA	240
35	TAAGCTTTAA CGGGTTTGAA TTTAAAGTGT CTGTGATGAA GAGACATGAC GGTATCAGTA	300
	TACAAATCAA GGATATGAAT AATGTTCCAC TTAAATCGTT TCATGTCATA GATTTAAGCG	360
	AACTATATAT TGCGACGGAT GCAATGCGTG AYGTTATAAA CGAATGGATT GAAAATAACA	420
40	CAGATGAACA GGACAAACTA ATTAACTTAG TCATGAAATG GTAGGAGGTA TGANAAGTGA	480
	ATGATTTACA AGAGAGAA TTAGAAACAT TCGAACAAGA CGACCGATTC AAAGTAACTG	540
	ATCTAGACAG TGCTAACTGG GTTTTTTNAG AAACTNGGAT	580
45	(2) INFORMATION FOR SEQ ID NO: 1204:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 139 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

	ATCUTATUGT TUAGGUGAAT TTAACTGAAA AATTAGACAA CGAATCTTGA TGAAAAGANA	. 60
	ATGATTGGCT AAAATAGCAG CTAATCAAAT CAACGATAAT GAATGCTTAT TTATCGTGCT	120
5	GGTTCATCTA CATTGGAGC	139
	(2) INFORMATION FOR SEQ ID NO: 1205:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 229 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1205:	
	AGGAGGATAT CAGaCTTACA FACTATTCTT TATCATACTG FAATTCAAAT AGACACCTTA	60
20	ATTGAAGAAG GCGTTGACGC GCTACTTTTC rAAACGTATT ACGACCTnGG AAGnGTTAAC	120
	AAATGTCATT TCCACGGAAC GGGGAAAGGA AATACGGCGT TGCCAATCCA TTGCTCCAAT	180
	TGAACCGGTT GCAAACACAA ATTGACTTGG TTGAAGGGGC AGGCATGCA	229
25	(2) INFORMATION FOR SEQ ID NO: 1206:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 399 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1206:	
	TCGACAAGTT TITAACAGTT CGTTATTATA TGAATGTAAG TAAAAATTTC TTAGCTACAA	60
	CTTACATATT ATAAATGCAT AAATTAAACA AAAAGGGGCG AAAAAAGTTG ACTCATTTAT	120
40	CAGATTTAGA TATTGCGAAT CAATCAACAC TACAACCAAT TAAGGATATT GCTGCATCAG	180
	TAGGTATTTC AGAGGATGCA TTAGAACCTT ATGGTCATTA CAAAGCTAAA ATCGACATTA	240
	ATTAAAATTa CGCCAAGAGA AAACAAAGGG AAGTTGTTTT AGTTAACTGC GATGAGCCCA	300
45	ACACCAGCTG GTGAAGGLAA tCMACGGTTA CAGTTGGtTT AGCTGaTGCA TTCCmTGaGT	360
	TaATGAAAAC GTTATGGTTG ccTTaGGGGG CCTGCCTTT	399
	(2) INFORMATION FOR SEQ ID NO: 1207:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 138 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1207:	
	ATAAACAATA CGATTTGTAT GCTACTTGTC TGAAGACAAC ATAAAACAAT ATGTTAACTG	60
5	ATATTGAGGA TATGGGCTTT CAAAATCCAn TTCAAAAAAG GTTATGTTGA AATATGACGC	120
	GGTTGTTGAA AGAGACCC	138
	(2) INFORMATION FOR SEQ ID NO: 1208:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 655 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1208:	
20	AGTCGCCTAA CTTTTATTAT CAGTCCAATC AGTTTCATCA AGTATAAATG TTATTGCTTA	60
	TTTTTGTATT CTTGGCGTAT TTTTTGTTCT TCTGCATAGC GCTCTGGATT TTTCTTATAA	120
	AAATCTTGGT GATAGTCTTC GGCTTTGTAA AATTGTGACG CTGGTArTAT TTTTGTTGCA	180
25	ATTGCCTTAT CAGCATTAAT CGTATTTTTA AGCTGCTCGA TATAAGTCTC AGCGAGTTCT	240
	TTTTGATGAT CATTAGTGTA GAAAATAGCT GTTTNATATT GAGGACCACG GTCTTGATAT	300
	TGACCACCTG TATCTAATGG GTCAATGACT GAGAAAAATA TTTCTAATAA CTTATTGTAT	360
30	GAGAATAATG CAACATCATA TTGAATTTCA ACAGTTTCTA AATGACCACT CGTACCTGAT	420
	TTTACTTGTT CGTAAGTAGG ATTTTCAATA TGTCCGCCCA TATATCCAGA AGTTACTTTT	480
<i>3</i> 5	TCTATGCCGT CAAAGGTGTC AAATGGTTTC GTCATACACC AAAAGCAACC TCCGGCAAAA	540
	TAAGCTGTAT TAATATTCAT TTTTGACATC CTTTCCATTA GACCTTAGTA CGATTTATTA	600
	AGAAATCACT TGCTTTTGA ATTGTTTTTA TATAACGTTA ATANGNGATT ATNAT	655
40	(2) INFORMATION FOR SEQ ID NO: 1209:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 213 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1209: CCGnCCCCAA TGGAAATTAC CTTTGGTnCC CCATTTTAAT TGTTAAATTA TTGGAGTGTT	6

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	AATCTCACTA TCTTCAAATA AGCTTGTGTA TAGTTTAACA GCTTCTTCAG CTTGGTTATT	180
_	AAACATTAAA AATGTCGTGA TTTTTGGAAT ATC	213
5	(2) INFORMATION FOR SEQ ID NO: 1210:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 149 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1210:	
	TTGATTGCAA CTTTGATAGT GAAAACATTT ACATGATGTT GTCACTGGTG CACGGGCGTC	60
	GAGAACAATC ATTGCGTTAT TGACGGTGCT GCCCTGCTGT CTCAGTTTGT TGATGCAAGC	120
20	ACTACACGAA ACCCAATAGC nTCACCAGG	149
	(2) INFORMATION FOR SEQ ID NO: 1211:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 142 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30		-
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1211:	
	AATGTTTCTC CTAATTTTAA ATGTTTAGGA ATATTAACTA GGATAATAAA TCCAGCGACA	60
3 5	TCCCAAATGG GATTCATATA AGAATGTTGG ATGATAATnT TGGCCGTTAA TATACATATT	120
	TTCTATTATA AAATTGGGCA AA	142
	(2) INFORMATION FOR SEQ ID NO: 1212:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 163 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1212:	
	TTTAAATTTA GTCACTTCAC CTTTTAAAGC ATGTTCATAA AATGTTTGCA TCATCAATGC	60
50	ACGTTCTGAA CCAGAGCCTT CAACACAAAG ATAAATTTGT ACAGCAATAC CGCCTCTAAC	120
	TCTTCGTTGC GATGATGGCA ATACCACTCA ATCCAACGCT Cng	163

(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 765 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1213:	
	GTCACCTTTC ACGTCTTGAA GAAAAAGGCT ATATAAGAAG AGATCCAACG AAACCACGTG	60
	CTATAGAAAT TGTAAGTGAT CAAACAAATG ATAATATTAA TATGGAAGAA ACGATTCATG	120
15	TGCCAGTTAT TGGTAAAGTC ACAGCAGGTG TTCCTATTAC CGCAGTAGAA AATATTGAAG	180
	AATATTTTCC ATTACCTGAA CACTTAACAT CGACACAA TAGCGACATA TTCATATTAA	240
	ACGTCGTAGG CGACAGTATG ATTGAGGCTG GTATATTAGA CGGAGACAAA GTAATTGTnC	300
20	GCAGTCAAAC CATAGCAGAA AATGGAGACA TTATTGTTGC TATGACTGAG GAAGATGAAG	360
	CAACTGTCAA ACGCTTCTAT AAAGAAAAAA ATCGTTATCG ATTACAACCT GAAAATAGTA	420
	CAATGGAGCC AATTTACCTA GACAATGTTG CTGTAATTGG GAAAGTAATT GGTTTGTACC	480
25	GCGAAATGTA ATATTTTAAA CCGTTATATA TTATCGTAAT TGTTAAGCCC TCATTTTAT	540
	AAATTTTGGG nCTCTTGAAA AAGTTACGTT TTCAAGAGGT TTTATTTATT CTAATCTAAA	600
30	TTCAGTTCAA ACAGAAATTG CGAATTGTTA GATAATCTCA TTCTTTArTA TAAATnTTGA	660
30	ATTACAGATT TCTGCAAAAT GTTACACAAA TTAAAACTCG CCCCGTAAT AATTTACAGG	720
	AGCGAGCCAT TATTATTTT TTCnTTCTTT TTTATTAAGT ATATC	765
<i>3</i> 5	(2) INFORMATION FOR SEQ ID NO: 1214:	•
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 495 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1214:	
45	AGTTGCCATC AAAAATACAG AACCTAATNA TNACCTTTTA TGATTTTTTG TGAATTCAAA	. 60
	GTCACTTTCT TTTTnAAGCT TTAAATTTCT CCCCATTTTT TTAGCCCCCT ATAAGGATTG	120
	AATATCAATG CCTTCTTTCA TTAAAATTTC TCTAATTTTC GAAACAAATA ATAATGCATG	180
50	TTCTCCATCA CCATGCACAC AAATTGTATC TGCTTGTAAC GTTACTTCCT TATTGTTTTT	240
	TGAAATAACT TTATYYYCCE TCACCATCTT TAAAACCTGC TTAAGTGCTT CGTCAGTATC	300
	INCREMENTAL PROPERTY OF THE PR	

	ATCAGCAAAC ACTTCAGAAG CTGTAATTAA TCCGACATTC TTTGCTTCTG AAATTAGATA	420
	TGAATTTGCT AATCCTACTA ACACTAGTGA TGGATCAAAG TCATAAACAG CTTGTGCTAT	480
5	AACGTTTGCn ATTnC	495
	(2) INFORMATION FOR SEQ ID NO: 1215:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 243 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1215:	
	ANTGTCCAGG TACCCGTGGT CCAAAATTCG ATGTACGTAG ACCATTGNCT CGTATTTGTC	60
20	AGATTGTGTT AATGATTGTC TCTGTATTAG GAAGTTTATT CTCCATTTTA ACAATTAGAA	120
	AAATAGATCC GTTAAAGGCG ATTGGGTAGG AGGTGTGCAA ATGTTGAAAT TGAAATGTAC	180
	AAGTCATTAA GTGGATCTAC ATGAGCGTAA GGTCATTGGA ATAGGTTTGC TGTGACTCGC	240
25	CGA .	243
	(2) INFORMATION FOR SEQ ID NO: 1216:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 256 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1216:	
	GGGCTTCTTT CTARARTARC TRAGTGRATT ATCTATATAT GRAGAGGTCT CCRATACTTT	60
40	TTATATAATT CGTGATTACA TTCTATACTT TTAATTGTAT TTTCTGCGTA GGAAAGTGGT	120
	TTTATTAATT CGATTAGTTC GAACTACADT CAAGAAAAGG TAAAATTTGT GCATGAGCAA	180
	GAGAAACATA CCTGAACCAA AGGCACCCGA ACAGTACCTA GGCCTAAGCG GCTAATTATA	240
45	AATGCTCAAG CGCAnG	256
	(2) INFORMATION FOR SEQ ID NO: 1217:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1217:	
	TITATTTTTT CTTCTAAACG AAACATTGCT TCTTTTTGTG ATTGTTTTGT ATTCTTGTTC	60
5	AACACAACAC TTACGCGCTT CCATTTATCT GTGTATGGAT CTTTATACTT CTCGTAGTAT	120
	CTGTATTTAG TTTCGTTATT TTTGTTTTTA AATTTTTCAA TCCACATGTT TATACCTCCT	180
10	GAGAGAACGT ACGTTCTGTA AATTTGTAAA AAATAATAAG GGTAGGTGGG CTACCCAAAA	240
	TTTAGTACTA GGTACTAAAT ATGTTATAAT AAAATAAAAA GTAGGTGATA AGATGACTCA	300
	ATTTCTAGGG GCGCTTCTTC TTACAGGAGT TTTAGGTTAC ATACCATATA AATATCTAAC	360
15	AATGATAGGT TTAGTTAGTG AAAAAAACAA GATTATCAAT	400
	(2) INFORMATION FOR SEQ ID NO: 1218:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1218:	
	CCAAGTGTCA ATTTTAGATG ATTTTTTTGT TGACCTATCG CCTTAACTGA AGAAACTGAT	60
30	AAATCATCCA TTTCAAAAAT AGGTCTAGAA AAATCTGTTC CGAAGGLCTT AAACGATTCA	120
	TATCACGAAT ATTTTTAATC GTTATATCAT TTTCTGTTAA TAATACATCT ACTTGCTTTA	180
25	CGGGATCTAA CGAAGTTGTT TTAGATAATT CTTTCATCCA TTTATTTAAA CCTTCAGCTA	240
35	ACGATTCTAT ATTTTCAATA TCCATCGTCA TACCTGCAGC CATATGATGG CCGCCAAATT	300
	TAGCGATTAA CTCTTGATGT GCTGATAGTA TTTCAAACAT CGACACTTGA TCAATTGATC	360
40	TGGCGGAGCT TTTGCATGAT TTTGCTCCCT ATCAATATTT	400
	(2) INFORMATION FOR SEQ ID NO: 1219:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 458 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1219:	
	AAGATATTAG ACATAAAATC TAAAAACAGC AGTAAGATGA TTTATGATTA GAAACTATCT	60
55	TACTGCTGTT CACTTTTAT AATACTTCTG AATGTCTTCA CTTATACTTC TAGTCACAGA	120

	GCATTCATTT CTTGTcTAGC AACGTTCTAC TCTAGCGGAA nTAALTAGCT ACCATCCTCG	240
.	CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGcTCTCGC	300
5	TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG	360
	TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT	420
10	AAAAAAAGAG ACCTCACGGT CTCAACTTGG CCTGGGCA	458
	(2) INFORMATION FOR SEQ ID NO: 1220:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 494 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1220:	
	CAAAATTTAT TTCTTGTAAA GTACAATATA AGTTAAATGT TGTTGTTAGG ATTGATTCTT	60
25	TCATCTGAGC ATTTAATTGT AAGTCGCTAT ATTTAATTTG TTCAGTATTT AMAAATAAAT	120
	TGAAAAATTC AACTGATAAT AAAGGTGTTC TAATCATACA AATACTTGAC GGTTCGTAAA	180
	TAGTGTTCAT TTGTAAGCAC CTCACATATT TGAATAGACA AATAGAGCCC TTTCAGGCTC	240
30	TATTTGCTGT AATCTTAACA GCAGAAGCTA TTAAAACTAC CAGTCTTAGC ACAACCAGGA	300
	GTACATAAAC TATGACTTGT AATACGTTCG TCACCTGCTG AATCATTTGA GTnATTGTTT	360
	GCTTTAACTT GCACGTCTAA ATCAAGAACT TTTTCCATAG ATAAAACCTC CTATTATTAG	420
35	TTGAAGTTAA GGCCTACTTC AATTGTCATA TTATCCCTTT TCACACAACA AATCAATAAA	480
	TTATATATT ATAT	494
40	(2) INFORMATION FOR SEQ ID NO: 1221:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 148 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1221:	
50	ACTATTATTT TAATAGTGAC GACAGTTTTA ATTTTATTAA GTATTGCTTT AATTACCTTT	60
	ATGCAATACT ATTTCACACA AGAMACCGAA AATGCCATAA GAGAAGATGC TAGACGTATA	120
55	AGTTCACTGG TCGAACAATC ACATAATA	148

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

5	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1222:	
	TCGCTTTTAC ATCAAATAAA TTATCTTTAT ACAATTTCGT ATGAATTACT TCTTTATAAT	60
	TATAAAAATG AGGAATTTTT TGATTGTTTA ATTCACTTGC TAATTGATTA GCTTTTTGTT	120
15	GGTCTTTAAT TGTAACGTCG TGTGGTGCAG TATATTTTAT TTCACTTGAT AAGGACGCTC	180
	TACTTATAGC AGCAAAGCAA AGAACTGAAA CAGTAATCGC TGAAATGATT GCCATGACCG	240
	TAAGTGAAAA AGCATTTTC TTAATACGAT ACATAATAGA TGATGAGAAC ATGACATCAT	300
20	TLACACTTAT AACACCTTKT CTAAACLTCT TCACCATTTT AAAAACTAGA GArACAGAGC	360
	TTTTAAAAA TAAGnGTGCC CCAATCACAG TTGACAANAA A	401
25	(2) INFORMATION FOR SEQ ID NO: 1223:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 176 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1223:	
35	CTTGACCAAA TCCATTTTT AACAAAAGTG GTCAAGTGAA ATCCCATCTT TCCAAATCAA	60
	AAAAGAGCTA AAGCAAAATG CTCTAGCCCT TGATATTACT GATTTCCCAT CATTGTnTAG	120
	CGTATTAATA TTGCTTCATG TACTGATCTC TTTCCCATTC AGAGACTTGA GTTCTG	176
40	(2) INFORMATION FOR SEQ ID NO: 1224:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 283 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1224:	. .
	AATACTTTTA CGATAATTAT AAAGGTTCAT TCAAATCTTA GGGCAAAATG TATAATATTT	60
<i>55</i>	TTATGCAAAT TTAAAACAnT AACACTTATT TCAAGGTTCA ATATTTTGAG AATAAGGAGT	120

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	AATGCCAATC AAACTCGCTC GAAATAGGGG GAAACGAGGC nATCATTTTT GACAATGAGT	240
5	GTCAATAGGG AAGAATAACA ATTAGGAATG ACTCATAGGA GGA	283
	(2) INFORMATION FOR SEQ ID NO: 1225:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 217 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	•
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1225:	
	AAAAGAAGAG AAGAAAGTTG AAGAACCTCA AGCACCTAAA GTTGATAACC AACAAGAGGT	60
22	TAAAACTACG GCTGGTAAAG CTGAAGAAAC AACACAACCA GTTGCACAAC CATTAGTAAA	120
20	ATTCCACAGG CCATTACAGG AATTTAAGTC GGATACCACG TGAATNACGT CAGGATGTCn	180
	GCCGTTCACA TGACACGCTC TACATATTCA CCACTCG	217
25	(2) INFORMATION FOR SEQ ID NO: 1226:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 176 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1226:	
35	TGGGTACTAT TTATTACGTA AAACTTTTCG TTAGCGATGC CGGCATTGCA AGAGCAAGGT	60
	TTACAAAAGC GGACTAGGTT TGCACTTTCT GCTGTTCCAT CGCATATGGA TTAGTAAGGT	120
40	CTTTATGGGn ACTGTAAGTG ATCCGAGCAA TGTCGGATAA TCTAGGTCTT GGATAG	176
	(2) INFORMATION FOR SEQ ID NO: 1227:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1227:	
	AATGAAAATA AAGAAGATGA TTTTGTTGCA TATGGGTCTC CAGAACATAA TTATCAATTT	60
<i>55</i>	GGTGGAAGTT TAATCAAAAG TAAAAATTTA AGCACGTTAT TAAAACCAGT ACATCAAACC	120

	GCGGCCGTTT TAATTTTGTT TTCAAGTTAA TCATACTTAC ATATAAAAAT GAAAAGTTGA	240
_	ATTTTTAGTA CAATTTCCAC TGTATTTATC TGTTAACCAC TTTATACCCG CAATATTTCG	300
5	TTGATCTTAT ATAAACACTT TTGGCTGCTT TTCCTTGACC TAGATTAAAA TTATAGATTT	360
	TCCTTGTAAG AGTGTGTTTG TAGTATCATA AATATGTAAA	400
10	(2) INFORMATION FOR SEQ ID NO: 1228:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 150 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1228:	
20	ATCTAGCATG CTTTTGGAAA ACGATAAGAA TTTGGTGTTT GAATTTCATA ACCAACACCA	60
	GCAGTTTCAA CAACTACGTG TGTAGGATAT AAATGTGTTA CTTGACCTTT GACATACGCG	120
25	TACATTATAG GCACATCCTT ACATACTCAn	150
	(2) INFORMATION FOR SEQ ID NO: 1229:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 138 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
3 5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1229:	
	TCGGTACAGT GCATTTGGTG CGTCATGGTT TACAAGGNAA AAATAAGTGA TCACTATTTA	60
40	TCAGTATGGG AAAAAGCAAC GACGTATCAA ATGTACCATG GCTTAGCATT ATTAATTATA	120
40	GGTGTAATTA GTGGTACA	138
	(2) INFORMATION FOR SEQ ID NO: 1230:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 182 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	. •	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1230:	
<i>55</i>	TTGGTATGTA CCTCCAATAG TAATTTCAAT AACTTTGTCT GTTGAACACT AAGAGCAATT	60

	CCTTGATTAT nCTAAGAAAA GTAAAAGCAC ACGGAGTATC CTATCAGAAA ACCAGTATAC	180
	CA .	182
5	(2) INFORMATION FOR SEQ ID NO: 1231:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 233 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1231:	
	TCTCTTTAAA TTGTACACAA TTCTGGATAA CTATCCCCAT TTCTGTGGAT AAACACCTTG	60
	ATGTCTTATT ACTTATCCTC GTTTTTATAT CCCATATTTA TCAACGGKTA TCGCTTTTTT	120
20	TCATAAAAA aCACTACCGT ACCYCTTATT TAAGAAATAC AGTAGTATTA TTTTCAATAT	180
	ATTTTAGCTA GCnTTTCTAC GTCGTACAGT CGCGATTAAA CCTATACCTG CTA	233
25	(2) INFORMATION FOR SEQ ID NO: 1232:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 385 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1232:	٠
35	GTTTTTGGTA AAAGTACTAA TATTAACCAA GTATTGAGTC ATATGTTAAA ACAAGATGCG	60
	AATGATATTG GCTTTGCTAA ATTACTACAA AATGAGAATA ATCGTATGAG TTATAACGAG	120
4.0	TTAATGAGTG AATGGCAATC ACATCAACGT GCATTTTTAG AAGAGTTGAG GCATGTTGAA	180
40	ATGTTAAAAG AAGAATCTAT TAGAGCATAT GATGTTTATA AAAATTGTGA GTCTTTCTCT	240
	AAGATTGAAC AGGTTATTAA TAGTGAAAAA ACAAGTATTG AAGAACAGGT ATATCATTTA	300
45	GATAATGAAA CGTTACGAGA CAATAAAGAA ATAGAAGTTT GGGATAATCG ATTTAATTAn	360
	ATTGNTAGCC CAATGGNCCC TTTAA	385
	(2) INFORMATION FOR SEQ ID NO: 1233:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 180 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
55		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1233:	
	CTGAAAAGAT TCAACTAATC TGAGTCAGGT TACAATCTCA TGATAACCGC TCGCACCTCG	60
5	GAGAAAGACG CTCAAACAGT ACAGAGCTCG ACCGCAGGAT ATTTTTTGTG AAAATGAACG	120
	TATGAGCTGT TCAGAnGGCA CTTTATTGCG CAATAAAACG GTAAAAATCC TGAAGTGAAG	180
10	(2) INFORMATION FOR SEQ ID NO: 1234:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 453 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1234:	
20	ACCATTTAA TTIncnTTAT GACCTTGTAT GCCATTATCA aCAGTTATGA TTAATGTTAT	60
	GCYTTCATCA TGAGCATTTC TAAATGCTAG TTCGTTTGGT CCATATCTTC GGTAAAGCGG	120
	TTAGGAATAT GCCATCCTAC TTGTGCACCT AAAAGTTGTA ATGTTATCAC TAAAATTGTA	180
25	GTTGCGGTAA CACCGTCGGC ATCGTAATCA CCATAAACTA GGATTTTCTC ATCATTCGCT	240
	ATCGCTCTTT TAATTCTTTC AATAGTCTTA GTCATATCGC TCAATTGNAG TGCATCATGA	300,
30	TTGATATCTG TATCTGAAAT GATGGATTCT ATTGCTTGTn CATCAATAAT CGATTTACTT	360
	nCTAATATTT TTTTTACGAT TGGCGTTAAC TTTAATTTTG ATGTTAATTC ATCACTTATG	420
	TATTCAGCTG GTTTAGTTAA TTTCCACTTA TAC	453
35	(2) INFORMATION FOR SEQ ID NO: 1235:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 163 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1235:	
	CGTGATTAAG TTGGATACTA AAATTTGGGA TGTTAGAGAA TGTGATGAAG ATTTnCAGCA	60
	ATGTCCTGAA ATTAATGAAA TAAGAGACAT TGTTTTAAAG CGGTGGTTTG ATAGGTTTAC	120
50	CAACTGAAGC AGTTTATGGA CTTGCAGCGA ATGCGGCAGA TGA	163
	(2) INFORMATION FOR SEQ ID NO: 1236:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 144 base pairs	

(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1236:	
	GTTAACACAT CGCTTATAAC GTGTAAATAT AAACACTGTT TTATAAAAAC TTTTTATACC	60
10	ATTACCGGCA CCGATAAATG TGTACTATGG AGCACAACAA TAACTGGAAT ACTTmGATTT	120
	AATCCCGCTA TAACATTTCC TAAT	144
	(2) INFORMATION FOR SEQ ID NO: 1237:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 204 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1237:	
25	ATAGTTTAAG GTGATATTCA AACAATATTA GGTTTGATTT AACTATCAAG CATCTACTTT	60
	GTCATGTTTA ATACCAGCAA ATAATAAAAT CCATGTCACG ATAATAAATG GCATGTTAAT	120
	GCAGGGTAAG CCCAACCGGT CCAGCCATGG TGGTGGTACC CTANTTGGCC NCCACCTACC	180
30	GGTTAATTAA CCACCCCAA AAAA	204
	(2) INFORMATION FOR SEQ ID NO: 1238:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 157 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1238:	
	CGGTCATTTT GGTTATTNAA CAACTATACC TGAGGGGTGG TGGGTAATTC GTATTGCCGA	60
45	TTCAGTTTTG TTAATATGCT GACCACCTGC ACCAGAAGCT CTGAATGTAT CAACTGTGAA	120
	TAGCATCCGG ATTGGTTTCA ATCTGCTATG GCATCAT	157
	(2) INFORMATION FOR SEQ ID NO: 1239:	
50 55	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 164 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1239:	
	TTAAAGCATG TTCATAAATG TTTGCATCAT CATGCACGTT CTGGACCGAG CCTTCAnCAC	60
5	AAGGTAATTT GTACAGCATA CCGGCTCTAA CTCTTCGTTG CGTATGCCTG CAATTTCTTA	120
	CCTCGATACT TAAGTCAATT TTCCGGGCAT AAGGGTGTTC ATTT	164
10	(2) INFORMATION FOR SEQ ID NO: 1240:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 239 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1240:	
20	TTGAAAAACT GAAAACGGTG AAGTTTTACA AACAACTAAA ACAGATAAAG ATGGTAAATA	60
	TCAATTTACT GGATTAGAAA ATGGAACTTA TAAAGTTGAA TTGAAACACC ATCAGTTACA	120
05	CACCACACA GTAGTTCAGA ACTATAAGTT GATCAATGTC TCACACAGTG CATAATNGAA	180
25	CAACATGCCG GTCTCAACAC TCACTAGGCA GAGGATCATA ACGGTCGTnG TAAGCTCGG	239
	(2) INFORMATION FOR SEQ ID NO: 1241:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 152 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1241:	
	TGATAAATAA TAGCGCCATC ATAAGTTGCA GGGTGGTAAT CATAATTTCT ACCATGAGTC	60
40	TTTGCCTTGA AAGACCGTGC ACCACTTTCT TTTAAATCGG TAAACGATAA TGnCAAGTTT	120
	AAAATAATTT GGCGTGTTGG CATTTGAGTA TC	152
45	(2) INFORMATION FOR SEQ ID NO: 1242:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 148 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
<i>55</i>	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1242:	

	AICHTACCT TICACIGTIC ACTTATGTAC CATAATACTT CTGACAGTTA CTAATTAACA	120
_	GCAACTCTAA CTCATTTATA TTTAACTA	148
5	(2) INFORMATION FOR SEQ ID NO: 1243:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 588 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1243:	
	GGTACCAATC GATCGTTACA AACGTTTCGT TAAAGACGAT AAAAAAGTAC CAACAGGCAA	60
	TGAATATCGT GAATTAGTAT TAAAAGCAAT TCACATGATT ATGCTTGGTT TCTTGTATAA	120
20	ATATATTGTT GCTTACTTTA TTAACACATA TGCAATCATG CCGTTACAAT TAGACTTACA	180
	TGGCTTTGTC AATTTGTGGT TATATATGTA CGCATACAGC TTATATTTAT TCTTTGACTT	240
25	TGCAGGTTAT AGTTTATTTG CGATAGCATT TAGTTATTTA TTCGGTATTA AAACACCACC	300
	AAACTTCGAT AAACCTTTCA AAGCGAAAAA TATTAAAGAT TTCTGGAATA GATGGCATAT	360
	GACATTATCA TTCTGGTTCA GAGATTGTAT TTACATGAGA TCTTTATTCT ACATGTCTCG	420
30	TAAAAAATTA TTGAAGAGTC AATTTGCAAT GTCCAACGTG GCATTCTTAA TCAACTTCTT	480
	CATAATGGGG ATTTGGGCAT GGGAACGAAG TGTAATACCA TTGGTTTAAG GGGTTAAACC	540
	ATGGCCAGCC TTGGTTAAAG GGTAnGGnCC AATAAGGACG GTGGGCGG	588
35	(2) INFORMATION FOR SEQ ID NO: 1244:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 376 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1244:	
	ATTGCTGGAG AAAGGCAAGG CTTTGCAGGC GGATTGAACT CGACATTCAC TAGTATGGGT	60
	AATTTCATAG GTCCTTTAAT CGCAGGTGCG TTATTTGATG TACACATTGA AGCACCAATT	120
50	TATATGGCTA TAGGTGTTTC ATTAGCAGGT GTTGTTATTG TTTTAATTGA AAAGCAACAT	180
	AGAGCAAAAT TGAAAGAACA AAATATGTAG CATAAGTATT TTGGTGTATA TTGATATAAA	240
55	GTAAAGCGTA ATATTATGAA TGATTAGCAT CGTTTTTCTT ATGAATTTTA TTAAGAAAAT	300

	GTTATATGTn ACAAAA	376
	(2) INFORMATION FOR SEQ ID NO: 1245:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 288 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(5) 10102001. 12.101.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1245:	
15	CAATITGTTC TAAAGCAAAT TCTTTACATT TCTCACGGAA TTCAGCTGTT GACATTTTCT	60
	TTCGGTCAAC ACCTTTTTTC GTTAATGGCT TGTTCAATTG GGTAAACCAT GTGGTTATCC	120
	CCCAACCTGG GTACCGTATG GGGTGGCCAT TAGGAAACCC CTTGGCAATA GGTTTTTTAA	180
20	TAAACCGGTA nCAAATTAAA AGGTCCTTTT TTAAAAAATT TTTGGTTTCC AAAGGGGCCA	240
	ATGGnTCCCC CAATTAATGG TTAAAGGTTT TAACCCCAAT TTTCCGGC	288
	(2) INFORMATION FOR SEQ ID NO: 1246:	
25 30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 161 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1246:	
35	CATCATCAAT AGAACGGTAT TCGCAACGTC GTAGAAATCC CTTAAACGAC GAGAACAAAG	60
	CAAGTCGACA TCAGTAAAAC ATTAAAGATA TTATGGCTGA AGCAGAGAAC TTAATAACTT	120
	TTTATAAATC TATACCnTCC AAAATGTAAA ACTACCAAAA T	161
40	(2) INFORMATION FOR SEQ ID NO: 1247:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 421 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1247:	60
	TCACTACGTT GTTTAATTGT GGTAATTGCA GTTTTACAGG CTTGTCTAGT GAAGATTTAA	
	AACTTAATTC AAGTGTTTTA GTCATGAATA TGTCCTCCTG ATTAAATTGA TAAAGATTTG	120
5 5		

	TTAATTTGGT CGTTTGATGC ATCAGGGTTA ATGTTAGCGA ATCGACGCTT AAATTCTGTT	240
5	TGTTTGCCGT TAGCGTCtAC TTTAGTAAAT GATAATACAA TAGTGATGTG GTTTATTTtA	300
	CTCATATTTT AAAACCTCCT TTCACACTAT ATATCGAAAC AAAATAATAA AATGGCTAAT	360
	TTTATTTTCT ATGTTTAAAA TCTATAAAAN AGGCAATAGA TATGTGTAAC TAAAATATAN	420
10	G	421
	(2) INFORMATION FOR SEQ ID NO: 1248:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 409 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1248:	
	ATAAGCTGCT GTTGATAATC CAAGTGCTAA AGTTAAATAT AATATAGTGC CAAAAATTTT	60
25	ATTCTTCTAT AAAAACACCT CTTCATATTT AATCCATATC TCTTTTTCGT TATTTATACA	120
	GAATTTCTG AAAATAGTCA AGGTTAATTT ATTTGCTGCA AATTTCAACC ACTTTATGTT	180
	AAATGGACAT CAAAGTATAA TTGTATTATT ATTAAATTGT GCAGTGTATA AATAGACGAT	240
30	ATGCAGGAAC ATGTCGCCTA TTGAGCCCGT TAAAAAGACG GTGACTAAAT GAGATTTTCT	300
	TTAACCATCA TTCGTTGTCA AAGTTTGGAA ATGATGGTTG TTTTTTTTTT	360
	TCATTGCGAC TTCTATATCA ATGAAAGTTA TCTTAATATA TGAACTTCA	409
35	(2) INFORMATION FOR SEQ ID NO: 1249:	
1 0	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 217 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
1 5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1249:	
	CTTTCAATTA CGAACAAATC ATTACTAGTT TATTTAATGA TAATGACTGn AATTTAGCAA	60
	AAAACGTAAC ATGATCATTI AGCTTGAATT GGTAAAACTG TTTATCCAAC ATTTCCAGAC	120
50	CAAATCACAC CGGTAAAACG TCAAAATATA TTGTnTCTAT GCCCGTTTTT ACCAGTTATC	180
	TCATTGCAGG TATATTGATG AATTCACAAG TTGGTAT	217
	(2) INFORMATION FOR CEO ID NO. 1250.	

5	(A) LENGTH: 176 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1250:	
		60
10	CAGAACGTGC GGATCGTTTT TATGCAACCT AAACCAGGTA CGGATTTAGC GTGGTTAAGT	120
	GGCAGTGCAC TAAGTATATT CATTGATCCT GCATTTACAC GATGAAAGCA TTTATTGCAT	
	GAGTGGGTAG ATGCATTTTG CTGGAATGAT TCACAAATGC ATTAGAGNAC ATTTAC	176
15	(2) INFORMATION FOR SEQ ID NO: 1251:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 212 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1251:	
25	TTTCAACTTT CTAAATTATA ATATATCTTT TTAAAATAAG CTAGAATTTC TATATAATAA	60
	ATGTTAATAA CGAAAAGGGA TGATGCATAG TGATCGCAAG CACGCCAGAG GCCGATTTGA	120
	TATTGCGAGT TAGTTTATAT GGTTTGGGAT GATATGGATA GAATTGGTAA ACATCTCCTA	180
30		212
	AAGCATGGTA TAGTGCAATT nAAAAnCTGT GT	
	(2) INFORMATION FOR SEQ ID NO: 1252:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 131 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1252:	
45	CAGTAAGTCA ATTGAAATGG CTAATTTATT AAATCTATAA AAGCATAGAG CACTGTTGTG	60
	AGTTCATAAT CAAAGATTTA TAAATGTnTC AGACTGCCAA TATAACATTT AGGACCTAGA	120
	ACATTGATTA T	131
50	(2) INFORMATION FOR SEQ ID NO: 1253:	
<i></i>	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 462 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1253:	
_	TTAGTAGTCA TCGGTATTGG TGGTTCTTAC TTAGGTGCAC GTGCAGCAAT CGAMATGTTA	60
5	ACGTCATCAT TTAGAAACAG CAATGAATAC CCTGAMATTG TATTTGTTGG TAATCACTTA	120
	TCATCAACAT ATACGAAAGA GTTAGTTGAT TATTTAGCAG ACAAAGATTT CTCTGTAAAC	180
10	GTTATTTCTA AATCTGGTAC AACTACAGAA CCAGCAGTTG CATTTAGATT GTTCAAACAA	240
	TTAGTTGAAG AAAGATACGG TAAAGAAGAA GCACAAAAAC GTATATTTGC AACAACGGAT	300
	AAAGAAAAAG GnGCTTTAAA ACAGTTGGCT ACAAACGAAG GTTATGAAAC GTTTATCGTA	360
15	CCTGATGATG TAGGTGGAAG ATATTCTGTT TTAACAGCAG TAGGATTATT ACCAATTGCA	420
	ACAGCTGGAA TTAACATCGA AGCTATGATG ATTGGTGCTG CA	462
	(2) INFORMATION FOR SEQ ID NO: 1254:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1254:	
30	ACTCATAAGT GAATGGTTGA TTACCACTAG TTAAAACTTC ATATACTATA GTTTCTTTTT	60
	TTATTTTGCA ATTAGTTATT TTCATTATAA ACTTCCTTTC AAACACTGCT GAAATAGACG	120
	TCTTTTTCAA ATAAGCATGA TTAATACTTC AATTCTTTAA TCCACATATA TTTAAAAGTG	180
35	AGGTAGTAGG TAATAAATAT AAGACTTAAA GTTAAGATTG CTTTTTTCAT GTTTCATAAT	240
	TAAAACCTCT GTAAATTTAA GGTTAGTATT ATGAAATAAT GGATTGGTTT ATTCTTTAGT	300
10	ACTAACTTCG TAGTAAATTA TATAGTTCGC TAAATTGTAT TTATCTACTA TATTTTTGGA	360
40	ATAAACAATT TCCTTTCTT TCTTCAGTAA ATTATAAAAA	400
	(2) INFORMATION FOR SEQ ID NO: 1255:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 137 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
50		
	(xi) SEQUENCE DESCRIPTION: SEO ID NO: 1255:	

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	NAATCTATGT ATGGGGGCAT CCAAAGATTT CATAGACTAC TTATTTGTTG ATGAAGCCGG	120
	ACAAGCAATC CTCAAGC	137
5	(2) INFORMATION FOR SEQ ID NO: 1256:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 139 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1256:	
	TGAAATGTAG AAATTGAATT AGAAATGAAG ATTAAAAATC nACACGTATC GTTCAAGTGG	60
	TGCAGGTGGT CAGCCGTAAA CACAACTGAC TCTGCGTACG TATTACCATT TCCACTGGTG	120
20	TCATTGCAAC ATCTTCTGA	139
	(2) INFORMATION FOR SEQ ID NO: 1257:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 177 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
<i>30</i>	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1257:	
	TTACCANTTA TTTTAACACC ATGTTTAGAC CAATTTGATC TGACTAAATT AATCGCTGTT	60
35	TGTACCTCCA AATTGTTACA ACGTACACCT TTAGTTTTTC TAAATTAATG TATATTCATC	120
	ACATCTTCTT CAGTTAAGGG TCAAAGTATA ATTTGTCGAA ATTGTGAAGT CGTTGTA	177
	(2) INFORMATION FOR SEQ ID NO: 1258:	
40 45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 250 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1258:	
	(xi) SEQUENCE DESCRIPTION: SEQ 10 NO. 1230. AAGACCAACC GAAATGAATA TCGACATGGA TTAAGCCTAT ATTCAGATGT AAACGCCGAT	6 0
50	TATATTAAAA AGCCAATTAC AGAATGTAGT GGTTAATGAA ATATGCCCAA GAATGGGCTG	120
	TATATTAAAA AGCCAATTAC AGAATGTAGT GGTTAATGAA TATTAAGGCCA AAAACCATGC	180
	TATCACTIAG GIGIAICANA CIGACCARRA MARGOLINA	

	TTAATTTTC	250
	(2) INFORMATION FOR SEQ ID NO: 1259:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 170 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(b) TOPOLOGY: Timear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1259:	
15	ACATTTACGG GACATTTCAT TACATCACCC TGCTTTATTT TGGATTATGG CCTAATTTAT	60
	ACTGATAAAT CTAGGAGGTG GAAAAAAGAA TGCCCTGCAA TTTAATTnCA TTTAACCAAA	120
	TAATGAAACA ATAAAAAACA TTATATCGTT ACTTATTAAG TAATTTGGCA	170
20	(2) INFORMATION FOR SEQ ID NO: 1260:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 313 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1260:	
30	TTTGTACTCC GATACGTTGT ATTCAGGTTG ATGACACTAG GAATTTGTAA TGATCAATTT	60
	CTCTAATTCT TTACAATTGA TAGAATTCTT CGATTTGTGG ATAGACATTC ATATCATTGT	120
3 5	CTAATGATTT TTGGTGATTC ATAAATTGTG ACTAAAGCTT GGATGCTTTA GGATTGTAGC	180
	TGAGACACAT GTTGCGTGAC TGNGGATTTA TCANATAATC TCAATCACGT GATCCNATCA	240
	CATTCATCAG CTCACTAAAT CAAGATGATC GTCGTTTATG GGCGATTAAT GGCGTACCGC	300
40	CAGTGTCCGC ACG	313
	(2) INFORMATION FOR SEQ ID NO: 1261:	
4 5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 206 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1261:	
	TAGCGATCAT TTAATCAAGG TTAGATTATT TAATGTCAGC ATTACGTTTG ACAATGAACT	60
55		

	GTTTGAGGTT ATCACAATGC CATTTAACAC TATGCGCACA TGGCTGAACT AATNAGCGAC	180
	GAGATGACTT CAAACCTTGA TTAGGT	206
5	(2) INFORMATION FOR SEQ ID NO: 1262:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 144 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1262:	
	AAGTGTGTAC ACGATAGCTA AACTCAAATA TCACAGAACA ACAAATGTCT TAGTACTTTG	60
	TGCCGGTGGT GGTACAAGTG GATTATTAGC CAATGCACTA ATAAAGCAGC TGAAGAATAT	120
20	CAThTGCCAG TGAAAGCGGC ACTG	144
	(2) INFORMATION FOR SEQ ID NO: 1263:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 132 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1263:	
	ATAACGACAC CTAATGCAAT TTGAATAAAG CAGTAGAATT TGTGGGAATC GATTATTGAT	60
35	AACCGAACTA ATAATCACAG CAAAAATAAA ATTAAAAATG CTCTAATAGT GCCTACATnC	120
	TCCTCAAATT TT	132
	(2) INFORMATION FOR SEQ ID NO: 1264:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 159 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1264:	
50	TATGTCAATT TCGTAGAATI GGTTTTANGC GCTATTTAGA ATAGCCATCA GATAAAATCA	60
	TTATTTAAAC GTATAATAGG TCAAAATATA GAGAGTTACT ATACAAATTT CTAACTTTCA	120
	CTTAAAATAA AATATATATA ATTAAAGTGG AGGAGAAGG	159

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 132 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1265:	
	ATAGCTCAAG CAATCATTAT GTTTATAATG ATTGTATGGT TCTTTATAGA TGCTTTATTG	60
	ATTAATTAAT AAAAAGCTTA TTGCAAAATA TGTTTTTCGG TAACTGTAAT TTAGTGATTT	120
15	TATCATTAAC AG	132
	(2) INFORMATION FOR SEQ ID NO: 1266:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 405 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1266:	
	CATGGATTTA TCTTAGCGAT TGGTCTAATT TTACCTTTAG GTGCACAAAA TGTATTTATT	60
30	TTTAACCAAG GAGCTAATCA ACCAAAATAT AGATATGTAT TGCCTGCAAT AATTACAGCC	120
	GGGTTGTCAG ACAGCTTACT TATTATTATT GCAGTGGTAG GAGTWTCTAT CATTATTATG	180
	TCTTTACCTG TACTTCAWGC AWTTATTTAT ATAGTTGGTT TAATTTTCTT GATGTATATG	240
35	GCTTGGACCA TTTGGCATGA TAAACCCTCA ACAGATGGAG AAACTCAAAT TATGTCTCCA	300
	ATGAAACAAG TAAGTTTTGC TTTATCAGTT LCATTACTCA ATCCACATGC TATTTLAGAT	360
40	ACAATTGGA: TAATTGGLAG TAGTGCTGCA TTATATAGTG GCnGC (2) INFORMATION FOR SEQ ID NO: 1267:	405
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1267:	
	TCTTTATATT GCAGTACAAA ATTCGCGTGG AGGTTTAACA CAAGTAGACC GCACAAGATT	60
	TAGCGTCTGA AGGTATTACT GTGTAATGCA TTCGCACCTG GNTATCGTTC AAACACCAAT	120

(2) INFORMATION FOR SEQ ID NO: 1268:

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 247 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1268:	
	TTTGCCCAAG TGACGTAAAG TACCCAATGT CCATTTGTAC TTGTATCGCC ATCAACAGTA	60
15	ATCATATTAA ATGTATGGTC AGTCGAAGAT TTTAATAATT GATGAAGTGT ATTCGATTCA	120
,,	ATCGATGCAT CGTGTTATAA AAGCAAGCAT GTAGCCAATT GGGAATCAAC CCGAnCTTGG	180
	CACACATGTA CGTTACACAT TAGAACNCAA GTGACCGACG GTAATCCTAC CCGCTCAACA	240
20	CAAGCGC	247
	(2) INFORMATION FOR SEQ ID NO: 1269:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 215 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1269:	
	TCATTGTATA TGAGCAGATT GGCTAGGCGG TGGCTGGACT GACGGAATCG ACACCCGGCT	60
35	GGGGTTGGGA AAAGTACAAG ACGCAACATG CTATGATTTT CCTATGTGGT TATCGTCCGA	120
	TTTAAAGTGA GCAGCGCACG GTCAGTCATC TCTCACAGNA CCTAAAAAGA ACAGTAAGCN	180
	CAACCTAAAG CAGTGGAACT TAAAATCATC AAGGT	215
40	(2) INFORMATION FOR SEQ ID NO: 1270:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 119 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1270:	
	ACAATAAAGA CTATTAAAAG AGATATAGGT TAGATATTAC ACTTTTAGAG CAAGACGGTA	6
	TAAATGCAAG TAAATTCGTG TATTTATCAA TACAGCAGGT NGAGTGAAAG GCCCAGCAG	11

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5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 223 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1271:	
	CGTGGCACGT TAAGCGTTTA ACCATAGCAT TAAGATGATT GTCTAGCAGA GGCGATTTGC	60
	GGGCTCACTA CAGTGCATGA TGAACTTAAT GCTTCAAATG TAACATTAAA AATAAAAGCA	120
15	ACGATGTCAC TTCTTACTTC TACATCTGCC ATnTTCGTGA TTTCGTATCT ATCCCGCATC	180
	TCATCTTGAA CGTACGAGCC TAATCGCCCn GCGCGATCCT GCC	223
	(2) INFORMATION FOR SEQ ID NO: 1272:	
20 25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1272:	
30	TAGTTACAAT ATCTGTCAAT TTCTGGAGAA CCACTAAAGC TATGCATAAT CCCGCCTACC	60
	TCTTCAGCAT GCTCCTCCAA TAAGATATCG GTACAGTCTT GAGnTGCTTC ACGGTTATGA	120
	(2) INFORMATION FOR SEQ ID NO: 1273:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 126 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1273:	
45	TTGCGCGGCA GTAAAATTCA AACTATTGGC GTCATTTTGC CTAGCTTAAC AAATCCGnTT	60
4 5	TTCTCAGCAC TGATGCAAAG TATTCATGAC CATAAACCAT CTGATGTTGA TTTATGCTGG	120
	TTAACA	126
50	(2) INFORMATION FOR SEQ ID NO: 1274:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 131 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
55	(C) STIGHTDDNESS. GOMPTE	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1274:	
	GATTCTGAAG GATCAATACn ACATGTACAA TTTTGGCGTA GGTGCAAAGG CATCAGGTTT	. 60
5	GCTTGCTAAT CTACATCGAA GCGGCTACCT AAATTAA'IGA GAAATCACAC TCAGTTAATG	120
	CATGTACTAG C	131
10 15	(2) INFORMATION FOR SEQ ID NO: 1275:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 159 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1275:	
20	TGGAGTATTA CCTCAAGTGA ATACAACATA CCTGTTGGAA GATTTTTCAA AACTTTAATT	60
	GGACCAAGTG ATGCCATTGA TGAGTTAAAT CCTAATAGAT TCAGGTTACC TCGGATGATT	120
	GATACTAATT TGGCCTGGCG CACGCTTTAG TANTAGTGG	159
25	(2) INFORMATION FOR SEQ ID NO: 1276:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 577 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1276:	
	GAAGTAAATA ATATATAGAA TATAACAGGA AATAAAATAG ATAATATTAA TGTTGTTTTT	60
	TTACGCATTA TAACTTTAAA TTCGATTTTC AAGTAACTTA GTATCATAAT TAGATCCCCT	120
40	TTGCTTTTTA TTGnTGAAGT ATGAATCAAC AATTGAGACT LTTTGTATTT CAATATCATC	180
	CAAATTAATA TGAAGTTGTT GAAGATATAA AATCGTATCA TTTACATTTG AAGTAATAAT	240
	TTTSATAGTG CCATTATGAT TTTYYCTGAA TAACTAAATC ATCTTTATCT AGTTTTAACT	300
45	TTCTTATATA TTCATCGGAT AACGTAATCT GAGATTGCTG ATTGGTTCTA ATATGTGACG	36
	TTGAATCATT AAGTATTATT TCTCCATTTT CAATGAGAAT AATTTTGTCT GACATACGTT	42
50	CGACTTCTTC AATATAGTGC GATGTATAGA GTATCGTTCG ATTATCTTCT TTTAAATTTT	48
	CAATAATTGA CCAAAAATAT TCTCTAATTT CTATATCCAT AGTCGATGTT GGTTCATCTA	54

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	(2) INFORMATION FOR SEQ ID NO: 1277:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 131 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1277:	
	CTAAAnTAAG GTAATAGTTA CCAAGTACCA TATCTTGTGG ATGGTGTACT ACAGGTTTAC	60
15	CATCTTTAGG TTCAAGATGT TTTGATGACT GCTAACATCA ACATTCTTGC TTCAGCTTGT	120
	GCCTCTTTG A	131
	(2) INFORMATION FOR SEQ ID NO: 1278:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 166 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1278:	
	GTTTGCGATA TTTTAGGCAG ACAACCTAAC TTTACAGAAA CAGGTATCTT TTCTGTTATG	60
30	TGGAGTGAAC ATTGCTCTTA TAAACATTCT AAACCGTTTT TAAAGAATTT CCTACGCAGG	120
	TGCCATGGTT TGGGCTGGAG TCAGGTGCGT TGTGTATAGC TGATAA	166
35	(2) INFORMATION FOR SEQ ID NO: 1279:	100
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 418 base pairs	
40	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	च् र	
46	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1279:	
45	CATAATTATG AAAATGATAT GATTTTATT AGACCATTTA AAAAAGCATA ATTTAAATCG	60
	AAGGCAGGAC ATTGAAATAT GAAATTTTCA ACTTTAAGTG AAGAAGAATT TACCAACTAC	120
50	ACCAAAAAGC ACTTCAAACA TTATACGCAG TCTATAGAAT TATATAATTA TAGAAATAAA	180
	ATAAATCATG AAGCACATAT TGTGGGAGTG AAGAATGATA AAAATGAAGT TATAGCTGCA	240
	TGTTTATTAA CAGAGGCACG AATTTTTAAA TTCTACAAAT ATTTCTACTC TCATAGAGGT	300
55		

	ATTCATTTAT AAAAATAGAG GAGTATTTAT TCTTGTTGAT CCATATHTAA TAGAGAAT	418
	(2) INFORMATION FOR SEQ ID NO: 1280:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 449 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1280:	
15	GACATATCAT AAATTACATG GTGATAAAAT ThTCGGCTAC GATACTAACG GATTCCCGAT	60
	TACCTGGTTT TATCCATTAG GTGAAAAGAA AGTTGAACGT AAGGCACCAA AATTAGAAAA	120
	ATAATTAAAT AAAACAGCTT AATGATGTAA TGAAATTAGT GAGTTAATCA CTGACTTCTA	180
20	CGTCATTGAG CTGTTTTTT GTGCTTTGTT ACAAAGCATT ATTGAATTTA TTTTACGTGT	240
	TCATATTTTG AAACATCAAA GCCGTCTTGT TTAGCTTTGT TGATAATGTC TTTGATTGAA	300
	TGTAGTCCTT TATCGGCGAA GTATGATCTT AAGTTGTCTT TTGTAGCTTG GTCAGCATTC	360
25	TTATCTAATA ACACATCAAT ATAACTTAAT TCATGTTCTA AGAAGTTTGC ATCATCATGT	420
	AGTACGAGTC CATTTGAGA ATAAACTTT	449
	(2) INFORMATION FOR SEQ ID NO: 1281:	
30	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 289 base pairs(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1281:	
40	TATTTATATG TACTGATGAT GAAGTTTATT ATCTATCAAG TGGATCAAAT CCGAAATATA	60
	ATCAGTATAT GGGTGCATAT CATCTACAAT GGCATATGAT AAAATATGCA AAATCACATA	120
	ATATTAATAG GTATAATTTT TATGGAATAA CAGGCGTCTT TAGTAATGAG GCGGATGATT	180
45	TTGGTGTTCA ACAATTTAAA AAGGGTTTTA ATGCACATGT TGAAGAATTA ATTGGTGATT	240
	TCATCCAACC AGTAAAACCC ATTCCAATAT TAATnTGCCA AACCTnAAT	289
50	(2) INFORMATION FOR SEQ ID NO: 1282:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 402 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1282:	
_	ATTCAGGTCG AGGTGGCCCG GCTCCATGCA CCGCGACGCA ACGGGGGAGG CAGACAAGGT	60
5	ATAGGGCGGC GCCTACAATC CATGCCAACC CGTTCCATGT GCTCGCCGAG GCGGCATAAA	120
	TCGCCGTGAC GATCAGCGGT CCAATGATCG AAGTTAGGCT GGTAAGAGCC GCGAGCGATC	180
10	CTTGAAGCTG TCCCTGATGG TCGTCATCTA CCTGCCTGGA CAGCATGGCC TGCAACGCGG	240
	GCATCCCGAT GCCGCCGGAA GCGAGAAGAA CTAATTGATA CAACACTTTC TCAACCTGAT	300
	CTTCTTTACC TTCTACATAG CGCGTGAGCA GAACCATCTT GATGGCACAG CTAAATAATG	360
15	CAATGGGAAT GATGTATGAC ATTCGGGGTG CATAATTTCT CT	402
	(2) INFORMATION FOR SEQ ID NO: 1283:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 224 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1283:	
	TATTGACAAC CAGAGTACAA ACAGCAGCTA TATTATAGAC TTAGGTCTGA AGTGGTAGTG	60
30	GCGGTGGACT ATTGTTGCGA CTGGACACCC GAGATATTGC TCAGCANAGC ATCATATACA	120
	GGAAGTATTA AAAGAGACTT GnCGAGTAAC AAATACTGAA GTAATAAGAT TAAAAGAGTG	180
	AGGTGTATAA TTATCCTCGT TCTTTTATAT TAGTATGATA GAGA	224
35	(2) INFORMATION FOR SEQ ID NO: 1284:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 146 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	RAM CONTRACTOR CONTRAC	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1284:	
45	CGTGGGAGAT TGTGCATATT GATTATGCAA GGAAGNACGC CATAAAAGTG GATGGCCAGA	60
	CATCATTAAT ATTATTGATA CCACATCAGA AGGTATTCAA AGTGAATCGG TGATAAGTGA	120
50	ATCAATTAAG TCTGCCAAAG AAAAGA	146
	(2) INFORMATION FOR SEQ ID NO: 1285:	

5	(A) LENGTH: 137 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1285:	
10	ATTTCGCGTG ACTGGACTTG GATCCGCAAC TTGGTAATTT AAGGAATTCT TGTCATTATA	60
	AGCCCTCCAT TTCATGATTT GATTTGCCAC TCGGTAACCA TTGGGGTTAC AGCTTCACTA	120
	GGGGANATAC GAACCTC	137
15	(2) INFORMATION FOR SEQ ID NO: 1286:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 594 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1286:	
20	GCTATTGATT ATGGTTAGCm TGTTGTTCwC TTTACTCATT GTTCCTTGGt TAAGCTCrAA	60
	AAAAGCACGT ACTTTAAAGA AACATGCAGC TAATGAACAG GCCCGATTTT TAAATCATTT	120
30	TTATGATTAT AAAGCTGGTA TGGATGAACT ACGTCGATTT AATCAAATTA ATCATTATCG	180
	AGATAATTTG ATGGCTAAAT TAAATCATTT TGATAAATTA CAACTTAAAG AGCAACGCTT	240
	TTTAACGATT TATGATTTTA TATTAAATAT TATTGCTATG CTTTCGATTT TTGGTAGTTT	300
3 5	AGTTCTAGGA TTAATTCAAA TTAATGCAGG CCAACTAAAT ATTATTATA TGACGAGTAT	360
	AGTTTTAATG GTCTTAACTT TATTTGAACA AGCTGTACCA ATGACAAATG TCGCGTATTA	420
	TAAAGCGGAT ACTGACCAAG CATTGCACGA TATTAATGAA GTGATATCTG TACCTTCTAC	480
40	TAATGGAAAA AAACGTCTTA ATGATAAGTA TGATGCAACG AACATTTATG AAGTTAAGGA	540
	TGCTAGTTTT AAGTATTGGA ATCAGCAAAC GTATGTnTTG TCGGATATTn ATTT	594
45	(2) INFORMATION FOR SEQ ID NO: 1287:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 233 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
50	(D) TOPOLOGY: linear	
	·	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1287:

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	TGAAGTAGTA ATAAACCCGG AACCCTAAAA CTGGATGGAG GATGAAACCA AAAAGGAACC	120
5	AGCCAAGCCA AATTGGGGAA ACCAGGACGG CCCAATGGAG GTCCAACCAA TCCAAACCCC	180
	ATTCCGCTAA TGnCTATGGG TCCCAATTAG GAATCCAATG GATGGATGGA TTn	233
	(2) INFORMATION FOR SEQ ID NO: 1288:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 132 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	·
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1288:	
	AATCCCTGTA CGTTCGTAAA GCTAGCTGGn TAATAAAAAA GAGTCTGGAA AGTAGGCAAC	60
20	AATCAATGAC AATGAGCAGA TCCAATCGCA GTATGCTTAC TCGTGTAAGA AACGCAAACA	120
	TGGTGCGTCA CG	132
25	(2) INFORMATION FOR SEQ ID NO: 1289:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 154 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1289:	
35	TATCTGATAA TTCTGTACCC AGGCGTTTTA ATATGTTTAT CTGGTGTCAT GATACATAAA	60
	CATTGTACCT TTAGGTCATA CGATGTCGCA AATAACTGCT CTTGCCGTTA CAACACCATT	120
	ACGGTTATAC ACTTNTAGCC AATCATTATC TGGG	154
40	(2) INFORMATION FOR SEQ ID NO: 1290:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 145 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1290:	
	AAAAGTGGCA CATGCGGCTG TAAAGTCCTC TGTTTCTGAT AAATCATAAC CTATATACAT	60
	GTCTACCTTC CAACTCATCT AAGAAATAAG TCATATTTTT TTGAATGTTG GATAATCAAT	120
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(2) INFORMATION FOR SEQ ID NO: 1291:

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 360 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1291:	
	CTTAATGCTA TATATTCTTT GTTTTTGATA CCATTTCATC GTCTTCTCTT GATTTCTAAA	60
15	CAATTTAGAA AATAAAAGAA TATACGCTTC AGACTTATTA AAACCCGCTA TATCATCTTG	120
	ATATTGTATT AACAATTGAG TAAAGCTGTG TATTAAGTCA TCTTTCTTCG ATGCAATGGT	180
	AGTTAATGAT TTTACACGAT AAGCATATTT ATCTGTAAAT AACTTAGCAA CTACCCCACC	240
20	TAAATCATGT CCTAGAATAT GTGCCTCATG AATATTTAAC TTCTCCATTA GAATTTTAA	300
	ATCCTCAACG TGATCGTTTA AATCGTATGA TTCACTTTTA GAAGACTTGC CATGACCTCT	360
25	(2) INFORMATION FOR SEQ ID NO: 1292:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 164 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1292:	
35	TGTGTTAGTT GTTTATGTTG TTGATATATA CTGCTCGTGC ACATGGTACC CAGACGATTC	60
	AACGNTGAGT ACACAAAATA CAAAATCTAC GGCACATGGT ACCGTTTATA AAAGATGTGG	120
	AACCTTACTA GCATTTGTTG AGAACGCTAC ACGTTTAAAT CAAG	164
40	(2) INFORMATION FOR SEQ ID NO: 1293:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 132 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1293:	
	TTAATTTTCT ATATATTTCT TAGGTTATAT TGGTATCTAT GCCAGTAAGT GACATGACGT	60
	TAGATCATTG AATCCAAGAT CGANACATTG GGACATATTT ATTAACGACA TGGCTTCAAC	120

	(2) INFORMATION FOR SEQ ID NO: 1294:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 213 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1294:	
	GTCATGCnTA ACAGGTGAAT ACCTAGTAAT TCAGATATTA TCATTTATAT ACCCTCTTAT	60
15	ATTTTAGTGC ATTATCTCGA AATCGAGATA CTTAATGTAA ATTTTTAGTG CAGCCTACAC	120
	TTCGTGATTG GGCAnTAGTT CTTAAACGCT GTGGTAAGAT GTTAATTCAT CCTTGGTTAA	180
	CACACAAACG CTTGGTTAAT GCTCAGCAGC TAG	213
20	(2) INFORMATION FOR SEQ ID NO: 1295:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 163 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1295:	
	AAGAAGTTTG AAGTCTATGA AAACAATCAA AAATTGCCAG TGAGACTTGT ATCATATAGT	60
	CCTGTACCAG AAGACCATGC CTATATTCGA TTCCCAGTTT CAGATGGCAC ACAGATGAAA	120
3 5	TGTTTCTCGn CCAATGAGAG GGAGAACATA GTATCAATAG ATG	163
	(2) INFORMATION FOR SEQ ID NO: 1296:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 207 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1296:	
	TAGCTTTAAT ACATTCTGAT TTTTAAACGC TTCGAAATGT TTTCAGTAAC TAATTTTGCC	60
50	ATAATCCCAA AAACTCCTTG ATTATTAACT GCnTTTTGAT TGGCTACATT AAGGCTTTAT	120
	ACACATCAGC TCACCATGCC CATATCTACT AATGGTTATA TCCCTAGAGT CCCAGCGATA	180
<i>55</i>	TAACATCAAC GCTTACnGGA GTTTCAG	207

5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 145 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1297:	
10	ATGGCATCGG TTGGTTATGA AAAGnCAAGC CATGGGGAGG CCATATTTGG GGTGGAATCA	60
	TACCTGGAAC CTTTGGTGCC TACCACCAAT TGGTAACGGT TTTACCATCG GATTTTTAGT	120
15	GATACAGCGA TATGTTTTGT ACAGG	145
	(2) INFORMATION FOR SEQ ID NO: 1298:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 139 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1298:	
	TCCAAAAGTT AAAGGTCAAT TGAAACAGAN AAAGCTTATT ATGTCTGGAA AAGTATTAAA	60
20	AGTAATGGTA TCAAATGACA TTGAACGTAA TCATTTTGAT AAGGCATGTA ATGAAGTCTT	120
30	TCAAGCGTTG AATTGTGGT	139
	(2) INFORMATION FOR SEQ ID NO: 1299:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 399 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1299:	
	GATATTGGCA ACCTTCAGCC GATGACCTCA TGGCAAATGA TTGGGAAGTT ATAAACCCAA	60
45	CTAGAGACCA GGAATTATTG AAGCAATTAT AGAAATGCTA TCAATGATAC TTTTTAAATT	120
	GTTTTTAAAC TCATTTCAA AGTAAACAAC AGTCTTGTCT GAAATTGTTA CATGATAAAT	180
50	AGTGTTACTA GCATACACGC CGTTTAGGAA CCCAGAGTTT TTAAGTTTAT TTAAATCGTA	24
	TTTTACATCT TCGAAATGTA GTTTTTGAAA ATACTTTGTA TGTATATCTT TAGCACTTCC	30
	AAAATTTATT GGCAGGTTAA TTTAATCGAA CCTAACTTTA CACATTCTAA ATAATCTTTG	36

(2) INFORMATION FOR SEQ ID NO: 1300:

5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 693 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1300:	
	CTACAGTGCA ATTTAACCAT GAAGTTGTTG ATTTTGAACA ATTATCAAAT GGTCAATGGG	60
15	AAGTTACTGT TAAAAATCGC CTAACTGGTG AGAAATTCAA ACAAGTAACT GACTACGTAT	120
	TCATCGGTGC TGGCGGTGGA GCAATTCCAT TATTACAAAA AACAGGTATC CCTGAAAGTA	180
	AACATTTGGG TGGATTCCCT ATCAGTGGTC AATTCTTAGC TTGTACAAAC CCACAAGTTA	240
20	TTGAACAACA CGATGCCAAA GTTTATGGTA AAGAGCCACC TGGTACACCA CCAATGACTG	300
	TACCTCATTT AGATACGCGT TACATTGATG GTCAAAGAAC ATTATTATTT GGACCATTTG	360
25	CTAATGTTGG ACCTAAATTC TTGAAAAATG GTTCTAACTT AGATTTATTC AAGTCTGTTA	420
20	AAACATACAA CATTACAACT TTATTAGCAG CAGCAGTNAA AAACTTACCT TTAATTAAAT	480
	ACTCATTTGA CCAAGTAATT ATGACAAAAG AAGGTTGTAT GAACCACTTA CGTACTTTCT	540
30	ATCCAGAAGC ACGTAATGAA GATTGGCAAT TATACACTGC TGGTAAACGT GTACAAGTTA	600
	TCAAAGATAC ACCTGAACAC GGTAAAGGAT TCATCCAATT CGGTACAGAA GTGGTTAACT	660
	CACAAGACCA CACTGNAATT GCATTATTAG GTG	693
35	(2) INFORMATION FOR SEQ ID NO: 1301:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 471 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1301:	
	CATACTTGGG TAATGCTGCC CATGGNACGC TGGNACAAGG TAAAGTTGCA CGTTTAATTT	60
	GTGNATGTAT ATAAAACAGA TGGGAACACC ATTTGAAGGG GATCCTCGTG CAAACTTAAA	120
50	ACGTGTATTA AAAGAAATGG AAGATTTAGG CTTCACAGAC TTTAACCTAG GACCTGAACC	180
	AGAATTCTTC TTGTTTAAGT TGGATGAAAA AGGGGAACCA ACTTTAGAAC TTAATGATGA	240
	TGGTGGATAT TTCGATTTAG CACCTACAGA TTTAGGTGAA AACTGTCGTC GTGATATTGT	300
55		

TITAAATTGG TIGTTAAAAC AATCGCACGT AAACATAATT TACACGCAAC A (2) INFORMATION FOR SEQ ID NO: 1302: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1302: CATGTGATTA AGAACGTTCA CTGATGAATT TTGATGATC GTTCGGTTTT TGTTTGGATT TTAATGATTA TITATACAAA AACAGCCGTA TTTCAAGCCG TACATTTTAA ATTTAACTAA ATTTGCATCT AGTTAATAAT TGCATTTATC AAATTTGTCT TATTGATCCA ATCTAATTTG TACTCACAAA CTAGTTTTAA ATCCTAACTT TATCTCTCAG TTCGTTATCA ATCATCAGAC ATAAACCAAT GAAGCAATCA GAAAACACTC TAATTTTCTA TTAGAAATTT GGTTTAATAT GCTTGGTGAT CTNTTATTCT GCGTAATAAT GCTAAACCTG (2) INFORMATION FOR SEQ ID NO: 1303: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 128 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303: 40 AAAAGACTGG GGTAAACTTC AACGTATCTT AGCTACTGAA GGTGCAGAAG TTTTAGAAGC AAAAGACTGG GGTAAACTTC GCCTAGCTTA TGAAATCAAT GGATTTCAAA GATGGGCTCT ACACACTC (2) INFORMATION FOR SEQ ID NO: 1304: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	CATGIGATAA TATCCAAACA 420	TCAACATGAA ALTGACTTAA ATATG
(2) IMPORMATION FOR SEQ ID NO: 1302: (a) SEQUENCE CHARACTERISTICS: (b) TYPE: nucleic acid (c) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1302: CATGTGATTA AGAACGITCA CTGATGAATT TITGATGATC GTTCGGTTTT TGTTTGGATT TTAATGATTA TITATACAAA AACAGCCGTA TITCAAGCCG TACATTTAAA ATTTAACTAA ATTTGCATCT AGTTAATAAT TGCATTTATC AAATTTGTCT TATTGATCCA ATCTAATTTG TACTCACAAA CTAGTTTAAA ATTCTAACTT TATCTCAG TTCGTTATCA ATCATCAGAC ATAAACCAAT GAAGCAATCA GAAAACACTC TAATTTCTA TTAGAAATTT GRITTAATAT GCTTGGTGAT CTRITATTCT GCGTAATAAT GCTAAACCTG (2) INFORMATION FOR SEQ ID NO: 1303: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 128 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303: 40 AAAAGACTG GGTAAACTTC AACGTATCTT AGCTACTGAA GGTGCAGAAG TTTTAGAAGC AAAAGACTG (2) INFORMATION FOR SEQ ID NO: 1304: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	TACACGCAAC .A 471	TTTAAATTGG TTGTTAAAAC AATCG
(A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1302: CATGTGATTA AGAACGTTCA CTGATGAATT TTTGATGATC GTTCGGTTIT TGTTTGGATT TTAATGATTA TTTATACAAA AACAGCCGTA TTTCAAGCCG TACATTTTAA ATTTAACTAA ATTTGCATCT AGTTAATAAT TGCATTTATC AAATTTGTCT TATTGATACCA ATCTAATTTG TACTCACAAA CTAGTTTAAA ATCCTAACTT TATCTCTCAG TTCGTTATCA ATCATCAGAC ATAAACCAAT GAAGCAATCA GAAAACACTC TAATTTCTA TTAGAAATTT GNTTTAATAT GCTTGGTGAT CTNTTATTCT GCGTAATAAT GCAAAACACTG (2) INFORMATION FOR SEQ ID NO: 1303: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 128 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303: 40 AAAAGACTGG GGTAAACTTC AACGTATCTT AGCTACTGAA GGTGCAGAAG TTTTAGAAGC AAAAGACTGG (2) INFORMATION FOR SEQ ID NO: 1304: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double		(2) INFORMATION FOR SEQ ID
CATGTGATTA AGAACGTTCA CTGATGAATT TTTGATGATC GTTCGGTTT TGTTTGGATT TTAATGATTA TITATACAAA AACAGCCGTA TTTCAAGCCG TACATTTTAA ATTTAACTAA ATTTGCATCT AGTTAATAAT TGCATTTATC AAATTTGTCT TATTGATCCA ATCTAATTTG TACTCACAAA CTAGTTTAAA ATTCTAACTT TATCTCTCAG TTCGTTATCA ATCATCAGAC ATAAAACCAAT GAAGCAATCA GAAAACACTC TAATTTTCTA TTAGAAATTT GNTTTAATAT GCTTGGTGAT CTNTTATTCT GCGTAATAAT GCTAAACCTG (2) INFORMATION FOR SEQ ID NO: 1303: (i) SEQUENCE CHARACTERISTICS:	-	(A) LENGTH: 400 h (B) TYPE: nucleic (C) STRANDEDNESS:
TTAATGATTA TITATACAAA AACAGCCGTA TITCAAGCCG TACATTITAA ATTTAACTAA ATTTGCATCT AGTTAATAAT TGCATTTATC AAATTTGTCT TATTGATCCA ATCTAATTTG TACTCACAAA CTAGTTTAAA ATTCTAACTT TATCTCTCAG TTCGTTATCA ATCATCAGAC ATAAACCAAT GAAGCAATCA GAAAACACTC TAATTTCTA TTAGAAATTT GOTTTAATAT AAAAAAACAG GCTTACTTCA TATAATTTAT GAAATAAACC CGTCAATTTT TGTTTAATAT GCTTGGTGAT CTNTTATTCT GCGTAATAAT GCTAAACCTG (2) INFORMATION FOR SEQ ID NO: 1303: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 128 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303: 40 AAAAGCTTAG TTGAACTTC AACGTATCTT AGCTACTGAA GGTGCAGAAG TTTTAGAAGCC AAAAGACTGG GGTAAACTAC GCCTAGCTTA TGAAATCAAT GGATTTCAAA GATGGGCTCT ACAACATC (2) INFORMATION FOR SEQ ID NO: 1304: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	1302:	(xi) SEQUENCE DESCRIP
ATTTGCATCT AGTTAATAAT TGCATTTATC AAATTTGCT TATTGATCCA ATCTAATTTG TACTCACAAA CTAGTTTAAA ATTCTAACTT TATCTCTCAG TTCGTTATCA ATCATCAGAC ATAAACCAAT GAAGCAATCA GAAAACACTC TAATTTTCTA TTAGAAATTT GNTTTAATAT AAAAAAACAG GCTTACTTCA TATAATTTAT GAAATAAACC CGTCAATTTT TGTTTAATAT GCTTGGTGAT CTNTTATTCT GCGTAATAAT GCTAAACCTG (2) INFORMATION FOR SEQ ID NO: 1303: (i) SEQUENCE CHARACTERISTICS:	GTTCGGTTTT TGTTTGGATT 60	CATGTGATTA AGAACGTTCA CTGA
TACTCACAAA CTAGTTTYAA ATTCTAACTT TATCTCTCAG TTCGTTATCA ATCATCAGAC ATAAACCAAT GAAGCAATCA GAAAACACTC TAATTTTCTA TTAGAAATTT GNTTTAATAT AAAAAAACAG GCTTACTTCA TATAATTTAT GAAATAAACC CGTCAATTTT TGTTTAATAT GCTTGGTGAT CTNTTATTCT GCGTAATAAT GCTAAACCTG (2) INFORMATION FOR SEQ ID NO: 1303: (i) SEQUENCE CHARACTERISTICS:	TACATTTAA ATTTAACTAA 120	TTAATGATTA TTTATACAAA AACA
ATAAACCAAT GAAGCAATCA GAAAACACTC TAATTTTCTA TTAGAAATTT GNTTTAATAT AAAAAAACAG GCTTACTTCA TATAATTTAT GAAATAAACC CGTCAATTTT TGTTTAATAT GCTTGGTGAT CTNTTATTCT GCGTAATAAT GCTAAACCTG (2) INFORMATION FOR SEQ ID NO: 1303: (i) SEQUENCE CHARACTERISTICS:	TATTGATCCA ATCTAATTTG 180	20 ATTTGCATCT AGTTAATAAT TGCA
AAAAAAACAG GCTTACTTCA TATAATTTAT GAAATAAACC CGTCAATTT TGTTTAATAT GCTTGGTGAT CTnTTATTCT GCGTAATAAT GCTAAACCTG (2) INFORMATION FOR SEQ ID NO: 1303: (i) SEQUENCE CHARACTERISTICS:	TTCGTTATCA ATCATCAGAC 240	TACTCACAAA CTAGTTTrAA ATTC
GCTTGGTGAT CTnTTATTCT GCGTAATAAT GCTAAACCTG (2) INFORMATION FOR SEQ ID NO: 1303: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 128 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303: AAAAGCTTAG TTGAACTTTC AACGTATCTT AGCTACTGAA GGTGCAGAAG TTTTAGAAGC AAAAGACTGG GGTAAACTTC GCCTAGCTTA TGAAATCAAT GGATTTCAAA GATGGGCTCT ACAACATC (2) INFORMATION FOR SEQ ID NO: 1304: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	TTAGAAATTT GnTTTAATAT 300	ATAAACCAAT GAAGCAATCA GAAA
(2) INFORMATION FOR SEQ ID NO: 1303: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 128 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303: AAAAGCTTAG TTGAACTTTC AACGTATCTT AGCTACTGAA GGTGCAGAAG TTTTAGAAGC AAAAGACTGG GGTAAACTNC GCCTAGCTTA TGAAATCAAT GGATTTCAAA GATGGGCTCT ACAACATC (2) INFORMATION FOR SEQ ID NO: 1304: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	C CGTCAATTIT TGTTTAATAT 360	25 AAAAAAACAG GCTTACTTCA TATA
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 128 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303: 40 AAAAGCTTAG TTGAACTTTC AACGTATCTT AGCTACTGAA GGTGCAGAAG TTTTAGAAGC AAAAGACTGG GGTAAACTTC GCCTAGCTTA TGAAATCAAT GGATTTCAAA GATGGGCTCT ACAACATC (2) INFORMATION FOR SEQ ID NO: 1304: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	g 400	GCTTGGTGAT CTnTTATTCT GCGT
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 128 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303: 40 AAAAGCTTAG TTGAACTTTC AACGTATCTT AGCTACTGAA GGTGCAGAAG TTTTAGAAGC AAAAGACTGG GGTAAACTTC GCCTAGCTTA TGAAATCAAT GGATTTCAAA GATGGGCTCT ACAACATC (2) INFORMATION FOR SEQ ID NO: 1304: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double		
AAAAGACTTAG TTGAACTTTC AACGTATCTT AGCTACTGAA GGTGCAGAAG TTTTAGAAGC AAAAGACTGG GGTAAACTNC GCCTAGCTTA TGAAATCAAT GGATTTCAAA GATGGGCTCT ACAACATC (2) INFORMATION FOR SEQ ID NO: 1304: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double		(i) SEQUENCE CHARACTE (A) LENGTH: 128 (B) TYPE: nuclei (C) STRANDEDNESS
AAAAGACTGG GGTAAACTnC GCCTAGCTTA TGAAATCAAT GGATTTCAAA GATGGGCTCT ACAACATC (2) INFORMATION FOR SEQ ID NO: 1304: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	1303:	(xi) SEQUENCE DESCRI
ACAACATC (2) INFORMATION FOR SEQ ID NO: 1304: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	A GGTGCAGAAG TTTTAGAAGC 60	40 AAAAGCTTAG TTGAACTTTC AAC
(2) INFORMATION FOR SEQ ID NO: 1304: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	AT GGATTTCAAA GATGGGCTCT 120	AAAAGACTGG GGTAAACTnC GCC
(2) INFORMATION FOR SEQ ID NO: 1304: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	128	
(A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	,	(2) INFORMATION FOR SEQ I
		(A) LENGTH: 141 (B) TYPE: nucle (C) STRANDEDNES

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	TCCTTCGGAT TCTAAATGGC ATTGGACAGT GTTTACAAGC TCGCATTTCT CCACTTTTTG	60
_	CAATTTCTTT TACAATTTCT AAAGCTTCAT CAAAGTTTCC TTCAATAGNA AACGATTTCT	120
5	GCACCATACA TTACTGACTT G	141
	(2) INFORMATION FOR SEQ ID NO: 1305:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 162 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1305:	
	GACTGGTAAA CACTAAGTGA ATTAGCTGGA CAATGAAAAA TATCCACAAT CATTAATTAA	60
20	CGTACGCGTA ACAGATAATA TCGGTTGAAG AAATGTTGAC GTTAAGAGTT ATGACTAAnT	120
	AGAGTAGAAT GATGGTGAGG TCGATTTTAG TAGACTCTGG AC	162
25	(2) INFORMATION FOR SEQ ID NO: 1306:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 282 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1306:	
35	TTCTTAGTTG CTCGAACTAA TAATTTGCTT AATAATGATS TAGCTGTTAT TGTGTCATAT	60
	TCTAAAGGTG CCATAAATTT AAAAACTATA GTAGTTGTTT TAAATTTAGT TGTTGGTGAA	120
	ACTTTGATAT GTATATTTGG TTGAGATTGT CTACTCAAAT ATATAGCCTC CTCTATATCT	180
40	TCTTACATCT ATATTTTTCT AGTGATTTTA AATTGAACTA AGCTATTTTT CATATAATTT	240
	AATGAATACA AAATAGGTTC ATCTGATTCA TTATAGTGCG TA	282
45	(2) INFORMATION FOR SEQ ID NO: 1307:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 276 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1307:	

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AAGGAAAAA CCCTTGGCCT TTGGAAAAAA CCCAAAAGGA AAGGGGTTTA AAAAAAAAA	120
AAGTTTAACC CGGTTGGCCC CAATTCCCGC CCGGGGAACC CAAAAGGAnT TTTAAAAAAG	180
GAAACCCAAT TCCCGGCCGG AAAAGGGTTT TTAAGCCCAA CCGGATTTTA AGGAAAACCA	240
TTTTAAGATT ACCTGGGAAA AAAAACCGTT TAGGAA	276
(2) INFORMATION FOR SEQ ID NO: 1308:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 692 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1308:	
TGTATTTAAT GCTCGTACAC ACAATTACAA AACTGCAAGA GAAAAAGCAT TGAGTAATAA	60
TCATATTCCA GAAAATGTAT ATGACAATCT AGTAAAAACT GTACATAAAT ATTTACCATT	120
GCTACATAGA TATACTGAAT TGCGCAAAGA ATTGCTAGGT TTAGATGACT TGAAAATGTA	180
TGATTTATAT ACACCATTAA TTAAAGATAT TAAGTTTGAA ATGCCTTATG AAGAAGCTAA	240
AGAGTGGATG TTAAAAGCAT TAGAACCAAT GGGTGAAGAA TATTTAAATG TAGTTAAAGA	300
AGGCTTATAC AATCGTTGGG TCGATGTCTA TGAGAATAAA GGTAAACGTT CAGGTGGCTA	360
TTCATCAGGT GCACATTTAA CTAATCCATT TATTCTACTT AACTGGTCTA ATACTATTTC	420
AGACTTATAC ACATTAGTTC ATGAATTTGG GCATTCAGCA CATAGTTACT TCAGTAGAAA	480
ATTCCaACCG TCaAATTCtA GTGACTACaC TATTTTTGTC GcTGAAGTTG CaTCAACTTG	540
TAACGAAGCA CTTTTAAGTG ATTATATGGA TAAACATCTT GATGATGAAA AACGCTTATT	600
ATTATTAAAC CAAGAATTAG AnCGTTTCAG AGCTACATTA TTCCGACAAA CAATGTTCGC	660
AGAATTTGAG CATAANATTC ATGCAATTGA AG	692
(2) INFORMATION FOR SEQ ID NO: 1309:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 151 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1309:	60
CONCENTRACE ATCATACCTT TTTTGACTGG ATTTACTAAA ATGAAAGCAA GTACTATATA	61

	atCGAGTAAT ATCTATATAT GACATTTTAA A	151
	(2) INFORMATION FOR SEQ ID NO: 1310:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 115 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1310:	
15	TGTGCATTTG ATAATATTCA CTATGATTCG TGGTCATTCA CATCGTCTAC GCTCACCGGT	60
	CTAAACGTAC CTAACCCAAC ATGTAATGAA CAAATGCGAT ATTANCACCT TTATT	115
	(2) INFORMATION FOR SEQ ID NO: 1311:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 164 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1311:	,
30	CACCCAACTG ACCTCAATGG TATAATGCAT TTGTGAATAC CGAATATCAT TGGAATATCT	60
	CCTATCATAG GAATATAATA TGTATATATC TTCGTAATCn TGTTCATTTT TAAGAAAATC	120
	AATAGAAGTG TATCGATTAA AACTACATTT GAACCATTAC TTTG	164
35	(2) INFORMATION FOR SEQ ID NO: 1312:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
		·
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1312:	
40	GAGGAAAATC GAAGTGAAAT TATTAAAATA TGGCGATGGT GGAATACGAA TAGATGGTGG	60
	TTTAATAGGC GGCTTTATTC GGGTGTTATT GTATGTAAAG TGAAAAATTT AAnCCCATTT	120
50	CAAATTGGTG ATATCGTTGC G	141
	(2) INFORMATION FOR SEQ ID NO: 1313:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 133 base pairs	

(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1313:	
	AATTGGTATT ATGCATAGTG CAATGGATGC TGGTATTAAA nTCCAGAGGA TTACAATTAT	60
10	TAGTITCAAT AATCACGATT AGTTGAGATG GTTAGCCACA ACTTTCTAGT GTATCACCAT	120
	TATATGTATC GGT	133
	(2) INFORMATION FOR SEQ ID NO: 1314:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 629 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1314:	
25	TTGCAATTAG AATGCTGTTT CACCCCTTTA AACCATACTA TATATTTAAA TTTAGAGTCC	60
	CATTTACACC AGGTTTAATA CCGAAAAGAC GCGAAGAAAT TGCAACTAAA ATTGGCCAAG	120
	TGATTGAAGA GCATTTGCTT ACAGAAACTT TAATTAATGA AAAATTGAAA AGCGAGCAAT	180
30	CACAGCAAGC AATAGAATCT ATGATTCAAC AGCAGTTACA AAAGTTGACG AAAGATCAAT	240
	TGTCAATAAA ACAAATTACT TCTCAAATCG LATTGATTTA GAACAAGTAT TACAAACTAA	300
	TGGAAATCAA TATATTGAAT CACAATTGAA TAATTATTAT aCAAAGCATC AAAACCAAAC	360
35	AATAGCATCT TTATTGCCAA ATCAACTTGT AACATTTTTA AATCAGCATG TAGATAACGC	420
	AACAGACTTA TTATGTGATC GTGCAAGGAA TTATTTATCA TCTGCAAAAG GCACACAAGA	480
	TATTAATGAT ATGTTGGATA CTTTTTTCAA TGAGAAAGGT AAGTTAATTG GTATGTTGCA	540
40	AATGTTTATG ACAAAAGAGA GTATTGCAGA TCGCATTCAA CAAGAACTTA TACGTTTAAC	600
	ATCTCATCCT AAAGCAAGAA CAATTGTGA	629
45	(2) INFORMATION FOR SEQ ID NO: 1315:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 399 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1315:	

	ATACAGGTAC GTTCGTTATC AATGGTGCAG AACGTGTAAT CGTATCTCAA TTAGTTCGTT	120
	CACCATCCGT TTATTTCAAT GAAAAAATCG ACAAAAATGG TCGTGAAAAC TATGATGCAA	180
5	CAATTATTCC AAACCGTGGT GCATGGTTAG AATATGAAAC AGATGCTAAA GATGTTGTAT	240
	ACGTACGTAT TGATAGAACA CGTAAACTAC CATTAACAGT ATTGTTACGT GCATTAGGGT	300
10	TCTCAAGCGA CCCAAGAAAT TGnTGACCTT TAAGGGGACC AATGGAATAT nTACCGTAAT	360
	ACCTTTAGGA GGAAAGACCG GCACCTGAAA CCACTGGAA	399
	(2) INFORMATION FOR SEQ ID NO: 1316:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 778 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1316:	
	ATAAACATTT TAANATGTAA TTNAGAAATT TTTTTAGTAC AAAATCTTTC TTAATAATGA	60
25	TTAAGGAGGT CAGTAATGAT TGAAATTAAA ACATTAACGA ATAATGATTT TAATGAGTAT	120
	AAGAGACTTG TTTCGACAGT CAATGAAGAA TTCACTCAAG ATTCACATTA TAGTCAAACA	180
30	ATGACLGACA CCTTAATACA TGACATTTTA AATCAAGGTT CACCGAAATG TATTGTATTT	240
	GGCTGTTATG AAAACGAAAC ACTTATCGCA ACAGCTGCCT TAGAACAAAT TCGATACGTT	300
	GGAAAAGAAC ATAAATCATT AATTAAATAC AACTTTGTTA CTAATAACGA TAAATCGATT	360
35	AATAGCGAGC TCATTAATTT CATTATTAAT TATGCACGGC AGAACAATTA CGAATCTTTA	420
	CTTACATCAA TTGTGTCAAA CAACATAGnn GCTAAAGTTT TCTATAGTGC ACTAGGATTC	480
	GACATTCTTG GTTTTGAGAA AAATGCAATT AAAATCGGAA ATACCTATTT CGATGAACAT	540
40	TGGCTTTTT ATGATTTGAT TAATAAGTAA TACAGTTTTA TATATTCTAC +TTTCTCATA	600
	AATTCAAATC ATATAGGTTC TATTTTCAT ACAACTACTC TACTATTGAG TAGTTGTTTT	660
45	TTATTTGATA TGATAACAAT AAGTTTTTTT CAGAATATTC TATGTTTTAG GGGTGTCAAA	720
45	ACTTAATGGG TAACCGCAAT TATTCATGGA nTTATCNTAA GCGATTGGGT CCTAANTT	778
	(2) INFORMATION FOR SEQ ID NO: 1317:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 465 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1317:	
	TGCACAAGGT GGTGCAGCAA TTGCAGCGTT CTTTATTATT AAACAAAATA AGAAGTTAAA	60
5	AGGTGTGGCA TCTGCCGCAG TATTTTCAGC ATTACTTGGT ATTACAGAAC CGGCTATGTT	120
	TGGTGTTACT TAAAACTAAG ATATCCATTT ATTGGCGCTA TCGTTGGATC AGGTATTGGT	180
	TCAGCATATA TTGCTTTCTT CAAGGTTAAA GCAATCGCAT TAGGAACTGC TGGATTGCCA	240
10	GGATTLATTT CAATCAATCC AGTACATGCA GGATGGTTAC ACTACTTTGT TGGTATGACA	300
	ATATCATTCA TCATTGCTAT AACAGTTACT TTAALTTTAT CLAAAAGAAA AGCAAATAAA	360
15	GAAGTTGTAG AATAAAAAA GAGGTATGAC AGTAATCAAA GTATCAGTCA TTGCAAATGC	420
	AATAGGATGA AACTTTAAGC TGTCATACCT TTNAATTTAG TTATA	465
	(2) INFORMATION FOR SEQ ID NO: 1318:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 150 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1318:	
	GACTTAATAT AACTGATCTT TTGCTATTAT TGAAACATAT TTATAAAGAA AATAGCATTG	60
30	CATAATACCC AAGCAATAAA TACTATAATA TTTTGGAAGT AACTAATCAA ACATCTAAGA	120
	CATGATTGAT AnCACCACAG AAAAATAAGA	150
35	(2) INFORMATION FOR SEQ ID NO: 1319:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 131 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1319:	60
45	CCACCTTTTA ACGTACGTAT CCATGAATCA TATGATTAAT TTAATATCAT TATTACTTAT	120
	TTCTTATCTT TATTNTCTTT TTTTCTTCTG AAAAGTAGTA ATGAACCTAT TGATGCTAAT	131
50	AATCCCCAAA T	
50	(2) INFORMATION FOR SEQ ID NO: 1320:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 140 base pairs	·

(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5	(wi) CROVENCE PROGRESSION OF THE WAY	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1320:	
	TAGTGTCCAA ATGAAAGTGT GGCTACCTAT AGCTGGTCCA TGAAGCTTTA TTTTTAACTG	60
10	GTTTGTACAA TATTTAAATA TCAAAATCTT CTCGCGnTTT GGACAGTTTT TTTGGTATTA	120
	ACCATTAATA AACGGAAAGA	140
	(2) INFORMATION FOR SEQ ID NO: 1321:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 140 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1321:	
25	CTTATTATAT AATTCTAATC CTAGTACATT ATACATTTTA TCAAATAGTC AACTGGATAA	60
	CTTTGAAAGT GAATGATnCT TTTAAAATAA AGAAGATAAT ATAAAGTGCT TGATAATGGA	120
	TTTGTAGTTG ATGATTTAAA	140
30	(2) INFORMATION FOR SEQ ID NO: 1322:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 185 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1322:	
	TCGTTGCAAC ACAGGCACTA TTTTACCTTT ATATGTTGTA ATAGTTTGAT TGCTGCCATT	60
	TAAACAACCA CCTTTCTTAC TCCACAAATT TACCATGAAT AGCGCGCGCG CCATAGCGGG	120
45	ATACTAAAGT GTTCTGCACC TTGCCTGTCT CCTTCAAnTT TCGATTACTG TAGAGCACAA	180
	GTACG	185
	(2) INFORMATION FOR SEQ ID NO: 1323:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 148 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1323:	
	ACCTGCAATT TTCGTTATTC AAAACAATAA CTATGCAATT TCAACACCAC GGAGCAAGCA	60
5	AACTGCTGCT GAAACATTAG CTCAAAAAGC AATTGCTGTA GGTATTCCTG GGTATCCCAA	120
	GTTGGTGGTA TGGTGCGGTA nTTGGTTT	148
10	(2) INFORMATION FOR SEQ ID NO: 1324:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1324:	
20	GAAAGCATTG ATGGACAAAG ATGAACCACC AAATGAATGG CGATTAGATT CCAATTGATA	60
	TGGCTCACGG AAAATTTATG CTACAATTGC GTCCAGTAAA CAGTGGCACT AATAGTCCAC	120
25	TTANGCTCCC TAGTGGATGA A	141
20	(2) INFORMATION FOR SEQ ID NO: 1325:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 204 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1325:	
	TTATACTATC GTGAAGGGTT TATTACTCAA TTAATGCCTA AAAAGGATAA AAGTTATTTA	60
40	GTTATTGATA ATTTTAATCG TATAGATACA GACATTTTCC AAACGTATAT TAATGTGTTA	120
40	GAAGGCTATG AAGTAACATT ACCACGTTAT AATAAAGACG GTAATATGAT TAAATGGTCA	180
	CGACAAAAG ATTCTTTCTA TTAT	204
45	(2) INFORMATION FOR SEQ ID NO: 1326:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 147 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	A GROWENCE DESCRIPTION: SEO ID NO: 1326:	

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	TITGITAAAA GICITCATIT CGGATGAAGC TTTATCTATT GAACGCTCCA AATTATTTAA	120
5	AGCAGCTTTT TCTTTATTAA CAGCTGT	147
3	(2) INFORMATION FOR SEQ ID NO: 1327:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 530 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1327:	
	CATTNAATGA AGAAACTGAA CCCNGAACTA TACGACGCAG AAGGCAATTT AATTAATAAT	60
	AGTAAAACAT CCAGCTTAAT CCATTGATGT GTTATAAAAG TGAAAAGCTC CAATCAAAGT	120
20	TGACGCTCAA ATAGTTTAAC TTTGATCGGA GCTTTTTTAT AATGTATACC GAAAGGTTCA	180
•	AATATTATAT AATGGTAGAA TTGAAAGAGA ATATAAAAAA GTGAGGATAT AAAATGAAAG	240
25	TTAATCCTAA TAATATAGAA TTAATCATTA GTGCAGTAAA AGAAGAACAA TATCCAGAAA	300
	CAGAATTGTC TGAAGTGCAC TGAGCGGTCG ATCTAATGTA GGTAAGTCTA CATTTATCCA	360
	ATAGTATGAT TGGCAGAAAA AATATGGCAC GTACATCACA GCAACCCGGC AAAACGCAAA	420
30	CGTTAAATTT TTATAATATA GATGAACAAC TTATTTTTGT GGATGTTCCA GGGTATGGAT	480
	ATGCTAAAGT AAGTAAAACA CAACGTGAAA AATTTGGGAA AATGATTGAG	530
	(2) INFORMATION FOR SEQ ID NO: 1328:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 153 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40		
	(vi) SEQUENCE PROGREDATION ORD TO ME TO SE	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1328:	
45	AAGAAAGTTT GATCTAGGCC AACCTTTCTA ACAACGATAC GACAGTTTAA TAATGTCTCA	60
	TATCTTGACT TCCCATGATG ATATGGTCGT TAATCACATC AATGACTTAA ATCTGGATNA	120
50	ATAGATGCGA ATGGATCTTG AAAAATCATT GTA	153
	(2) INFORMATION FOR SEQ ID NO: 1329:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 115 base pairs (B) TYPE: nucleic acid	
<i>55</i>	(C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1329:	
_	TGTAGTTCGT TTGTGCTCTA ATTAAACGGT CGAAACCATG GATTAGACCT GCGATTACAA	60
5	CTGCAATGAT ACCTGAAGCA TGAACTTCTT CTGnTAAAAA GTATACGACA AAAGG	115
	(2) INFORMATION FOR SEQ ID NO: 1330:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1330:	
	AACAAGTTAT CTACATCTGC TGATAGGCAT ACTATTACTA ATAAATAATG CATCTTTTTG	60
20	CCAGATGTTT TCTTAATCAA TTGCACCAAC GAATGGCACT CTCATCTGTA Gn	112
	(2) INFORMATION FOR SEQ ID NO: 1331:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 203 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1331:	
	TTCATTGCAG ACAnTTGGTG AACCATGTGG ACGAACTAGT CCTAGATTAA GATAAGAGAT	60
35	TAGTGAnCAT TGCCACCACT GCAATTAAAC ATTCTTGGAA AAATTAACTT AAGTTAGAAT	120
	CTTAATGCAT ACAGATACGG CGAAGATGAT GCCAAAGAAC GTCACGACTT TATGATGATG	180
	ACTGAACCCA GTTTTTACGG AAG	203
40	(2) INFORMATION FOR SEQ ID NO: 1332:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 269 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1332:	
	ATGATGTACT AATATCTAAT AAGCTTGCTA AGTCTTGAGA CCTCATTTTA ATCACCTTTT	60

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	GACIAICIAI TICIGITAGI ACGTITGACA TATTAATCAC TCCACYTTAA CGCAATAWAW	180
	TTTAWTAGCG TTGGCTATTG TTGTTTAACG CGATGGNATT TACAACTTGT AACGTAAGAG	240
5	AATGAAAAAT AAGCTGnATA TGTTGTTTG	269
	(2) INFORMATION FOR SEQ ID NO: 1333:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 142 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1333:	
	TAGCTTTTGC CCAATATGGT GAATCATGCG CCGTTCTGTA ATAATCTTCA CTTGGCATTC	60
20	TTGGAATTTG AACAACATCC TGTTCATTTT TATAGAnTGC TTAAATGGTA CAGCTGAAAA	120
	ATCAAAGTAA TGTCCTTTTC TG	142
	(2) INFORMATION FOR SEQ ID NO: 1334:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 211 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1334:	
35	ACTGATGCCC AATATGCATC TTGnCAATTG CAGGTGTGCA TGACTAAACA CATGACAAAT	60
	CTGCCTGACT TTTTGCTGAC CCATAAATAA TTGGnCTAAC TTTTTGCATC TTGATCTTGC	120
	ATCCTTGCCT TCCTATTTAA AATGCTACAA ATAAATTTGC CGGCGAGTGA ATTTTAATGT	180
40	TTTACAACGC TGTTCAATAC CTGGGAATAA G	211
	(2) INFORMATION FOR SEQ ID NO: 1335:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 129 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1335:	
	CTTGAATCTC TTGTGCCTCT GTGATGTATC ATCAAATTAT TTGCACTGCT TCTTCTTTTA	60
56		

	TCCGCTCGC	129
	(2) INFORMATION FOR SEQ ID NO: 1336:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 633 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(b) Toroboot. Timedi	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1336:	
15	CATGATGGCn TCTTACCAAA GGCGATTTTA AGAGCAATGA TACCAAGATA TTTTTAATAC	. 60
	TGATCAAAGT TCAGGTGGTA GCACAATTAC ACAACAACTT GTTAAAAAATC AAGTTCTTAC	120
	CAACGAAAAA ACATATAGTA GAAAAGCAAA TGAATNCGCC TAGCAATTAG ATTAGAACAC	180
20	CTACTCTCAA AAGATGAAAT TATATATACA TATTTAAATA TAGTTCCLTC GGTAGAGATT	240
	ATAATGGCGC TAATATTTCC GGAATTGCAT CCGCTTCATA TAGTCTATTT GGTATTCCAC	300
	CAAAAGATTT ATCAATTGCA CAATCTGCAT ACCTTATCGG TTTGTTGCAA AGCCCATATG	360
25	GCTATACACC CTACGAAAAA GATGGAACGT TAAAATCGGA TAAAGATTTG AAATATAGTA	420
	TTCAAAGACA ACATTATGTA TTAAAGCGTA TGTTAATCGA AGATCAAATC ACTGAAAAAG	480
	AATACAACGA CGCATTAAAA TATGATATTA AATCACATTT GTTAAATCGA AAAAAGCGTT	540
30	AATTGATGCT CACTTTTTAA AGTAACCACA ACAATGAATC CAAATATTAA AAACAGCAGT	600
	AAGATTATTT TCAATTAGAA AATTTCTCAC TGC	633
<i>35</i>	(2) INFORMATION FOR SEQ ID NO: 1337:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 317 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1337:	
45	ATCAATATTT AGCAGTTATC ATTATGCTTG AACGGGTGGT AAAGGCGGAG AAGTCATCCA	60
	CTTTTCCTA TACTACAAGG ACCTTTACTT TAAAACAACG AATTTACAAA ATAAAAGGCA	120
	TAATTTCTTT TCTGTCACAT CGCTCATTCT AACTACTAGA CTTTTAAAAT CGTTCCTGTA	180
50	ATTTAAACTC AATCAACTNT CAATTAATGA TGCATAATAT GATTATAAGT ATAGTAGTTA	240
	ACTICAAATA TCTTAGAAAT GTCCTGTACT ATATCTCTTT TATTCTCAAA AGTCATAGGT	300

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	(2) INFORMATION FOR SEQ ID NO: 1338:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	·
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1338:	
	TACGGCATAT ACCTCGTTCA TCAATGTTCG TAAACATTAT TTAAAACATC TCTTACATCT	60
15	TGCGTTGGAA GTTCTTCATA GTCGAATTTC ATTGTnTTAT CAAAGTTTTC CATTTGCGAC	120
	ACTCC	125
	(2) INFORMATION FOR SEQ ID NO: 1339:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 111 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1339:	•
	GAGCTTCGTT CCATTGTTAT CAAACGATTG CCATTCTGAA ATGCTGTAAA TAGCATGCTT	60
30	CAAATCATCT TGTGCCTGCA GCAGTTTCTT TGNAATATGC TTCATATCAT T	111
	(2) INFORMATION FOR SEQ ID NO: 1340:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 158 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1340:	
	TCACACGTTT AGTTTTCTAT GAATACCAAT ATTTTAACAC CATGTTTAGC CAATTTGTCT	60
45	GCTAAATTAA TCGTGTTTGT CCTCCAAATT GACACGCACC TTTAGTTTTT CTAAATAATG	120
	ATATCATCAC ATCTCTCAGT TAAAGGTCAA ANATATTG	158
50	(2) INFORMATION FOR SEQ ID NO: 1341:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1341:	
	GCTTCAGGTC AATTAAAACG TTCAAGAGCT TTCACATCTC ACTTATTCGC AAACAAGAGC	60
5	ACTAAACAAA AACGTCAATT ACGTAAAGCT AGATTAGTGT CTAAGAGCGA TATGAAACGT	120
	GTAAAACAAT TATTAGCATA CAAAAAATAA GAACAAATAC AGAAATCGGT AGGAATTACC	180
10	TAAGGAGGAA TTTTTTATGC CACGAGTTAA AGGTGGAACA GTAACAAGAG CGCGTCGTAA	240
	AAAAACGATT AAATTAGCTA AAGGTTACTT CGGTTCAAAA CATACATTAT ACAAAGTAGC	300
	TAAGCAACAA GTAATGAAAT CAGGTCAATA TGCTTTCCGT GACCGTCGTC AACGTAAACG	360
15	TGACTTCCGT AAATTATGGA TTACACGTAT CAACGCAGCA	400
	(2) INFORMATION FOR SEQ ID NO: 1342:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1342:	
	GTTGAACAAG GGCAACAAAA ATTTCGAGCG AAACAGATTT TTGAATGGTT ATATCAAAAA	60
30	AGAGTAGATT CGATTGATGA AATGACGAAC TTATCGAAAG ACTTACGACA GCTTTTAAAA	120
	GATAACTTTA CTGTTACAAC TTTAACAACT GTAGTAAAAC AAGAAAGTAA AGACGGTACA	180
	ATTAAATTCT TATTTGAATT ACAAGATGGC TATACAATTG AAACTGTTTT AATGAGACAT	240
35	GATTATGGAA ATTCAGTATG TGTAACGACA CAAGTAGGTT GTCGCATCGG ATGTACGTTT	300
	TGTGCTTCTA CACTTGGCGG CTTAAAAAGA AACCTTGAAG CTGGCGAAAT TGTTTCACAA	360
	GTTTAACAG TTCAAAAAGC CCTTGATGCT ACAGAAGAGC	400
40	(2) INFORMATION FOR SEQ ID NO: 1343:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 399 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1343:	
	GAAAATTTCA TCAGGTGTTG GCGTGGAACG TACATTCCCA TTACACACAC CAAAAATTGA	60

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	TTTACGTGGT AAAGCTGCTA GAATCCAAGA AATTCGTTAA TCAGCATTTA AACAAAGCTA	180
	TGTATGAGTC AAATTCGACT CAAACAATAA AGCCATCTAG GTCACTTTTA TGGAGTGATA	180
5		240
	TAGATGGCTT TTTTTGCTGT TTAGTTAATG TAAAGTTGAT AATGTAATTG TTTATTCCTT	300
	CTCTATTCAT AACGTGTTTG CTCAAAATGG TTATATAAAC AAAAATCTAC TAAGTGCCAT	360
10	TGAAAAGGAC TTAGTAGATT TATTAAATAT ATGCGTAnA	399
70	(2) INFORMATION FOR SEQ ID NO: 1344:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 134 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1344:	
	AACTTACAAC ACCAGGTAAT AACAGCAATA AAGGCACCAG TTAGTGCGGT AATGCCAnTA	
		60
25	TCTAGGCCTT TAGGTTGCCA TAGTACGAGA TGTAGAGGTA CTAGAGGAAT GAGTGTCGCT	120
	AAAGTTGTCG TCGT	134
	(2) INFORMATION FOR SEQ ID NO: 1345:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 109 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1345:	
	TCATAATAAA CAAGTTCACA TGAATCACAA CATCTGAAGA CAATGTTCAA AATGAGGCTG	60
40	GCACAATAGA TGATCGCAAG TCGNATCATC ACACAGTACT GAAGCAAGA	109
	(2) INFORMATION FOR SEQ ID NO: 1346:	103
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 113 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1346:	
	CCATATCTGG nACGACCGAC ACCTTTACCA CCAACGATTG GTGCCATTTG TTTGCATAAG	60
55		

	(2) INFORMATION FOR SEQ ID NO: 1347:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1347:	
	CAATTGAAAG GTGAATTTTA TAGGTCCATG ACAAACTAAG GCTTGTTAAA GCTTATTAAC	60
15	ACAGTTTCAT CAAATAGTTA AATTAGTTTT TGTTTTGCAA TAAATTGGGT ATAGATTACA	120
15	AnTG	124
	(2) INFORMATION FOR SEQ ID NO: 1348:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 337 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1348:	
	CATCAGTGGC CTGATCACCC CAACATTTGA CATCAATGCA TACCAGTTGA TTTGAACAAT	60
30	GATTGCATTG AGCTATCATC AAGTTTGTCT TTAAGCTACT AAACCCACGA ACCATGTTAA	120
	CCCCGTGGTC ACCATCACCA ATTGCTCGAT CTAATTCAGT TAATTCAGAT TCATGTTTTT	180
35	TAAACGTTTC TTCTAAATTT AATAAACGTG CTTTCATATC ATCALTTCAT TGTGCaCtaT	240
35	AAATGLATAT TATTCATATT CACTTCTnAT TTAAAGTATG ACTTGTTGTT GGTGCTAAAA	300
	ATGCTTCCAA ATATTCTGGT TTATTAGGCA CGATAGT	337
40	(2) INFORMATION FOR SEQ ID NO: 1349:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 162 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1349:	
50	CAGCACGTAA ATACAACAAA GCGATCCCCA GCTTGTGGCA CATCATTAAT ACCTGTAATT	6
	TCAACAGGCG TTGATGGACC AGCCGTTTTG ATTCTTTGAC CTAAGTCATT ACATGCCGAA	12
55		

(2) INFORMATION FOR SEQ ID NO: 1350:

5	(A) LENGTH: 399 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1350:	
	CAATTITACT TTGAATTICT TTTTTATCTT TTCTAGTTTT ATCGTCCCAC TCTTCAATCC	60
15	ATTTTTTAGC TTTATCTTCA TTATTAGTCA ACTTGCCTAT TTCTTTTAAT ATTCTTTATG	120
15	ATTGTATTTA TTGTATGTAT ATGGGATTGT TGGCGCTATT TTTTGGTATT TTTTTATATT	180
	TTTATCCATA GCATCTACAA CAATTAAATC TGGTTTLGCT TTAGCAACTC TTTCAACATC	240
20	ATTITCTCCA ATATAATCAA CCCCTTTTAA ATAAGGTTTT AAAATTGAAG AATCTTTAGT	300
	TATATCTGAA ACAGCAATTG GTTTGATTCC TAACTTTATA AAATCACCAA CATAAAATCC	360
	AGTTAATACA GCAACTCTTT TAAGGTTCTC nGGGACTTT	399
25	(2) INFORMATION FOR SEQ ID NO: 1351:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1351:	
	TAAAACTTAG GCGGTTTTGC ATGATTATAG CGCTCAACAC GTTTGAAATT ATAGGTCATC	60
	TCTGGTATTC TTGTACGATT CTTTTTCCAA TCTAAATCAA AGTTTTCAAT TTCTTCTTTT	120
40	GAGTTTAGAC TTAATCGATC ACGTTCATGT TCTTTAAAAG ATGGAATAAC TTGTTTAAGT	180
	GACCCTTCCA TTCTTAATTG ACCATGTGAA AACCAAGCTA TGTAGTTACT CACTTGTGAA	240
	ATTTTATCAA TATCATCACC AATTGACACA ATCGTTAAAT TATTTTCAAT ATAATCATTT	300
45	GTTAATTCAA TCGCACGTTC CATAAATTGT GGTGTTAAAT AGTCAATAAC ATGATTTAAA	360
	ATAATAATAT TTGATTTTGA TGAGCGTGCA ATACTTAATA	400
50	(2) INFORMATION FOR SEQ ID NO: 1352:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

and the sales of the

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1352:	
5	AAGGGAACAA AAGCTGGAGC TCCACCGCGG TGCGGCCGCT CTAGAACTAG TGGATCCCCC	60
	GGGCTGCAGG AATTCGGCAC GAGCATATCT AGTATTTTAG GACGGAGGNA GTACATT	117
	(2) INFORMATION FOR SEQ ID NO: 1353:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 153 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1353:	
20	AGTTCAGGAG AGTTATAAAT ATTAGGGTGG TACATGCCCG AAATCATTGG AATTGTTAAA	60
	GTAGATTTTA CAGTTTAGAG ATAACAGACA TGTCTATATG AAGGGCTGTC TACCCTCGTA	120
	AGGTTATATC CTACAGNTGA ACGTATCAAG CTT	153
25	(2) INFORMATION FOR SEQ ID NO: 1354:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 159 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1354:	
35	TGTTGTAACA GCTCTCTATG TTTACGTTGG AAGTATGGTT TATTTTTCAT CTTCACATTT	60
	AGTTCCTTAT TTAAAAGTGA TAGAGCAATT GCACTCGTAG GTCAAGAAGC GGGATGCCAA	120
	CACAAAGTTC ACAAGAnAAT ACACTTTTGA AAATATTGG	159
40	(2) INFORMATION FOR SEQ ID NO: 1355:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1355: CGNCTTCCTT CAACCATTGT AGAAGTTGTC TCATATACTT ACTACGGCTT GCTAATACTC	60

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	(2) INFORMATION FOR SEQ ID NO: 1356:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1356:	
	GGATTCATTG GTGCTTATTT ATTTACATTC AATAATGAGA NCTTTACACA ACCAATTGGT	60
15	CAAATTATAG ATGTCAACAT GTTTCTTCGA CACCTACAAA AGATGCACAA	110
	(2) INFORMATION FOR SEQ ID NO: 1357:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 133 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357:	
	TAATGGTGGG GTATATTTAT ATTAGTACCG AATTTTAGGn GCCTCACTAT CATTTATCAA	60
30	ATTATTTAAA GTGGGATCCT ATCGCAATCA ATTGGCAGGG GCAGAATAAT GGCATTAGTC	120
	GTTGAAGATA TCG	133
	(2) INFORMATION FOR SEQ ID NO: 1358:	
35 . 40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358:	
	GTGTCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACAAATG	60
45	ATATATCAAA ATCATTAAAT CGAGGAAAGC ATACTACAAG ACATGTCGAA CTATTCGAAC	
	GTCAAAACGG TTATATTGCA GACACCCTG GATTCAGTGC TTTAGATTTT GATCATATAG	120
5 <i>0</i>	ATAAAGATGA AATAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTAAGTT	180
	TAGGAATTGT AATCATATCA AAGAACCTAA TTGTAATGTT AAGCATCAAT TAGAGATAGG	240
	GAATATTGCG CAATTTAGAT ACGACCATTA TTTACAACTA TTTAATGAAA TTTCCAAATA	300
55		360

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(2) INFORMATION FOR SEQ ID NO: 1359:

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 392 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1359:	
	CTGTTTTAGT CTTATTGATT GCCTGACCAT TAACTAAGTA ATTTGTGTTT GAAGCGGTTA	60
15	ATTGAGCAAT GATTGGAATG TCGTATTTCT TTCTCGTTCG TGAAATGACA TTTGTTAACT	120
15	CTTCTAGGTC GTAATACGTT TCGAAAAGTA GCGCGTCAAC GCCTTCTTCA ATTAAGGTGT	180
	CTATTTGAAT TCAGTATGAT AAAGAATAGT TTGTAAGCTG ATATCCCCCT GTTTGGATAC	240
20	CTCTAAACCC CACCAACTGG GGCCCAATAT ÀTACGTAANC TNTAATTGGC NGGCTTTTTT	300
	GCGATGCGAC GGGGGGCTGG AGGATGCTTA ACCTTAACCT CCAGACCGAA CCGTTTAACC	360
	TTTCCAAAAT TGCACCATAG GAATGGGTGG AT	392
25	(2) INFORMATION FOR SEQ ID NO: 1360:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 160 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1360:	
	CCATGGTTAT TTTCTTCACA TTTCATGTAT ATATATTTGT TTATTATCTG TCTCTACTAG	60
	ACTGTAACCT CCAACATATC TGTTTTATAA ACCAGAGAGC AGTCATTCAA TAAATAAACA	120
40	GATCTGAGGG CCAACTGGCA TGTTGTCAAC TTATGATATT	160
•	(2) INFORMATION FOR SEQ ID NO: 1361:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 148 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1361:	
	GTATCCTAAA GATTCAGTTA ATCGGAGCGT TGTATTGCAT GAAGGTACAT TGCGGAATGC	6
55		

	ATATTTATTC ACGATNTTAT TTAGCGAC	148
	(2) INFORMATION FOR SEQ ID NO: 1362:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 147 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1362:	
15	AAAATTACTA TGAAGATTGC ATTAGGATGC GACCATATTG TTACAGATAC AAAAATGCGT	60
	GTATCTGAAT TTTTAAAATC AAAAGGACAT GAAGTCATTG ACTGACACTT CACTCATNAG	120
	TGGCGACAGT GTACGTATCA GACTTAG	147
20	(2) INFORMATION FOR SEQ ID NO: 1363:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 108 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1363:	
	CTGGCAAAGA AGACAACAAC AAGCTGGTAA AGAAGCAACA ACAAGCCTGG TAAAGAGACA	60
	ACAACAANCT GGCAAAGAAG ACGGCAACAA GCTGGTAAAG AAGCAACA	108
35	(2) INFORMATION FOR SEQ ID NO: 1364:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 153 base pairs	
40	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1364:	
45	GACAATGTTG CTGTAATGGG GAAGGNAATG GGTTGGTACC GCGAATTGAA TAATTTAAAA	60
	CCGTAATATA TAATCGTAAT TGTTAAGCCC TCATTTTTAT AAATTTTGGA CCTCTTGAAA	120
50	AAGTTACGTT TTCAAGAGGT TTTATTTATC CTA	153
	(2) INFORMATION FOR SEQ ID NO: 1365:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 184 base pairs	

(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1365:	
	TAAGAGAATT ATATGCATTC CAAACGAAAC NAACAGAAAA ACGGACCAAA CTAACTGTCA	60
10	CAAGTACAAT CGCTGTACTA CTGCAAAACA CGCAAAACGA ACACTTACGT ACACAAAAA	120
	AGACCACCAT TCACGTCGGG ATTATTAAAA AGGTAGTCTC GTACATTTAT TAAACTACTT	180
	ACGT	184
15	(2) INFORMATION FOR SEQ ID NO: 1366:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 452 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1366:	
	ACATTAGATG GGTCAATCAT GTTATACACG GTGATTTAGG GGAGTCAATC AAATATAAAA	60
	GGCCGGTAAT TGATGTTATT GAGGAAAGAA TTCCAAATAC AATATTACTC GGTGCTATGT	120
30	CATTAATTAT TACTTATATT ATCTCATTTG CTTTAGGAAT AACGTCAGGT AGATATTCTT	180
	ACAGTTTGAC GGATTATACT GTGCAAATAT TTAATTATTT GATGTTAGCC ATTCCATCTT	240
	TTATTGCGGG AGTATTTGCA ATTTNTATTT TTTCTTTTGA ATTACAATGG TTCCCGTTTC	300
35	AAGGTTCTGT TGATATTAAC CTTAAAGAAG GTACTTTTGA ATATLATATG AGTAAAATAT	360
	ATCACACATT TTTACCTGCA TTCACTTTAG GTTTATTATC TACTGCTGGT TATAWTCAAT	420
40	ATTTACGTAA TGATATTATT GAAAATTCTA AA	452
40	(2) INFORMATION FOR SEQ ID NO: 1367:	
4 5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1367:	
	TTGTGAGTAA TTGGACAATA TAAGTGTTGG TCTTGGATGG CATATCCTTG GTACGACCTG	6
	GGCAACTTGC TTCATAGCGC AGTTAGGAAC TGATCAATCA TTGGCGTTTT GATACCTAGC	12

	(2) INFORMATION FOR SEQ ID NO: 1368:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 126 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1368:	
	TGGTGCAAAT TAAAACGGTT GCATATGCAC GTACGACGTA TTGCTAAATA CAATCAATTA	60
15	TTACGTATCG AAGATGAATT ATTTGAAACG CTAAATATGA CGGTATCAAA TCATTCTATn	120
	ACTTAG	126
	(2) INFORMATION FOR SEQ ID NO: 1369:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) <u>LEN</u>GTH: 160 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1369:	
	TGnAAAGTTC ATCAGGGAGC CATTTTACA ACACAGGGCA CATACGGGTT GTGTTTAGGT	60
30	GCAATTGCCC CAAGCGGACA AAGCATTATT TAAAGTTTCA AGTTCTTCAA CGATTTATTA	120
	GTGCACAGGA TCCTGTTAAG AGGTATTTTG AAGACTTCCG	160
35	(2) INFORMATION FOR SEQ ID NO: 1370:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	,	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1370:	
45	AGTAATTCTG CAAATGCCGC AGATAGCNGT ACTTTGAATT ATGAGGTTTA CAAATACAAT	60
	ACCAATGACA CGTCAATTGC TAATGACTAT TTTAATAAAC CGGCAAAGTA CATTAAGAAA	120
50	AATGGTAAAT TGTATGTTCA AATAACTGTC AACCACAGTC ATTGGATTAC TGGAATGAGT	180
50	ATCGAAGGAC ATAAAGAAAA TATTATTAGT AAAAACACTG CCAAAGATGA ACGCACTTCT	240
	GAATTTGAAG TAAGTAAGTT GAACGGTAAA ATAGATGGAA AAATTGACGT TTATATCGAT	300

(B) TYPE: (C) STRAND (D) TOPOLO (XI) SEQUENCE D (XI) SEQUENCE D (XI) SEQUENCE D (XI) SEQUENCE D (XI) GATGATAA AATTATCAG (ACGATTATT TAAATTTAG (ACGATTATT TAAATTTAG (ACGATTATA CGATGATTGA (ACGATTATA CGATGATTGA (ACCAAGATAA TTGAATTTCA (ACCAAGATAA TTGAATTTCA (ACCAAGATAA TTGAATTTCA (B) TYPE: (C) STRAND (D) TOPOLO (XI) SEQUENCE D (XI) SEQUENCE	C AGGTGCTAAT GCACCAGGTA	400
(1) SEQUENCE CH (A) LENGTH (B) TYPE: (C) STRAND (D) TOPOLO (XI) SEQUENCE D (A) CACGATTATT TAAATTTAG (ACCAAGATAA ATGAATTGA (ACCAAGATAA TTGAATTTC (A) LENGTH (B) TYPE: (C) STRAND (D) TOPOLO (XI) SEQUENCE D	SEQ ID NO: 1371:	
(xi) SEQUENCE D CATCAAGAAC ATGTGAGAC GGATGGATAA AATTATCAG CACGATTATT TAAATTTAG GGTGATAATA CGATGTTTG CACAAGATAA TTGANTTTC (2) INFORMATION FOR (i) SEQUENCE CH (A) LENGTH (B) TYPE: (C) STRANN (D) TOPOLO (xi) SEQUENCE CH TTGAAAAGCA GTTTGGAT TTCCAAATAG GTTCATCT (2) INFORMATION FOR (i) SEQUENCE CH (ii) SEQUENCE CH (iii) SEQUENCE CH (iv) SEQUENCE	: 345 base pairs nucleic acid EDNESS: double	
GGATGGATAA AATTATCAG CACGATTATT TAAATTTAG CACGATTATT TAAATTTAG GGTGATAATA CGATGTTTG CACAAGATAA TTGANTTTG CACAAGATAA TTGANTTTG (1) SEQUENCE CH (A) LENGTH (B) TYPE: (C) STRANN (D) TOPOLO (xi) SEQUENCE I TTGAAAAGCA GTTTGGAT TTCCAAATAG GTTCATCT (2) INFORMATION FOR (i) SEQUENCE I (xi) SEQUENCE I (xi) SEQUENCE II (xi) SEQUENCE		
GGATGGATAA AATTATCAG CACGATTATT TAAATTTAG GGTGATAATA CGATGTTTG GGTGATAATA CGATGTTTG CACAAGATAA TTGANTTTG (2) INFORMATION FOR (1) SEQUENCE CH (A) LENGTH (B) TYPE: (C) STRANN (D) TOPOLO (xi) SEQUENCE INTOCAAATAG GTTCATCT (2) INFORMATION FOR (1) SEQUENCE CH (2) INFORMATION FOR (3) CACAAGATAG TATTTATCH (4) TAATACGATG TATTTATCH (5) INFORMATION FOR (6) SEQUENCE CH (7) SEQUENCE CH (8) TYPE: (C) STRANN (D) TOPOLO (Xi) SEQUENCE	ESCRIPTION: SEQ ID NO: 1371:	
GGATGGATAA AATTATCAG CACGATTATT TAAATTTAG GATTTTAGAA ATGAATTGA GGTGATAATA CGATGTTTG CACAAGATAA TTGANTTTC (2) INFORMATION FOR (i) SEQUENCE CH (A) LENGTH (B) TYPE: (C) STRANN (D) TOPOLO (Xi) SEQUENCE I TTGAAAAGCA GTTTGGAT TTCCAAATAG GTTCATCT (2) INFORMATION FOR (i) SEQUENCE CH (A) LENGTH (B) TYPE: (C) STRANN (C) TOPOL	C ACAATTTGAA TCACTTGAAA AAATAAATAA AGACATTGTT	60
CACGATTATT TAAATTTAG GATTTTAGAA ATGAATTGA GGTGATAATA CGATGTTTC CACAAGATAA TTGANTTTC (2) INFORMATION FOR (1) SEQUENCE CH (A) LENGTH (B) TYPE: (C) STRANN (D) TOPOLO (xi) SEQUENCE CH TTGAAAAGCA GTTTGGAT TTCCAAATAG GTTCATCT (2) INFORMATION FOR (i) SEQUENCE CH (A) LENGTH (B) TYPE: (C) STRANN (C) STRANN (C) STRANN (C) TOPOLO (SI) SEQUENCE CH (A) LENGTH (B) TYPE: (C) STRANN (D) TOPOLO (xi) SEQUENCE	G AACATCATTA AATTATCCAG TACTACAAGG TAAGACAAAT	120
GGTGATAATA CGATGTTGA GGTGATAATA CGATGTTTG CACAAGATAA TTGANTTTG 25 (2) INFORMATION FOR (i) SEQUENCE CH (A) LENGTH (B) TYPE: (C) STRANN (D) TOPOLO 35 TTGAAAAGCA GTTTGGAT TTCCAAATAG GTTCATCT 40 TAATACGATG TATTTATC (2) INFORMATION FOR (i) SEQUENCE C (A) LENGTH (B) TYPE: (C) STRANN (D) TOPOLO 45 (xi) SEQUENCE C	A TITTGAGCGA GAACATCGAC GTAAAGGTAG TATTTYATG	180
GGTGATAATA CGATGTTTC CACAAGATAA TTGANTTTC 25 (2) INFORMATION FOR (i) SEQUENCE CHAN LENGTH (B) TYPE: (C) STRANN (D) TOPOLO (xi) SEQUENCE INTO AN	A GAATTTMAAT CATAATACTA TTTTATACGG GCACCATGTC	240
CACAAGATAA TTGANTTTO 25 (2) INFORMATION FOR (i) SEQUENCE CH (A) LENGTH (B) TYPE: (C) STRANI (D) TOPOLO (xi) SEQUENCE II 35 TTGAAAAGCA GTTTGGAT TTCCAAATAG GTTCATCT 40 TAATACGATG TATTTATC (2) INFORMATION FOR (i) SEQUENCE CH (A) LENGTH (B) TYPE: (C) STRANI (D) TOPOLO 50 (xi) SEQUENCE	SA TGTGTTAGAA GATTATTTAA AGCAATCGTT TTATGAAAAA	300
(i) SEQUENCE CHAIN SEQUENCE	G CAATAAATAT GGTAATCTCC ATTGC	345
(A) LENGTH (B) TYPE: (C) STRANT (D) TOPOLO (XI) SEQUENCE I TTGAAAAGCA GTTTGGAT TTCCAAATAG GTTCATCT (2) INFORMATION FOR (I) SEQUENCE C (A) LENGT (B) TYPE: (C) STRAN (D) TOPOL		
(xi) SEQUENCE 1 (xi) SEQUENCE 2 (xi) SEQUENCE 2 (xi) SEQUENCE 3	HARACTERISTICS: H: 154 base pairs	
TTGAAAAGCA GTTTGGAT TTCCAAATAG GTTCATCT TAATACGATG TATTTATC (2) INFORMATION FOR (i) SEQUENCE C (A) LENGT (B) TYPE: (C) STRAN (D) TOPOL	nucleic acid DEDNESS: double DGY: linear	
TTGAAAAGCA GTTTGGAT TTCCAAATAG GTTCATCT TAATACGATG TATTTATC (2) INFORMATION FOR (i) SEQUENCE C (A) LENGT (B) TYPE: (C) STRAN (D) TOPOL	DESCRIPTION: SEQ ID NO: 1372:	
40 TAATACGATG TATTTATC (2) INFORMATION FOR (i) SEQUENCE C (A) LENGT (B) TYPE: (C) STRAN (D) TOPOL	TT ATGCTCAAAC CATGGACGAC GGTTAGGTTT ATGAATGTTA	60
(2) INFORMATION FOR (i) SEQUENCE C (A) LENGT (B) TYPE: (C) STRAN (D) TOPOL	AT AAAAACTAGT GGAAAGTGGA AAAAATnAGT GGACCTTCGA	120
(i) SEQUENCE C (A) LENGT (B) TYPE: (C) STRAN (D) TOPOL	GT TAGAAGCAGT AATA	154
(A) LENGT (B) TYPE: (C) STRAN (D) TOPOL	SEQ ID NO: 1373:	
(xi) SEQUENCE	HARACTERISTICS: H: 136 base pairs nucleic acid DEDNESS: double OGY: linear	
	DESCRIPTION: SEQ ID NO: 1373:	
GAGCCTAATT ATTCAAGC	CCA AATCGCATAT GAAATTGATA AAGAAGTTCA ACGAATCGTT	60

	CTATACNAGA ACTATC	136
	(2) INFORMATION FOR SEQ ID NO: 1374:	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 358 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1374:	
15	ATCTTTAACA ATTAAAACCA TACTATCTTG AATCATCATC AAATTTAACG CATGTGCGTC	60
	AAGTTGTTTC ACTTTAAAGA CTTCATTATT AAGACCGACC TTAGACTGCT TTTTAAAAAT	120
	AGGTACATTC GTAATCATAC CTATACTTTG ATTGTCTAAG TGTAATTTGT TTTGGTGATA	180
20	TCGATTATAA TCTTGTGCAG TAAAAGCTGT AATCATTACT GATTGTCTTG AAAATATCGC	240
	GCCTTCATTA CCAATGAAGT CTATTGGAAT aTCATCACTA GCCTGTTTTA ACTTGTAATA	300
	AGCACGATTC TNTTCTAAAG AAGCTCTAAA TAATGTCGTT TCATATACTT TGAAGTCT	358
25	(2) INFORMATION FOR SEQ ID NO: 1375:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 122 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1375:	
	ATATTGTGTG CTAAATTTGC TTAAGTATGT TTTTTGTTTG NAAGTAAGCA TATGTTATTG	60
	TCTTTTTAAT TGTTGTAAAA GTGCTGTTTT CATAGAATTA ATATCAGACA TCTTTATTAG	120
40	TA	122
	(2) INFORMATION FOR SEQ ID NO: 1376:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 467 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50		
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1376:	
	CATTITCTTC GGTTTCTGTC TTTTTATGCG TAGATTTATT TTCTTGTTCT TGGTTATTAC	60

	CGATAATTAC GATGGTAATA AGAAGTTTTT TCAAATATAA CGCCTCCATG TTAATGAAAA	180
	GTAGTTGATA CGTGAAGCTA AATAATTnAT TTCAATATTG CCATAATCAT TTTAAAAAAT	240
5	AAATATTAGA AAAGTAGGCG ATATTAATAT TTTCATTGTt TTTTGTGTAC TTCAATTAGT	300
	ATAACAAAAC TGTTATGTAT TTATAAATAT AATCATTAGT ATTTTTATGG CTGAAAAAGT	360
	TATAATAAA GTGTAAGGAA TAAAATATTT GTATGGAAAA GAGAGATAAT TATGAATAAA	420
0	ACCAGTAAAG TTTGTGTAGC AGCAACATTA GCATTGGGCA CACTGAT	467
	(2) INFORMATION FOR SEQ ID NO: 1377:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 128 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1377:	
	AGGTGTTAGA ATTTATTTTA AGTGTTATAC GTGTCTTCCA GAAATTGTAA TGGCATTATA	60
25	TTTATNAAAG TGTTGGCAGG TTATTTTCAG GTGTATTAGT TTAGGTATCA TTCGTAGTAT	120
	GCTTGGGA	128
	(2) INFORMATION FOR SEQ ID NO: 1378:	
30 35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1378:	
40	GGACGCTAGA GGATCCCGGT CTGGAAAATA TCGTCCAGAA CTTAGAAAATA TGAAAATATT	60
	CCCAAGACCA ATCGATAATA TATTGCCAAT ATGGCGTGCT GTTGGTGGTC CACCTGCAAG	120
	TGCTATTAAA GCGGGAAAAC AAGGTGTGCC AATGATGATT ACAACCCTTG GTGGCCCAGC	180
45	AATGAACTTT AAAGGTTCTA TAKATGCTTA TCGTCAAKCG GCAACTGAAG CAGGTTTCGA	240
	TGCTTCGCCT AAGTCTTTAC CAGTAAGTAC AGCGAGTCTG TTTTATACAG CTGAAACAAC	300
	TCAGGATGCT ATGAGAGAAT TTTATCCACA TTTGAATACA GGGATGTCAT TTATTCGTGG	360
50	TRGTTGGTTA TCCGAAACAG CAATRGCTAA TTCGTCAGTT	400
	(2) INFORMATION FOR SEQ ID NO: 1379:	

5	(A) LENGTH: 108 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	_
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1379:	
10	AACTACAACA ATTTAACGAC CAACCTTAAA AnAATACGCT CTTATGCATT GGATTAGTCC	60
	TGATTATACA ATTTAACTGA ACAAATACCC ATCATTTAAA AGACTTAG	108
	(2) INFORMATION FOR SEQ ID NO: 1380:	
15 20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1380:	
25	AAGTGGGGGG AATCAGTATG TTACATTTAC ATATATTAAG TATTAGCGAT TATTTTATTT	60
	ATCGCTACAT ACTTAACCAT TTCAAAAATT CAAGGCGGnT CACCATTTTC CAACCCGT	118
	(2) INFORMATION FOR SEQ ID NO: 1381:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 114 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1381:	
	TCATGAAAAC ATTTATTTTA AAATTTGATA TTTGTTCAAT AATATTCGAA ATTAACTTnT	60
40	GTGTATAGAT TTTCTTTATA TCCTGAGAGA CATGTACTAT AATGTTTGTG AATA	114
	(2) INFORMATION FOR SEQ ID NO: 1382:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 165 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(vi) SEQUENCE DESCRIPTION CTS	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1382:	
5 <i>5</i>	CGGTATTGAT CATATAAATA GTGTTTAGAT GCTATAGTCG GNTGACTTAA GTAATTTAAA	60

	GTTTTCTTCT GCCTTGCTTA AAGATATATG ACAGGGTGCT GGCAT	165
	(2) INFORMATION FOR SEQ ID NO: 1383:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 111 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1383:	
15	TTTGGTGTGA TGGAGTATAT TTAGGTGTGG AAATCAAGAG GGAATTCCAT TTTCAAACAT	60
13	CCAATTAGAG TCGnAATAAG AACTCGCTAT CGGTCCAATT AACTGATTCA G	111
	(2) INFORMATION FOR SEQ ID NO: 1384:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 144 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1384:	
	CATTTAAATA ACGTTGTGAC CATGTGCTTT ATGCTATGTG CTAGAAAATC CATGTTTTTA	60
30	TCTAATTTCT TAATAAATTG ACATTAAGTT GGATTCTTGT CCnCTTCACG TTTCGACATT	120
	GGATGACTGA ACGCATGAAA TCAG	144
0.5	(2) INFORMATION FOR SEQ ID NO: 1385:	
<i>35</i>	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 103 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1385:	
45	TCGTTGTGCA GCAACTGCAT TACGCTGTCT CATTAATGTA AGCGCAATGG CCATTTGGTT	60
	TTTCnATAGT GGAATACTTG TCAAAATTGA ACATTGTATC TTC	103
	(2) INFORMATION FOR SEQ ID NO: 1386:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 533 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1386:	
5	CCAGNACAAA TACAACGTTA TATTCAACAA TTAGAAGACT TAGNATAGAT ATAAATTGAG	60
	GGAGGACATC GATATGGCAT TTGAAGGGTT ATCAGAAACC TTGCAAGCGA CGATGCAAAA	120
	AATGCGTGGT AAGGGTAAAC TTACTGAAGC TGATATAAAG ATAATGATGC GTGAAGTAAG	180
10	ATTAGCGTTA CTTGAGGCTG NACGTAAACT TTAAAGTGGT AAAAGAATTT ATTAAAACAG	240
	TATCAGAACG CGCATTAGGT TCCGATGTAA TGCAATCATT AACACCAGGG CAACAAGTTA	300
	TTAAAATAGT TCAAGATGAA TTAACGCAGT TGATGGGTGG AGAAAATACG TCGATTAANA	360
15	TGTCAAATAA ACCACCTACT GTTGTTATGA TGGTTGGTTT ACAAGGTGCT GGTAAAACAA	420
	CAACTGCAGG TAAATTAGCA TTATTGATGC GTAAAAAATA CAACAAnaaa CCTATGTnAG	480
	TTGCAGCAGA TATTTATCGT CCAGCAGCGA TAAATCAATT ACAAACAGTA GGG	533
20	(2) INFORMATION FOR SEQ ID NO: 1387:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1387:	
	TTATTTACAA GCCATTAATA TATTTTAGGT TTGTTCTGCA TCGATTCATT GGTGCTATTT	60
	TATTTACATT CAATAATGAG ACTTTTACAn CAAACCAATT GGTCAAATAT AG	112
35	(2) INFORMATION FOR SEQ ID NO: 1388:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1388:	
	ACACCTACAG TTAATAGTAT CAGTGCACAC TAAAGTCCTA ATACTTTCAA CCATGACTAA	60
	TGATGTATCn TCTTGCCCAA CGAACGCGTT GTGCCAAATT GAATTAGACT GGACGGAC	118
50	(2) INFORMATION FOR SEQ ID NO: 1389:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 147 base pairs	
55		

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	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	(with converge processors and an Mo. 1389).	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1389:	
	CGACGACACA ACTITATAAT AAAATCTTAG ACAATAACGA AGGGTATTAA CAGAACTTGG	60
10	TGCTGTTAAT GCAAGTACTG GAAAATATAC TGGTCGTCGC TAAAGCAAAT TTTTGCTCTG	120
	ACCTnCAATG GTACTTGTTG GGGAATA	147
	(2) INFORMATION FOR SEQ ID NO: 1390:	
15 20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 161 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1390:	
25	TTTTTGATCA TGATTTTTGG GCATGGATCA ATCACTTGCT TGGCCAATGG TCTTTCAACA	60
23	ATTTGGATAT CTGACCTTAT TCGCTTTATC TAGCACTTTT GnCAATTTGT TGGCATTGGA	120
	AAACATGTGT TTAGATTTTT GTATGCCTCT CGCAGGCTTT T	161
30	(2) INFORMATION FOR SEQ ID NO: 1391:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1391:	
40	GCCGCACGCG CGCGATTCTC GGCCTAATAA GAAAACAAAT AATTCCAATT CATATATGNA	60
	CATTTTTGCC TCCTTATTTC TTGAAAATGT GGAATTGGAA TT	102
45	(2) INFORMATION FOR SEQ ID NO: 1392:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 412 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1392:	

	AAAATGCTAT TAACAACGTA TTAAATAATC AAGATTACCA TGGTATTAAA GATAAACCAT	120
	TCGCATTATT CGTAACTGGA TTTTTCGACA ATGTAACAGA TAATACTGTT GGTATTAACT	180
5	TTAAGACAAA AGACGGTTCA ATAGCAGTAT TTATGCGTCC AGATATTGGA GAAACATTTA	240
	GCGAGTTTAG AACATTCTTA GCCGTCTTGT TAATGTTGTT ATTATTTATC TCGATTTCAT	300
10	TAGTTATCGC ATCANCCTAT TCAATCATTC GTCCAGTAAA AAAGTTAAAG CTAGCGACCG	360
	AACGCTTAAT TGATGGTGAT TTTGAAACAC CTATCAAACA AACnCGCAAA GA	412
	(2) INFORMATION FOR SEQ ID NO: 1393:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 186 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1393:	
	AGCAANTGGA TTGCAATGAG TTTCTTATAT TTACAAGGTG GTAGATTGAT TGATGTTTTA	60
25	ACTGCGATAT TAGCAGTAGT CTAGATACCT AGTCACTGAG ATTTTAGATC GAGTTACACG	120
	CACATTATCC GATCTGTCTA TATGGATATC CGTATGACTA CCTATCCCAC GGACTGCACA	180
30	TACTGG	186
	(2) INFORMATION FOR SEQ ID NO: 1394:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1394:	
	TCTTTAAAAG AATCAGGAGC TTGGAAGAAG TATATCAGGA TCATTAAGTC AACAAATTAC	60
	GCGATATGAA AATTTGAATA ACAATTTGAA AAAGCATGCT TCCGATAATC AGCAAGCC	118
45	(2) INFORMATION FOR SEQ ID NO: 1395:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 175 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

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	GGTTACCTCG GATGGATGAT TACTATTTTG GGCTGGGCGC CGGCTTTnGT TATTAGTGGT	60
	GGCAATAGTG GCAAAGTGTC ACAAAAAAAT CCAATAGCTG GAAACCCGGG TATATTTGGG	120
5	TATTAACGCC GGTGGCCGGG ATTTGGCCAA TCGCATTAAT TTAATGGCCA TTGGG	175
	(2) INFORMATION FOR SEQ ID NO: 1396:	
o	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 132 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1396:	
	AGAAACTTAG ACGATTAGTA TCATATATTA GAACACNGCA CCGAACTTGA AATCATGGCT	60
20	GATATCGCAC CTTGAAGAAG CAAAAATGCC GCACGACTTG GCTTTGATAT ATTGGCACGA	120
	CTTACATGGC AT	132
	(2) INFORMATION FOR SEQ ID NO: 1397:	
25 30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 121 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1397:	
35	AGAGGTCCGG CTATCTATCA AATAAAGTGG TCATTTAAAG CGTACACTTC GGGTGCGTTG	60
	ATTICTIACT TIAGGIGIAG GACAATIGIA TCGCATCIAI CTITACNCIA CCIGCATIGI	120
	T	121
40 -	(2) INFORMATION FOR SEQ ID NO: 1398:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 202 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1398:	
	CGTTCGTATA ATCTCACTTG CATCnTGAAT TGAACAACAT CCTGTCATTT TAAGACTGCT	60
	TOTAL TOTAL SON ROMAN OF THE CONTROL OF THE CANADAM CA	120

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	AAACACCTCA TCCAAAGTTC AG	202
	(2) INFORMATION FOR SEQ ID NO: 1399:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 165 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1399:	
15	CGTTGGATCA CTGATGCATT CATAAATGGG TGAACNTAAT GTAATGTTAA ATCTATCACA	60
	GCGCGATAAC AGCAAGAATA TAGTGAACAC CATAAATTGA GCATATCAAT GCCATATTCA	120
	TGGATACACA TAGTTCACCT GGTGGTCGGT GAAAGCCTGT AGATG	165
20	(2) INFORMATION FOR SEQ ID NO: 1400:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(b) Torobogi: Tinear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1400:	
	ACACCTTTGT TTTTGCAAAG CTGTACCACA AAGTACTGGG TAGAATTCTA CGTTATATGA	60
	GNCTTGGCGT ATAGCTTCTT TTAATTCATA AACTGTAAAT TTCTTCG	107
35	(2) INFORMATION FOR SEQ ID NO: 1401:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	
	•	
	(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1401:	
45	TTTTGTCTAG nAACATCTGC TTCTAATAAT GATCGATCAG CAGCCATTGT GCTTAATCTT	60
	TCATCCCACA TCACAATCTC AATAGAAGGA TAAGCTTCTA ATAATT	106
	(2) INFORMATION FOR SEQ ID NO: 1402:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	-
55		

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1402:	
	CAATGTTAAA CCTACACCGT TAACAGCACA CATGATACTA AATTGTTGGG GTGTCATATT	60
5	ATACAATGTT GAGTAnTAAA TGGCGATGCA GATGAATAAC TA	102
	(2) INFORMATION FOR SEQ ID NO: 1403:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 169 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1403:	
	TTTATTATTT GTGCTACAAC TACTTAAAAA AATCAGTAGA TATAGCATTA AACATATTTT	60
20	CATCCCCYTG AATTTTAAAA ACTTTTTCAA AAGCAACACC TCTAAAAATA AATACAATAT	120
	ATTATAGCAA ATAGAAATTA TTATTTTGTT AAATTATGTT GTnCATGTT	169
	(2) INFORMATION FOR SEQ ID NO: 1404:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1404:	
35	TTAGTTGATA AGTAAATCCG AGTGACATTG GGATTCACCC CAACCGACTC TATTCCAGTC	60
	TGAAATACGT GAACCCATAA NATCCTATGT CCAGATITAT ATTTCT	106
	(2) INFORMATION FOR SEQ ID NO: 1405:	
40 45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 309 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1405:	
	TATTITTGCA GCAGAGATGT TCGCGACAAG GTTTACGCCA AATTGTCACT GCTACTGCGA	60
50	THE PROPERTY AND A PARTY AND A THE PARTY AND	120

	CTTTAATAAG CAATTTGTAC TGACTGTCGA CATTGCGTCA TGGTCTGTTT TTGTTTAACT	240
	ATACTATRGG TGCGAAGTAG GCCTATGTTT AGAGGTCTAA CATGCCGTAG GTCTAATGGA	300
5	TCAGGAACC	309
	(2) INFORMATION FOR SEQ ID NO: 1406:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 144 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1406:	
	GTGGACCTGC AGTTAATTCA ACGATTTCAA GATGGGCGCC AAGAACGAAA CGTGGCCGAT	60
20	ACTTAGGATT CTGGAATCAT CACATAATCG TGTGCATGAG GTGTTTCACT TTGGGGTCTA	120
	ATGATTCTTC ATGGAAnGTA TAGG	144
	(2) INFORMATION FOR SEQ ID NO: 1407:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 115 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1407:	
35	ACCTTTGCGT CCAGAATTAG CTACATGGTA AAGCTTCGTG TTACTATTTT AGGGATATCT	60
••	TCAACnCGTT TCACTTGTAT AATTTGTTTT TGTAATTGGT GAAGTCATAG TATAG	115
	(2) INFORMATION FOR SEQ ID NO: 1408:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 115 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1408:	
	ATTGGTATTG GCGCTGTAGT ATAGCTTCAT TATCTGATGC CATTAGTATA CGCACACTTT	60
50	TTATTTATGG GCGTGGTATT CATCCTTATC GGGATCAATT ATTGGGTTAC ATTTT	115
	(2) INFORMATION FOR SEQ ID NO: 1409:	

5	(A) LENGTH: 123 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1409:	
10	AACCAGATGA AAAGCAAATA TACATATATA ACTCTACATG GGGTCGTGGT TTGGATATTG	60
	TTCATGATGC ATTCGGTATG CCAATGACAA AGCAATATAA AGATAAATTn CAAGAAGATA	120
	AAA	123
15	(2) INFORMATION FOR SEQ ID NO: 1410:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1410:	50
	CTNTTTATAT TGAGGATTTT GTATCATATA TGGATAATCA TTAAAGGTGT ATGCTCTTGT	60
	TATCAGATCG CTACGGGTAA AATCGCTTCT ATAGGGCATT TACATGCGGG CTTCTGCCGG	120
30	(2) INFORMATION FOR SEQ ID NO: 1411:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 455 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1411:	
40	TCTCGTATTG CGTTTAGAGA ACATGCGCAC AAAGGACAAA TTCCAGGTGT TAAAAAATCA	60
	AGTTGGTAAA ATCAAATTTC GTACTTTAGC CCATTTACAA TATCAATAAA ACAATGTACA	120
	GTATATACGA ATGCTATAAA CTGAATGTTT TCTCATATTA ATAAGGAAAC ATTCGGTTTT	180
45	TAATTTGCAT TTAAAAATAA TTAGTTTTTA AAGGGGCTAT TTAAAGTGAA AATATTTGAT	240
	TACGAAGATA TTCAATTAAT ACCTAATAAA TGCATAGTTG AAAGTAGGTC TGAATGTGAT	300
50	ACAACTATCC AATTTGGTCC GAAAAAATTC AAGCTACCTG TAGTTCCTGC GNATATGCAA	360
	ACAGTTATGA ATGAGAAATT AGCGAAATGG TTTGCTGAAA ATGATTACTT TTATAATCAT	420
	GCATCGTTTT GATGAAGAAG CAAGAATACC TNTTA	45

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1412:	
	ACAATGTCAA ATCACAATAG CTGTTGTAGG CATTTGATTA CAATGAACTA AAGGCAAAAT	60
	TGGAGCAGTT ATCCATGAAT GATTAATAAC AACANAAAGT ATGGGGTCAA GTTTAGGG	118
15	(2) INFORMATION FOR SEQ ID NO: 1413:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 245 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1413:	
25	TGTTGACGAT ATAGGAATTA GCAAGAAATA GGCTAAGATA GTTTCGCACA ACTTGGGGCC	60
	CANCCACTTG CTTGTTTGTA GAATTAGGGG TCCATTTCTC GTGTTGGGGC CCGAACTAAT	120
	AGTATGAATA TATATATCTA ATATTAAAAC GGCAATATTT ATATGGTATA CATTTTTATA	180
30	TTTAGTnTTT GTATAGACAT GCTAATTAGC ACTTTCTAAA AAGGGTTGAA ATGATATACT	240
	GATGA	245
35	(2) INFORMATION FOR SEQ ID NO: 1414:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 252 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1414:	
45	TTTTTGTTAT TCAAAATTTA GAGTGTGTTA TATGATAACG GTTTTTTCAT AGCGACTTGA	60
	TCATTTTCG AAATGATGAA AGATATGCAA GTTCAATCAA TCGGAACAAA AATACTATAT	120
	TATGGTAAGA ANTTCCCGAA GACTAGCGCA CTCACACACA AGTGCATCCT CGCGAACAAT	180
50	GCGCACTTTT CACAAGCACA CAAACACAAG GCACAAGTGC ACGCANTATT AGACAATGGT	240
	CTACCTACCA GA	252

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(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 112 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1415:	
	ATCTGCTGGA AGAGAAAAA GACGCTCTTA AAACTGGCTT TAGAAGGTCA AGATATAGAA	60
	GNTATTAAAT CTAAAAAAGA AGGAACTTGA AAAAGTGATT CCAGGAATTT TC	112
15	(2) INFORMATION FOR SEQ ID NO: 1416:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1416:	
25	CTCAATTACA TTCAAGAAAA TGGGTGGAAT TACACAACGT TGGACTGAGA AGTATAGTTA	60
	ATAGCGCAAA TGCNATAAGC CTTATATAAA AATGGGCACA ATTATTTCAT GTACCAACAA	120
30	GAAC	124
	(2) INFORMATION FOR SEQ ID NO: 1417:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 121 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1417:	
	TTCAAGAGCA CATACTGTAA CTCGTACGAG AATTTTTTCA AAATGACGCG TCAATCTCAA	60
45	TATCATCATA TGGTATTCCG AGTAATACCC CTCGnCACCT TTTTTAGGTA GCGTCAATAT	120
40	T	123
	(2) INFORMATION FOR SEQ ID NO: 1418:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 123 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1418:	
	CTACGCCATC AAGAGGGTGT TAGTGCTATT AACTATTGCG GCGAGAGCAA TTAGTCGAAT	60
5	GCAAATTAGG ACAAGTTGAT GAGTAACTAC nGCCAATATC GGTAAGTTTC ATGGCGGTTC	120
	AGC	123
10	(2) INFORMATION FOR SEQ ID NO: 1419:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 109 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1419:	
20	CTTATAATCC TTACnGCAAT TTCACCTTGT ACGGAATTAA ACAACGGAGG CATTTACTTA	60
	CCCCCTTTAC TTAATACGTA CCAAAACTTG GTCGTATTCA ACCATTGGG	109
25	(2) INFORMATION FOR SEQ ID NO: 1420:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 121 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1420:	
35	GCTGTnGTGC TGCCAAGATG CTGATTGAAA AGTATATATG ATTGCATCAG TAGAAGAGCG	60
	AGCAGAAAGA AGATATAAAG ATAATCAGTT AAGAGGTGTC GAATCAAATT TTGAAGATTT	120
	A	121
40	(2) INFORMATION FOR SEQ ID NO: 1421:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 128 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1421:	
	TGTTTTTACA GTCACATACA CTAGGCATCC TAGCATTATC TAAATTTAAT ACCATCGCAA	60
	CTTGCGCTTT AATCTTCAAG GCCAATTAAA CCTCCTTCAT CTTTCTAACT GCTTANATAT	120

(2) INFORMATION FOR SEQ ID NO: 1422:

5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1422:	
	GCCAATCATT GTCAATGTTC AGGCATCANA TTTATCGAAT GATTTTCATT TGCCATGATC	60
15	AGTCAAGGCG GGGATTTATT CAAAAATTAT GACGCCTAGT AAAAAATTTT	110
	(2) INFORMATION FOR SEQ ID NO: 1423:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 111 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1423:	•
	ATTACCTTGC ATGAATTTCC ATCTGTCAAA TGTGCGCCTT CACGAATTTG TTCGATAAAG	60
30	ATACGTTGGT CACCGTGAAT AATTTCACCA GCTGCATTTn TCCATGGACC A	111
	(2) INFORMATION FOR SEQ ID NO: 1424:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 200 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1424:	
	TGTTGTGTGA TTGCGTATTC TCAGGTGAAT TCTTACATAT ATAGTACTTT TTGTTTCCGC	60
45	TTGATTTGAC CTTGCATATC TTTCACATTC TTCGAAAATT GATCAAAGCn CTATTGAAAA	120
45	ACCGTATCAT ATACAMACCT CTAATTTTT TGACTAACAA AAAGAATTCT TTGACGTATC	180
	AACTATATCA TCATGACTTC	200
50	(2) INFORMATION FOR SEQ ID NO: 1425:	
55	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 119 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double 	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1425:	
5	TTTCTATAAT TTTAGACTAT TTCTACCATG TTGCTGAACA ATTTACTTAG ATAAAAATTA	60
	THAAATTTTG GTCAATTAAC AAAGTTAGTT TGTTAAAACG TATACTTTAA TTATTCCGG	119
	(2) INFORMATION FOR SEQ ID NO: 1426:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 116 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1426:	
20	AAAATGGCGT TGCATTTTAC TCTAATAACG CTCAAGGCGA CGGCAAAGAT AAACTAAAGG	60
	CACCTATTAT CGAACATAGT ACTCCTANCG GACCTGGAAT TTAAATCAGA GCGGCC	116
	(2) INFORMATION FOR SEQ ID NO: 1427:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 212 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1427:	
	TTTTATTTAC GTATAAGTGG GCGTTAGGTG TCACAGCGGT TGTCGATCAA AATATCATCA	60
35	TCAATCTTGT ATATGGGTTT GCGGATTCTT ATTTTATGAT TTTACAGAAC TATCCTAGGC	120
	TTATTCTTTA TTAAAAGATG CAACHAGTTA TATAAAAAGA CGAATCTATC AACGCGAGCT	180
40	GCTCACAAGG CATCTCnTAT AGCGTCCACA TC	212
	(2) INFORMATION FOR SEQ ID NO: 1428:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 265 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1428:	
	GAAAAATTGG TTCTGAATAT AATGGTGCCG TATACTTTAC GCCTCAAATC AAAGATTTTA	60

	ATTITAATGA AAAACATCGG TCGAATATAA CATAAAAAAA CGTCTATATC AAAAGCATCA	180
	TGAATAAACA GAGGAGCACA AAAATGAnTA AAAATATAAT CATCAAAAGT ATTGCGGCAT	240
5	TGACGnTTTT AACATCAATA ACTGG	265
	(2) INFORMATION FOR SEQ ID NO: 1429:	·
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 145 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1429:	
	CGTACGAAGG ATTTGCAAAC TTCTTCATTC AACAAGCTAA AGAAGAACGT TTCCATGGAC	60
20	AAAAGATTTA TAACTATATT AACGACAGAG GTGCACATGC AGAATTCAGA GCAGTTTCAG	120
	CACCAAAAAT TGACTTTTCA AGCAT	145
	(2) INFORMATION FOR SEQ ID NO: 1430:	
25 30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 115 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1430:	
35	ACACCGCTAA GCGTATTAAG ACAGGATCTG AAAATGGACA CATCGCAATC GAATTATTGC	60
	AATGCCAAGT CATATCGGGG GTGAACCGCA ATTTCAGGNA TTAAGTGGAT AGGTA	115
	(2) INFORMATION FOR SEQ ID NO: 1431:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 211 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45	(5) 10103001. 1111001	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1431:	
50	nATGTATTNG TGAAAAGGTC CTGAGTGGAC AAAAGACCTA AATATTTAAT GGTCGATTAT	60
	CGCACGTCCA TAGTTGGTGA ACAGGAACTT ACACGTACAT CTAATCGCAG ACTATGCGTA	120
	AACTTTGGAA ACTGCTAGTC ATTGAAGCGT GGTATGTGTA TGCACGTAAA TATGCATTAG	180
55	•	

	(2) INFORMATION FOR SEQ ID NO: 1432:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 145 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1432:	
	GGAATGATTG ATAAATTGGA CTACTTAAAG ATTTCGGTAT CGTGTCATTT GGCTCAGTCC	60
15	ATGTTTAATC ACCTATGNTG ACATGGTATG ATATTAGTGA CTACCAGAGA TATGGATGAT	120
	TTGGAACGTG GAGGACTTGA TCGTT	145
	(2) INFORMATION FOR SEQ ID NO: 1433:	
20 25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 169 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1433:	
30	TTTATTGCAT TTACATAATA ATATCCTTTT GTTGTTTTGG TATTTCTATT CATATACAAG	60
	ACCATACCTT TAACTTTCAG AGCTTCCCCC TTATTTTGAG TTGCCATTTC AGAACCAATA	120
	ATCCATGTAC CTTTATCATT TTTATCAAAT TCGTCATCAC GATAACCTn	169
35	(2) INFORMATION FOR SEQ ID NO: 1434:	:
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1434:	
	GATCTATAGT TCTGTAATCT GACGTGCTTT GCCATGTGCA CCACTCGTCn TAAAAATCAC	60
	TTACACTTAA CCCTTTTCCA CCTTTATCGT ATCCACCTTC AA	102
50	(2) INFORMATION FOR SEQ ID NO: 1435:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 116 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1435:	
	TTCTTATTAT ACAAATAGAA GCCATGTGTG CTTATATCGC AGCATCATGA CTCCTTTTTC	60
5	ATTTGAATAT ATAAATAATA CAGnCGCTTT CGAATAAATT TAGGCTAATT CTACCA	116
	(2) INFORMATION FOR SEQ ID NO: 1436:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 144 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1436:	
	GGGGGTTTAT GTACTGGTGG ATCTGCAAAC TACTTGGCGT AAAGAATATA CAGATATGGT	60
20	AANGAAAAGT TTAGATTCAC ACGCCATCAC AATGGATTAG AAAAACCGAA TTTCTTCAGC	120
	AATTCTACAA TTTCTAGTAT ACGC	144
0.5	(2) INFORMATION FOR SEQ ID NO: 1437:	
<i>25</i> <i>30</i>	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 101 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1437:	
<i>35</i>	GTTGCTGGGn AACCTATGGT CGAACATGTA TTGGTAAAGT GTGAAAGGCT CTGGTGGCGA	60
	TCAAGTTGGT AACCATCGTA GTACATGGTG CTGTAAATGT A	101
	(2) INFORMATION FOR SEQ ID NO: 1438:	
40 45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 321 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1438:	
50	AAAGATGGTG ACATTTCATA TAATCCGAAT GTGCCAAGTT ATTCAGCAAA GTATCAATTA	60
	AGTAATGATG ACTACAATGT GAAGCAACTT AGAAAGAGGT ATGATATACC AACTANGAAA	120

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	AATTTAGAGT TTACATTTAT AGAAAATAAA GAAGAAAACA TCTATTTTAC GGATAGTATT	240
_	AATTTCAAAC CTACTGAATA GGGTTAATAG AAGTTTGAAA TGAAAATTTC hTAAAGTGTG	300
5	CAAAATAATT TGTCGCTTTA G	321
	(2) INFORMATION FOR SEQ ID NO: 1439:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 135 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1439:	
	CAGTTGTAAT GGGACCTGGG CCAATCGGAT TACTTGTAGC ACAAGTGTTA AAAAGTAAAG	60
20	GCGCAACTGT TGTGGGTACT GGGTTGGGAC AATTGACCAA GTCAGATTAG ATTAAAGCCA	120
	GAAnGCCATT GCCAC	135
25	(2) INFORMATION FOR SEQ ID NO: 1440:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1440:	
35	AAATTATTTT GAACACTTTA TGAAATTTTT ATTTCAAACT TCTATTAACC CTATTCAGTA	60
	GGTTTGAAAT TAATACTATC AGAAAAATAC ACATTTnCTT CTTTATTTCT	110
	(2) INFORMATION FOR SEQ ID NO: 1441:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 436 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1441:	
50	TCTCTTTTGG ATTCATTAAG ATTGCnGCAT CGATACCAAC GTTMAACGGT GATTGTGTAA	60
	TGAATTTTTG CCACCAAGCT TTTTTAACAT TATTCTTTAA TTCAACACCT AAAGGACCAT	120
	AATCCCATGT GTTTGATAAA CCACCGTAAA TATCACTACC AGGGAACACA AAACCTCTGT	180
<i>55</i>		

	GAAAACGCCC CATGGAAAAT AACAGCATAG TAAATATGCT TTACTTCCAT GGGACGAGTT	300
	AATATTTTAA ATTGTATATA ATACAAAANA AGTNACGTAT TTAACCCGCG GTTCCACCCA	360
5	AATTAGTGTA GTCACTCGCT TTTATTTTAA AATGATTCGT TGCGCCAATC TTATTGTTAA	420
	GCTTACACTA TCCTTA	436
10	(2) INFORMATION FOR SEQ ID NO: 1442:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 461 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1442:	
20	ATTTTAGAA GCATACTGCG AACGTCATCA CATCGATTTA CATATCAAAA AGTTAGATTT	60
	GTCGCATAGT CTCGACCGAA ATAACAGCAT TCAGAATGAA GCTCGAATTA AACGTTACGA	120
	ATGGTTTGAT GAAATGATGA ATGTATTAGA AGCGGATGTA TTGCTAACGG CGCATCATTT	180
25	GGACGATCAA TTAGAAACTA TTATGTATCG TATTTTTANT GGGAAATCAA CACGTAATAA	240
	ACTAGGATTT GATGAGTTAT CGAAGCGAAA AGGTTATCAG ATTTATCGAC CACTTTTAGC	300
30	TGTCTCTAAA AAAGAAATAY AACAATTCCA AGAGAGATAT CATATTCCAT ATTTTGAAGA	360
	TGAATCHAAT AAAGATAACA AATATGTTAG AAATGATATT CGTAANAGAA TTATTCCAGC	420
	TATTGATGAA AATAATCAAC TTAAAGTATC GCATTTATTA A	461
35	(2) INFORMATION FOR SEQ ID NO: 1443:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 143 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	`	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1443:	. 60
	AAAGGTGATA AAAAACAAAG GCATTGTAAA TTACTTGAAA ACCAAGTGAG TTATTACACG	120
	ATTCTAATTG GGATAATGCG CGATATTTTA TTCCACACTT GTTACATTAT TGCTTTACGT	143
50	GGGGGTTAGC GTGGANTCAT CAC	
	(2) INFORMATION FOR SEQ ID NO: 1444: (i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 90 base pairs	

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	1743
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1444:	
	TGGTGTTGGT TCATCAGTTG TAAACGCGAT TGTCACAAGA CTTAGAAGTA TATGTACACA	60
10	GAAATGAGAC TATATATCAT CAAGCATATA	90
	(2) INFORMATION FOR SEQ ID NO: 1445:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 218 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1445:	
	ATTGAACAGT GACAACAAT GACAACAATG AATGACCAAC TGAGTTGCAG AATTGACCGA	60
25	CCTGACTTGC TGTnAGATGT GCATTGCCTG TGACCAGTTA ACTGCTGTTT GTACATTATG	120
	ATTGTGCACG TGAAGTCTTT GCAAATGACT TTTAACATTA TGCTGCTAGA GCCATCTTTT	180
	AAAGATGTTT GGACTAACGT nCATGATGTG AATATCTG	218
30	(2) INFORMATION FOR SEQ ID NO: 1446:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1446:	
	TTTGACTTGA CATTATAGAA CACAAATTCA TTTGAAACTA TGTTTTCAAA TTTATTTATT	60
	GTTACTGGGA ATTTCACATT ATTAGATTTA TTTATTTTCT TTTGA	105
45	(2) INFORMATION FOR SEQ ID NO: 1447:	•
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1447:	

	AGACTGAAAA CTGCATATGC AGAGGCGATG AAACAAAATG CCAT	104
	(2) INFORMATION FOR SEQ ID NO: 1448:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(b) Topologi: Timear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1448:	
15	TTGAATTAAC TGAAGAANTA GCAGTGCAAG CAGGATTGTT GATATGACAA CATTCGAGTC	60
	AGAATGGCAA CAACAACGTG ATTCGTGCAC TCCAAGCACG TGCA	104
	(2) INFORMATION FOR SEQ ID NO: 1449:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 349 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1449:	
	TATTAATTTT TTTTAATATG GAATATTCAT TGCATCGCTT TCCTATTCTT CAAGCCCACT	60
30	TTTTATCTTC ATATACATTA ATTAACCACC KTCAAACATT GTCGTTAGAT TCGCCAAATT	120
	GAATCTATTT TTAGCACAGC AAAAAACCGA ACTGCTGAAA TAATGCATCT CCAACAGTCC	180
35	GGTCTATTAA ACTATTTACT TATCTTTATT AAACAATTGA CATGATTTAT TAGAATAACC	240
	CAATTGGCAT GACCATGCAT CAGTAACATC CATGTTTAAT GGCTGCTGGT TTTTTAGGTA	300
	AACCAGGCCA GAGTCATGGn TGGCACCTGn GCAACGCnAC GATAAAGCC	349
40	(2) INFORMATION FOR SEQ ID NO: 1450:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1450:	
	GATTTTATAT AAATATAGCT TTTCAACAAA ACAAATGATT GAATTTCTAG GAATTGAGTC	60
	ATTAAAAAA CACTTGAAAA ATTCAGGTGG GATTGCGCTA TTGCCGGAAT TTATTGTTGC	120

	AGAAACAACA TIGATAATTA ATCCTGAATC GAATAAGCAM GTACTTGAAT CITTTGTAAA	240
5	AGATGTTTTT TTATAATTAT TGGTGAAAAC GTGTAGTTAT GGTGAAACTC AAAGATAATA	300
3	ATTTAAATGA GATGTTAATG AAAAAGTAAT TCAATATANA ACAGGTGATT TANATCTTAA	360
	TAAGGnTAAT TCCAGGTTGA ATTCCAATTG CGGGCATCAT	400
10	(2) INFORMATION FOR SEQ ID NO: 1451:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1451:	
20	TGCGTTATAG TTGCTATTCT CAATTATGTT CGCGATAATT TTAAGTAAAA GTAAGCACAG	60
	ATATTGAATT TGATAGGAGT TAATTGATAT ATACATACGA ACTTTCATGG ATCACTTAAA	120
	TTnG	124
25	(2) INFORMATION FOR SEQ ID NO: 1452:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 126 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1452:	
	TGTATTAAAA ACCTTCCACC TTTAAAAGCA ACAATGCGGT GTCCTTTAAA TTCAAACATA	60
	ACCATATACG AATTACTCGA TAATTCTGTG TGTTTAATTG ACAGATGTCG TGTGAATTGA	120
40	TNATTT	126
	(2) INFORMATION FOR SEQ ID NO: 1453:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 280 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(with growning programmer)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1453:	
	ACTTTGGCAA CATCTGGAAT ATCATATAAA TCAAGTAACT TACCTAACCG ATGATTAATA	60

	CTAACAGTTG TTTCCATGCC TACACCTCAC GATATTATCA CTATTCATAT TAACATTATA	180
	TGTAAGAAAT TAAAATCTTT TGAAGCATTA AGATTACTTA TCATTTnTAA ATTTCAATTT	240
5	AAACTAACAG TAATTTATGT AGCTTTTGNA ATTCTCATAA	280
	(2) INFORMATION FOR SEQ ID NO: 1454:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 242 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454:	
	ATATTCTTTA AATTAAACTG ATCACTTGAA TAATTAACAT TACTTAATTC TATGGCATTC	. 60
20	ATGATGATTC CTCCTCATAA ATGAACGTTA AAATATCCTG CAGTTCCTCA AGTGACATTT	120
	CGATGGCTTG CGCTTCATTA ACCAATTCTT TAACCAAATT TTCAATGGTA AAAAATTGTT	180
	TCTCTTTTAA AATAGGAACT ATTCTTnGCT CCTTAACAAA GGnCCCTTTT CCTCTAATTG	240
25	TT .	242
	(2) INFORMATION FOR SEQ ID NO: 1455:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
3 5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455:	
	ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA	60
40	TTGATGTGAC AGATCAAGTG AGACTTGCAT ANTGGTATTT TATTCAGATG	110
	(2) INFORMATION FOR SEQ ID NO: 1456:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456:	
	ACCAGTGGTT GCCTTTTTAA GTCCCGCGTG GGACAAAAAT TAACCTCTTT ACACTTGCAA	60

1962

	AAAGCGCTTG CAATATATTT TCGATTTGTL ATTCAACMAA ACGTTTTATT LTATTCGCTG	180
	TAGTCAAATG TATACCCTTA TACTGACTCG aTAATCATTT GCTTATnATT TGAGACTAGG	240
5	ACATAAATCA ATGCTCTAGA ATCCAAAAAG TCACATTAGT AGTAGTTAAC CGAACGAAAA	300
	TGCACTTGTA ACAAGCTTTT TTCAATTAAA GTCAGGGGCC CCAACATAGA GAATTTCGAA	360
10	ATGAAATTCT ACAGGCAATG CGAGTTGGGG TGGGACGACG AAATAAATTT TGCAAAAATA	420
	TCATTTCTGT CCCACCTCAC TCAAAATAAA TTTCACTATC CGTAAAATAA ACAACTAACT	480
	ATTTAAGTAT CATCTCCCC CTAATTAACA ATTATAAAAA TAAGAACCAA TATTCGAGAC	540
15	AACCTAATTA A	551
	(2) INFORMATION FOR SEQ ID NO: 1457:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 109 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	\cdot	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1457:	
	ATCNGGGGCT GCATAAGCGA TATCAAGTGT GAGCATTGAA CGATTCAGGA CTGACCAGCA	60
30	CGCCGTTTGC CTGCTTTGAA AGATCCACCG ACAAATCCGC CAACATCGT	109
	(2) INFORMATION FOR SEQ ID NO: 1458:	
3 5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	-
40		
••	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1458:	
	ACCAGAGCCT CTTTGACTTC CTAAGTCGAA TAGCATCGTT GATATAGTTA AAGATGACGC	60
45	TAGATTTAGN AATCCAAACT CATAACACCT CCACCATTCC ATCACATCTG GA	112
	(2) INFORMATION FOR SEQ ID NO: 1459:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 224 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

1963

	CCCCAACCAA TTTTTTAAAA AAGGGGGCCT TTGGGGGGGC CAACCAAGGG GGAACCCCTT	60
	AACCCCAATT TTGGCCAATT TTAAAGGGAA GGCCTTGGAA CCTTTTTGGG AATGGGCCGG	120
5	TTTTAAACCC TTGGTTTCCG GAAGGGGAAA ATTTTTAAAA AAACCGGAAT TGGTTGGCCC	180
	CCTTTAAATT AAAAAGTTCC CTNAAAAANA AATTCCCCCA AGGG	224
	(2) INFORMATION FOR SEQ ID NO: 1460:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 135 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1460:	
20	TTTCGACAAT CAATTCGACG TCAGTGCCAC TCCATCTATA GTAAAGCGTT GATACTTTCA	60
	ATAATAACTG GATCACTGTC TAATTATAAA TGGATTCTTA CATCCCACCA TAATAAATTn	120
	CATATGTTCA TCACC	135
25	(2) INFORMATION FOR SEQ ID NO: 1461:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 114 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1461:	
	TTATAGAACC TCGTACTCCT nTCGACACTT GAATTTAAAT CAGAGCCGCC AGTGGAGAAG	60
	CATGAATTGA CTGGTACCAC TCGCAGAAAG TAATGATTCT AAGCCACTTG ATTA	114
40	(2) INFORMATION FOR SEQ ID NO: 1462:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1462:	
	GTTGAATTGT TGGTGATGTG GTTACACGAA TTTCGAATAA TTGTTCTTTA CGTCAAAACG	60
	TATCGTTCCA AAGTAATCCC CNGGTAATAG TTACCAACAA GTTCA	105

1964

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 162 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1463: TTGTATGACT CTTCGGACTT TGGTAAAATT GTGAACGCTG GnTGAATGAT TTTTGTTTGA	60
	CAATTGGCCT TATCATCATT AATCGTATTT TTAAGCTGCT CGGATATAAG TTCTCAGCGA	120
	GTTCTTTTTG ATGTATCATT AGTGTAGAAA ATAGCTGTTT GT	162
15	(2) INFORMATION FOR SEQ ID NO: 1464:	102
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 103 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1464:	
	TAAATTGGAA AGTCACATTC AAnATGCGAA AATGTTTTAA AATGTCCTGT AGGTGCTTAA	60
30	TAGTTTTGCA TTTGCAAATT TTACTGAACC GGTTTAAACG AAT	103
	(2) INFORMATION FOR SEQ ID NO: 1465:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 153 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	<u>.</u>
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1465:	
	AAATTGTATA ACTACCAAGC TTATATGAAA TGGTAAACAA AATATTATCA CTTGTTTGAT	60
45	AAGTAGCGTG GAAAATATTG TATCTTTCTA AATGTACACG TTAGAAnTCA TGCTTATGTA	120
73	TTACACGCGG GGCACTGGTA CCTAAGGGCC TAT	153
	(2) INFORMATION FOR SEQ ID NO: 1466:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1466:	
	TTTCAGTAAC ATATGAAAAC TTAATTAACG ATGTTCAGTA GGTTCATACA TTTTACTTTA	60
5	TGATGCTTAA TTGAATTACA nTTAAGATAT GACCAGCTAA AAAGAGTTAA TGTGATATTT	120
	AACC	124
	(2) INFORMATION FOR SEQ ID NO: 1467:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 354 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1467:	
20	AAGGAATTAA GTTTGCGACA CCAGCAAATA GTACTAATAA AGGAATATAT GGTAAGTCAA	60
	TAATTGAATA ACCGATATAT AAGAATATAC CTAAAATAAC ACTGACAGTT ACTTGACCTT	120
	GAATGTAAGA TTTTAATGTA AAGTTTAAAT CAGTTAATAA ATCTACGAAA AATACTTTAC	180
25	GTTCACCTTT GANAAATTTA GCAACAGCTG GGATAAATTT TTCATGGTCT TTTAACATAT	240
	AAATTAAGAA GAATGGAACC ATAATCAATA AGAAGATGGT TGAAATTAAT GATGTAATGT	300
30	ACTGTAATGA ATTAGATAAn ATATTAGNAA CGCCATCACC CATTGATTTA ACCA	354
	(2) INFORMATION FOR SEQ ID NO: 1468:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1468:	
	TGCAAACTAG GAACAATAAT GTTAATATAA CTATGATGNA AGTTAAAAAA TAAAAAGGAA	60
45	CACTCTATAA TATGAATTAG GGTTTACAGT TTTTTGAGTA TTTTACAGTA TCAAAGTTTA	120
45	(2) INFORMATION FOR SEQ ID NO: 1469:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 476 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

1966

	TCTAAATGCT GACTAAAACT AGCAACACGA GACTCATTAT TATTAGACAC GATTGTAATA	60
_	GTGATTCCTT TTTCATTAGC TTCCTTAAAC CATGCTTTAA CACGTTCTGT AGGTTCTTTA	120
5	ACATCCCAAC CTACTAGCGT ATTATCTAAA TCTGTAATAA TACCTTTAAC GCCTTTGTCC	180
	ACTAACTTGT CTAAATCAAT TTGAAATATT GATTGAACAT ATGAATTCGG CATAAAAAAC	240
10	TTGCGAACTA AACCCATTTA ACTCACCTTT ACCTTTTTAT AATTGAGACA CTAATGCTTC	300
	AACAGTTTGA CTTGATGATA CAGCTGCTTT TTCTAAAAAT GCTTCGAAGC TCATTTCCGC	360
	TTCTCCATTT GCTAAGTCTG AAACTGCACG AACTACAACA AATGGTACAT TAAATTGATA	420
15	ACATGTTTGT GCAATTGCAG TTGCTTCCAT TTCAACCGCC ATCGCATTTG GAAATG	476
	(2) INFORMATION FOR SEQ ID NO: 1470:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 156 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1470:	
	CACCATACAT GGGTAAGGAT ACTACTCAAA TCAACTTGAA ACCAATAATn CATGACCATA	60
30	TGTGTGCCAA TGAATTCAAT TGGAAAGACA ATGATGAGAT ACTATTAAAA CGATTATATT	120
	TATTGTCACT TGTTCAAACG CACTCCTTTT CCAAAT	156
	(2) INFORMATION FOR SEQ ID NO: 1471:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1471:	
45	AACAAAAGTT TTGAAAAGCC GGGTGCCAGC GAAAACTTAA AAAGCACTTT ATCAGAAAAA	60
45	GCTAAGAAAA AAGATTAATA TTCATTCATT AAATATAAAT CCAATTTAAT TTGTTGTTTA	120
	AGGTCTACAA GTGTATGTTT AATATACAAT TCATCGTTTG ACGGTAAATC AGATACTTTG	180
50	AAATCTTGTC GCTCAACCTC TAGTAAATCG AAATCGCTAC CAGCTGAATT ATAGGTTTTA	240
	AGTTCACCCT CTTCAATGAT TCTGTTTTCA AAGTCTTTAA TAACTATAAA TACTGGTTTA	300
	CCGTTGTTAT TAAACAACTT GTCTCTTTTG TCTAATAAGC TTATACAATC CAAATTCATA	360

(2) INFORMATION FOR SEQ ID NO: 1472:

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1472:	
	CTAGGATTNC ATCTATTTGG GATGAAAATA AGCGTTTCCT GAATCCACAA GAATATCCAG	60
15	TCGATTTAAG CCAGGCATGT TGGGGTAATA ACATAACGTT TTTTGA	106
	(2) INFORMATION FOR SEQ ID NO: 1473:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1473:	
	TATCTTACCT ACATTGTTAT CTGATGGCTG TAATCATTAA ATCTATAACA CCGAGTTCTT	60
	CCATTAATTT TCAGCTTCAT TCGACTGCCT TTTTATnTTT CGTACTATTA CGAATTT	117
30	(2) INFORMATION FOR SEQ ID NO: 1474:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 164 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1474:	
	ATGCATGGCA CTGGAAnCAG CTGGGAGATA TAGGTAGTAT CCTAAAGAAG TTCAGTTAAT	60
	CGGAGCGATT GTATTGCATG AAGGTAACAT TGCGGAGTGC CAACAGGCGA AGTAAAACTT	120
45	AACGGCAACC ATGCCTTATA TTAAATGCCC TTCCGGGAAA GGAC	164
	(2) INFORMATION FOR SEQ ID NO: 1475:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 210 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1475:	
	ACAGCAAGAC GTGACAAATC AGATACTATT AGTCATCAGC GTTAACATGT GGATANGTGT	60
5	GAGGTACGAA TANCCGAAAG GAAATACGAC CTTTAACATT CGCGCACAAA ATGAGCTCAG	120
	GCGCCTGCCT TGCCCATTTT TTAAATTATT TCCCTGGAAA TGATTCGCTG TGTGCTGTTC	180
10	TGTCCACAAC AACACGATTA ATGCCATGAC	210
	(2) INFORMATION FOR SEQ ID NO: 1476:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 128 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1476:	
	AGGGTGATTT CACGGTTCGT CTGCCCATTT AATTGCGCAT TTTGCACACC ATCTACCGTT	60
	TGCAATTTTG GTATTAATTG TTGCATGCAG TACTGTCCGT TGACTTTGnT GCAAGTGCAT	120
25	GCTCTTTC	128
	(2) INFORMATION FOR SEQ ID NO: 1477:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 641 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1477:	
	AAAATCTGGT AAAGTAACTA GAGTTTAATA AATATATTGC ACATAAAAAA TGTGACCTTA	60
40	TGTGGAGGAC ACATTTACTT AAGAACTAAG AGCTCAACCT CTTAGTTCTT TTTTTGTTAC	120
	CAAACAATÄC ATAATGGTTC ATAGTGAAAT TCGAACTATC AATATAATTT GGTTAATACG	180
45	TTTAATAATG GTTCTCTGTC AAATTGGACT TATGGGTTCA ATATCGATTT TGGCACATAA	240
45	ATCAATGTAC TAGGACCTAC AATTTTCCTT TCAATAATAA ATCACGCCAT AATCTTCATT	300
	AATTACAGCG TGATTCATCT ATTATTATGT TATAAATKCT ATCTATAAAC GTCACTTTAT	360
50	TAAATAACTC ATGCACTTTA TTAAAAATCC TCACAAATTT GAATATACTT AATTTAAATC	420
	TGTACTTCTA ATTTGCAAAA TCAACCCATC ATGTACAGTT ACTTTCGCTT GCAAAGACTC	480
	AATTTCATTT GAAATAGTTA AAGTAGAACC TATATNAAGC ATTTGTCTAG CTAAATTATA	540

	GATAACTCTT ATCTTTTCA ACTGTAGGTG ACCTTTAGGG C	641
	(2) INFORMATION FOR SEQ ID NO: 1478:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 121 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1478:	
15	TTAACCGTGA TGCAGAGTAG TAAGTGGATn CATGCTCTGT TATGGATGAC AAGACAAAGC	60
	AGCGAATATT GCGTACTGCG ATTGATGAGC AGATGCATAT GATTGGATTG	120
	c	121
20 .	(2) INFORMATION FOR SEQ ID NO: 1479:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 133 base pairs (B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
•		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1479:	
30	ACCATTGCTT AGATAAATAC CTCGCAGTGA ACCGCATTAG TATAGCACTT CTAGCTGATC	60
	GCATCAGTAA AGTATGCTAT TAATGTCTCA GTTTTATCTG TAATGCATGT TTAAGTTAGT	120
35	CATAGCATTA TTn	133
	(2) INFORMATION FOR SEQ ID NO: 1480:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 201 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1480:	
	TTTTGGGGnT TTTAAATTTT AAATTCCCGn TGGGGGAAAT TCCCTTAAAA ATTCCCAACC	60
	CTTTTAAGGG GTGGGGGTTT TTTTAGGGAA AAAGGGGCCC GGGGTTAATG GTTCCCAAAA	120
50	AATTGGGGAA AATGGCCCCC CAAATTTTAA ATTCCCGGTT TTAAAATTGG GGTGGGTTAA	180
	ATTGGAAAAA CCCCCAAATT T	201

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1481:	
	CAGTATCAAG CATAGTAAAA AATGAGGGTA GGACTGAAAA TACGGCGTTA TTGGTGGTGC	60
	ATTCACGGTA AATATGTTGC ATGACCAGCA AGTTTTGGnC TTCTGATGCA CC	112
15	(2) INFORMATION FOR SEQ ID NO: 1482:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1482:	
25	CAAAAAACAA GTTCTGATAT GCAGTAGCTG AATAATTTTG CTAGTTACAC CANAGTGATC	60
	TTCTGGTGTT TTACTTTTTA TAAATGTTTT CATATATTTC ATATGTATAA AAATGGGATT	120
30	TAGCGTA	127
	(2) INFORMATION FOR SEQ ID NO: 1483:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 83 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1483:	
	AGTGGTGTAT TGGGTGAGTA ATGCTTAACT TCATACCTGG TGCATTGGCT GTTCAGTATC	60
	ATTATATCTG CATGGGCGAT ACT	83
45	(2) INFORMATION FOR SEQ ID NO: 1484:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 201 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

1971

	-	
	TATTATTGAT GTTCTTTGGT TCATTCTTTG GTAATAATTT TGCACTTGAA AATTTACAAC	60
	CGTTAGCTGG AACCTAGnCA AAGGGATGGG TTTAGTGGTC TATTGTGGGT TTATTGGTAT	120
5	TCCGTGGGCC ACCCCATGGG GCCATTATGG TTTGGGAATT TTGGGAATAA ATTAATTTnC	180
	CCAACCAAAA ACCAGGCCAA G	201
	(2) INFORMATION FOR SEQ ID NO: 1485:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 210 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1485:	
20	CTCACAGCAA CATCAAAGAG GCAGATATTA GTCAAGTTCA ACGTAATAAC ATCTACCTTC	60
	ACAAGTCGAT AAAGGAGCAC CATCATTAAT AAGTAGATCA ACAAGTCAAC GAGAATTTTA	120
	ATGTGCAGAA TAGAGAAGTA CACCACACAN ATAATCAAGC GATGTAATTA CTACTACATT	180
25	TTnCATGACA GAGTGAACCT CAACAGCGGT	210
	(2) INFORMATION FOR SEQ ID NO: 1486:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 158 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
3 5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1486:	
	CAGGTTATGT TTGCATTAGA AGTTCTTGGA AAATCTTTAT GGAACGTGGT TTACACCCTG	60
40	ACTITGAATI GCATCGATCT GATGAAGATA AATGAAATTG AATGGGATGG CCNACATGGA	120
	ATGCAACCTA TGACTTGGAT GGAATTAGAT GAAGCGGG	158
	(2) INFORMATION FOR SEQ ID NO: 1487:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 114 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1487:	

1972

	TTGCAGCATA TAGAGGTAGA GGCATCGCGA CAAAGTTATT AACGTCATTA CTTG	114
	(2) INFORMATION FOR SEQ ID NO: 1488:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 108 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1488:	
15	TGCTAAGTGA TAAAAAGAAT GATAAGCCAG GTGTACCAAT GGGTCCTGGA TTAGACCATT	60
	TGGGAGATAT CGTTGTACCA CATGTTGATC AACTAACGTT nCCACATG	108
	(2) INFORMATION FOR SEQ ID NO: 1489:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 112 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1489:	
	CAAnaCGTAA TTTCATGATG AAAGTGGTCG ATAATTTCTT GAAACATCGC TTTCAGTAAT	60
30	AACGCCTGCT TTAAGGTCAC GTTCCGCATA GGTGTACTGA GGATGTTGAT GT	112
	(2) INFORMATION FOR SEQ ID NO: 1490:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 265 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	•
40	-	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1490:	
	CAGAACGTIT AAAACAAAGT TGGAAAAGTT TTCTAATCGT ATTAGCTGCA TGTTTAATAC	60
45	TTATTATTGC AAGTGAAACG CTTATTTTCC TTTAGTCATT TGACCGATGT TAAAGAGGTG	120
	AGATGGTTAT TTAGAATCAT TGTATTGATT GTTTTTGCGG TAGTGATGTT CACAATTTAT	180
50	ATCTCTTATC ATCATTATAT GAATGACTTT TTAGTTACTA AGTTATTTAA TATTTCCGCA	240
	GCGACGCCAL AGTTATTATG TCTAT	265
	(2) INFORMATION FOR SEQ ID NO: 1491:	

5	(A) LENGTH: 113 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1491:	
10	Charattggc Caggggctca tccartatta aartaggcgt acgagggatt aatagaccac	60
	CTAATGAAAC GCGTTGGTTG TTGGACCTCC AGATAAATCC TGGGGGTCGG TGG	113
	(2) INFORMATION FOR SEQ ID NO: 1492:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 276 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1492:	
25	ACTAAGAAAA TCCGAAATCT TTTCCGCTTC TTTTAAATAC GTAATACTTC CTTTTTTCG	60
	CTCTAAATGT TTGGCATTCA ACTCATAACT ATTCATTAGT TTCGTTAAGC CTTCTGCATG	120
	ACTCTCATTT TGAGAAAAA TTTCCAAATG GTACGAAGAT GTTTCAGGGT TATTCACTGA	180
30	GCCACCTGCC AGAAAAGCTC CTCTCAAGTA ACTGCGTCTC ATTTCGTCAT CTTGAATCAT	240
	TGAAATGATC AATTTCATGG CGnnAAAATG CCGTCT	276
	(2) INFORMATION FOR SEQ ID NO: 1493:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1493:	
45	GATGACGAGC GCCAATTATG TCACTTTTAT GGCAAAAGCT GGAACTAAAC AACCNAGCCT	60
	GCCAGTAAAA TTGGCAATTG GGACGTTCTT AGCAGGTGCG TCATACATAC	110
	(2) INFORMATION FOR SEQ ID NO: 1494:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 200 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1494:	
	AAAAAAAGG TTTTTTACCC GGAATTCCAA ANTTTTAATC CCTTAAAAAA AATTCCGGCC	60
5	AACCCCCAAA CCCAAGGTTT TTTCCTTAAC CTTGGAAnTA ACCAAGGTTT TTTTTCCAAA	120
	AAATTTCCA AAAAAGGAAT TACCCAAACC CTTAAAGGTT TTAAAATTGG GGGGGGAAAA	180
10	AGGCCCTTTT AGGGGGGAA	200
	(2) INFORMATION FOR SEQ ID NO: 1495:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 253 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1495:	
	AAAAAATTTG GTGCATTTAT CATATGGAGT ATTAATCTGT AGAAGTAAAG GCGATATAAA	60
25	TGTTACTTTG GTAATAAAGA TTACAGCGAA CGTTATTATT GCTCAGGTCA GATCAAGAAA	120
	TTGGTGTCCG GGTGACAAGA CTTGGTGGCG CGGTGTAGTT TGTCAGTTGT GTGGTCATCT	180
	TAAATAACGC TATCGTACGG TGTGTATCAC ATGAAGGGAC TCTTACTAAT TCTGCAAGTA	240
30	CACGTCACGC nnT	253
	(2) INFORMATION FOR SEQ ID NO: 1496:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1496:	
	ACGCTAGCTT CTGAAAAAAT AAGTGAACTA TGGATGCAAT GAnCCTATTC CTGAATGATA	60
45	TTAGACGTAG CGCACCTGGT GCAGAACGCC AATAAAAAGA CAAG	104
	(2) INFORMATION FOR SEQ ID NO: 1497:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 100 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

	AGGGAGGCGC CCAAATGGCT CTATATTAAA AAAGGACTCT CAGAGCATTA ATGAAAAGTT	60
	GAAGCTCAAA AGGAAnCGAA AGAAACAAGT ATCAAAACAT	100
5	(2) INFORMATION FOR SEQ ID NO: 1498:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 101 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1498:	
	TGGAACTTTG GGGAAGTCAA ACGGTTGTAA TCGTTGAACA TAAAGTTAAA CACATTCTGG	60
	ATCATGTCGA nCGCGTCCAT TTGATGGATA TAACGGGAAT A	101
20	(2) INFORMATION FOR SEQ ID NO: 1499:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1499:	
	AGTTCTGGTG CATCGTTTTT CATTGTATTT GTGACGATTA TCATTCCAGC ATTAGAATAT	60
	TATGCATTAT ATTTAGGTGT GATAGGTGCA TTTATAGGTG GTTTAACTGT TTATACACTT	120
35	TCAGGTG	127
	(2) INFORMATION FOR SEQ ID NO: 1500:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 560 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1500:	
	TCCCCGCTTT AATACCTTCC ACGATTTCTT TAATTGCTTG CGGTTGGTCA CCTTGAGGCT	60
50	CAAAATCAGA ATGTATTTTA AAAGGATAAT GTTCAACCAT TGTCACATAT GCCTCCTCTT	120
	TCAACGTATT ATTTATATTT CCGCTCAACT CTTTGCTTTC TCATNACATA TNTTAGCAAA	180
	GTAGTCACAC AAAAAGCAAA CGTTKGTTCG TAAAAATGTC GAACAAAGAA ANACAAACAT	240
55		

	AAATACACAT TATATTAATC ATCATTTTGT TTCAACAAAT TTGTTTGAAA CATTATTTTA	360
_	AAGTTAATCT TAGCGATCTT CATCTTGATG TTTATGAAAT TCGAGTTGAT CTATAATTAA	420
5	ATAACCAGCT AATAATGACA CTACATCAAT AAAAATAATC CACTCGTTAT GGAAATACTC	480
	TITATAGATT GAGGCACCAA TTAAAATTAA TGTCAGAATA GTACCGACCC ATTTACTTCT	540
10	TGTTATTACA CTAAATAATA	560
	(2) INFORMATION FOR SEQ ID NO: 1501:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1501:	
	ATTAAATCAT ACTnACAATT ACCGATGACA TTATTCCAAT TCAATCTAAT TCCGTGATGA	60
25	AAGAGCCACG TTTTGGTTAC TTCGTGGGCG TGAATTATTA TG	102
	(2) INFORMATION FOR SEQ ID NO: 1502:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1502:	
	TATGGTAGCT CCAAATGGTT GTATCGTCAC ACCATCATCT TCAAGTGCAA TGCGATGTAA	60
40	TCGATTGGCT GTTGTTTCTG TTACCCATAG TACTTTTTCA TCTGTACTTA AAGCAATACC	120
40	ATTTGCTACG CTAATATTTT GAATGATAGG CGTCACTGTT CTAAAGTCCG GCGAAACATA	180
	ATAAACGCCT CCTAGTGGAT TGGTAGAGTA TCCTCTAAAA TCTGTAAAAT AAAATCCACC	240
45	TTTAGAATCA AATACCATGT CATCAATACA ATATGCTGTT GAAAGATCTT CAATAATATC	300
	TTGTAAGTTG TCACCATTTT CTGTAGCTGC AAAAATGCCT CCnGGAGATT TAAAATCTCC	360
	nAAAATAACC AACGNATAAA TCGGGCANCT TATGGAATTG	400
50	(2) INFORMATION FOR SEQ ID NO: 1503:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 168 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1503:	
5	TACAGGTAGT TAACAGTTGA TGTTAAATGG CGTACTGGAT TCTTTACGCA CGATTTTTTG	60
	TTAATAAGTA TGGGATAGCA CATTACTATA TCCTACTTAC GACTTATTGG ATATGTCnTA	120
	GCTATTCTTA AGCTCGAAAA GTTTCACAGG ATACATAAGG GACCAACT	168
10	(2) INFORMATION FOR SEQ ID NO: 1504:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 237 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1504:	
20	CTACTGATTG TGTAATGTCG TTGGTAGGCT TGGGCTGTAC GCAGTATTAG GTGTAGGCAA	60
	CTTGGCTTTT GGCATCTACC TTGTATGTGT CGTGTATCTA nGGCTGGGGC TTGCTCCTTC	120
25	AGTTGTTAGA CAGTAGGGGG TAATCTCAGG GGTGCAATGT ACTCCCTCCG TCCTAAAATA	180
	CTNTATATGC TCGTGCCGAA TTCCTGCAGC CCGGGGGATC CACTAGTTCT AGAGCGG	237
	(2) INFORMATION FOR SEQ ID NO: 1505:	
30	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 209 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1505:	
	CGCATTTACC ACCATATGAT GGATCCANCG ACGTTTTAAT AAAGATAAAA GTGACAGTAG	60
40	CGGGAAAACA GGnCCATAAT TCACATCTCT TTTGAAAAAT ATGTTCAAGC TAGGATCATT	120
	AGGAGAGTCA TATTAATAAT AAAAATGTTG CAATCAATCG ACGTGCGTTG AATCTTAAAT	180
45	ACATAATAAA TGTTGTAGAA GATATGGGT	209
	(2) INFORMATION FOR SEQ ID NO: 1506:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 121 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

1978

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1506:	
	AAAATGTGGC TATTGATTTT GACTTGGAAC TTTTTGAACA TTTCTCTCAA GGATTTAAAT	60
5	GTAGGTAACA GGGCAGGTAC TACGGTACTT nCCTATTTTT TTATGCAAAT TTTAAAAAAC	120
	A	121
10	(2) INFORMATION FOR SEQ ID NO: 1507:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 144 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1507:	
20	AATGACAAGG TCAGCATTAA AACCATTTAA AAATAAACGC GTTATGGTTA CTGGACGTAT	60
	ACAACGTGTT TTGTTTAAAA ATTATTTAGA TAGACATAGC ACATTTAAGC CGAATGTAAG	120
25	GATATTATTA AAAGANGTAT TTGT	144
23	(2) INFORMATION FOR SEQ ID NO: 1508:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 139 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1508:	
	CCGATTGAAT CTGTGTACAC TTCACCAAAG ATATCTTTCT TCGTTTCTTC AGATAAACTT	60
	TCCATTGCTT TCTTATCAAC ACTTGTTTCT ACTAATAAGT GTGTTAATTT GTGCTTnTTA	120
40	ACAAACTCAA TAGCTTGTC	139
	(2) INFORMATION FOR SEQ ID NO: 1509:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 155 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1509:	
	TCTGCCTGCC TCGGCCTCCC AAAGTGCTGG CATTACAGGC ATGAGCCACC ATGCCTGGCT	60
<i>5</i> 5	·	

(2) INFORMATION FOR SEQ ID NO: 1510: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 87 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 87 base pairs (B) TYPE: nucleic acid	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1510:	
15 ATCCCAATGC TAATGAATTT GCATATACGA TAAATAATGC TTTTTATCAT CAATA	AAGCT 60
ATGAATCTTT CAAGATCTTC ATTGAAC	87
(2) INFORMATION FOR SEQ ID NO: 1511:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 217 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1511:	
ATAGGGGTTT ACCAGTTATT TTCGAATCCA TATAATTATG TTTGTCCGTT TGGTT	TAATC 60
CAATTAATTG ATTAAGTTTT TCCAATTCCT TTTTTTTTAA TTAAAATTCC AATCC	
AAAATTGGA AAAAAGCCTT AAAAAAAATT GGTTAATTTT CCCAAGGGAA TTAAA	
35 TGGGGTTTTT ThAGGnCCCT TTTGGGAAAA ACCCAAC	217
(2) INFORMATION FOR SEQ ID NO: 1512:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 101 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1512:	
TGACATTGCA TCGGATTATG TTACATCANG GACAACGGGC CTCAAAAAGC GGTGG	CACAAA 60
50 CGTTCCGTAA TCATATGCCA GTGCAATCGG ATGTAAAGAG A	101
(2) INFORMATION FOR SEQ ID NO: 1513:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 114 base pairs	

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1513:	
	GATTTTATTG AAATGATTTT ACCTGTGATC AATTATTGTA ACAAATCTAC AATAAAATTG	60
10	TCTTACTGCA TGACCTAATA ANATAGCAAC AGATATCATA CACACTTGTA ATTT	114
	(2) INFORMATION FOR SEQ ID NO: 1514:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 77 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1514:	
	ACATATACAG GTACGTGTTT AGTCCGTCGT ATACTGCAAA ATTATGTCCG ATGAAATTAG	60
25	GGGAAAATTG TAGAACG	77
	(2) INFORMATION FOR SEQ ID NO: 1515:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1515:	
	CCTTATAAAG TTAATGCAAG CAACATGGAC AAATTATTAN TTGAATAAAC TGCAAGAAAG	60
40	ACAACAATCA TTCTTCGGAA TGCTAGGAGA ATATATTTTA GA	102
	(2) INFORMATION FOR SEQ ID NO: 1516:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 89 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1516:	
	CAATTTTAAA TAGGATTTTT AAGACCTTGG TTGGGTTTTG GTACAATTAA TGGGGACATG	60
	ACTAGGTCTT GCCACGTTTA TATGCATCT	89

5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1517:	
	GTAAGAGTGC ATAGTTTTTA AATGTTGCTT GTCTGGTnTC ATTTTGGCAC CATACAGTTC	60
	GTACCTGGAT TAGGGAAATG CCAAATGTCC GCGTAGTGAT AT	102
15	(2) INFORMATION FOR SEQ ID NO: 1518:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 448 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1518:	
25	GAGAACTCCT TACCACAATC AAAAGTAATT GATTTAAATA TATGAGAAGA TAAAATGAAA	60
	AGGTGCAAGC AGTATTAAGA ATTTAGGTAG CAAGAAAACA AGAAGTGGTA CATACGATGC	120
30	TAACCTAAAA AGAATTGGAG ATTAAAATGA TTATTAACCT TGAAACACAA CAAATACATT	180
50	TTGATTTAGA ACATGAAATT CCCTATTTTC AAGCACCTGA GAAAAATAGG ATACGCTTAG	240
	ATATTGATGT TCTCAATAAA AAGCnAATTT CTAATATTAT TAATGTTATA TTTAATAACC	300
35	AATCAAAGAC GAAATGTACA TTTTTGTCTG AATACTTATA TCCTGTTAAA TTTAGAGAAA	360
	AAACAAGAAT TGGTCGTTTT TTTAATATTA CTAACTGGTA CGAAGAAATC CATTCTACCG	420
	ATGAGAAGTA TGTnATTGCA ACTATTAA	448
40	(2) INFORMATION FOR SEQ ID NO: 1519:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 304 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1519: ATGGACGAAA GAAGATGTCA TTGCTTTTGA AAACCTAACA AATATTAAAG TAAATTTAAA	60
	•	
	AGGTAGCGGT TTTGTGTCCC ACCAATCAAT TAGTAAGGGA CAAAAACTTA CTGAAAAAGA	120

	ATTCAAATTC AGATGGTMAA GAAGAAATCT GACAGTTAAA ACTGACAGGG ATAAGTCGGG	240
	ACTNAACAGG AATGGGCTAC nTTTAAATTT AGGGATGGTA TTGGGCCACT ATTTGGTTTT	300
5	TGAC	304
	(2) INFORMATION FOR SEQ ID NO: 1520:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 322 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1520:	
	ATGACGTCGC ATGCACGCGT ACGTAAGCTT GGATCCTCTA GAGCGGCCGC CCTTTTTTTT	60
20	TTTTTTTTT TTTCTGTTGG CCTTTGATAA TTTTATTGGA TCAGTAACAA CTTTTTGTGT	120
	TTCAACTAAG ATAGCTAAAA TTCTAACACT TATATGTAAA AATTACACTC CATTTTAGCA	180
	CAAATGTTAA CAGAAATTAA CAGCACAGTG CCATGAAGAA ATGANAAATA CACAGCTTTG	240
25	GTAGGGNAAT GGTCCTGGAA ATAATGTAAT GCCAAGTNTC TGATCATTTA ACATATCACT	300
	CACCTCCTTC TTCATCTGAT GT	322
	(2) INFORMATION FOR SEQ ID NO: 1521:	
30	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 105 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1521:	
40	TAAATACAAA CCCTTTAAAC ATATTTACTA AGTCGTTCAA TTGTTGATTT GATAAnTGAT	60
	GTGATGTGGT ATTTTGCATC GGTCCTGCTT GATTCCAGAC ATGTC	105
	(2) INFORMATION FOR SEQ ID NO: 1522:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1522:	

	GATCGTATTT CCCAGATGTA AATTCnGTGG ACAATTGGCG TCAAATAGCT TCTAGTGG	118
	(2) INFORMATION FOR SEQ ID NO: 1523:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 157 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1523:	
15	CNGCATATAA TCCCGCGACA TGTCTTTTAC GGGTGCACTT GTAATATTAT TACCCCCCGT	60
	ATAACCCATG TATATCTATA CTTTACCACA TAAAATAATT CCGGGACTAT TTGGCACATG	120
	TTTTGGGTGA ATTTCTTTAG TGGCACACCA CCCCTGG	157
20	(2) INFORMATION FOR SEQ ID NO: 1524:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 82 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	••
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1524:	
30	ACTGAGGTAG GTTATGTAGG ACGAGATGTT GAAAGTATGG TTAGACATCT TGTTGATCCT	60
	TGAGTAAGAT TAGTCAAGGC CG	82
35	(2) INFORMATION FOR SEQ ID NO: 1525:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1525:	
45	GATACAAAAA AGAAGTTCAA TTTGAACTAT GAAGAAATTT ATATTTTAAA TCATATTTTA	60
	AGAAGTGAGT CTAACGNAAT CTCATCTAAA GAGATTGCTA AGTGCTCAGA GTTCAAACCT	120
	TACTATTTAA CTAAAGCTTT ACAAAAGCTA AAAGATTTAA AATTGTTATC AAAGAAAAGA	180
50	AGTTTACAAG ACGAAAGAAC AGTTATTGTT TATGTTACAG ATACACAAAA AGCAAATATT	240
	CAAAAACTGA TTTCAGAATT AGAAGAATAC ATTAAAAATT AAATCAAGGT TAATTGCGTT	300

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	AAAATTAACT TAAAATTTAA ATATTGAAGA GCTTAATTAA	400
5	(2) INFORMATION FOR SEQ ID NO: 1526:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 125 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1526:	
15	ACTGTCTAAT ATTCACTCCC TTAAAGTGTT TTTCATATTT TTCTATTAAT GTTCATATTG	60
	TAGGGTGTTG AATGCATCTA AGCATTMCAA GTTATTCTCC AAGTTCATCA ATTTCAAAAT	120
	GGAAC	125
20	(2) INFORMATION FOR SEQ ID NO: 1527:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 base pairs	
25	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
•		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1527:	
	CATGITTATT TATGITTCGG CTTTAATGIT GAAGAGITTT ACAAAGITTA CCGATTGCAT	60
	TTTATAATTT TAATGCATTA TTGGAGCATT GGCTATCATC TATTACTGCG nA	112
35	(2) INFORMATION FOR SEQ ID NO: 1528:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 115 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1528:	
	GCGAAGATGA GGATGAGATG ACTAAAGGAA AATATTGAAA AACAACCAAA AAACTGATGA	60
	ACATTATTAA AAATTTACAA AATCAAATCG ACAACTTGAG CGCAAGAACN AACAG	. 115
50	(2) INFORMATION FOR SEQ ID NO: 1529:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
55		

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1529:	
5	ATGGATCTTC CGCTTCTCTT AATTGATCAA TTAAATCAGA CATTTCATGT TTTTGTAAAT	60
	AATGATTCGC TTTAATGGAT TTTTTACATG ACATCATGAT TGCTACATCT TCACGTAATT	120
	TTTTGATATC TACTTTTTTC TCTTCCAAAA TTAGCTCAAT CATATCTTTA ATAATTTCTT	180
10	CTACTTCATC TTTAGGGAAC CAAACTGGAT AGCTACTTAC AATATAATCA TGACCACCAA	240
	AATGTTCTAA CATGATACCT ACTTGTTGAA GCTCATTTTT ATATTGATCA ATGACTAATT	300
15	GTTCATCTTT TGAAAAATGA AATGTTAACG GGATTAATAA ATCTTGTACT TCATTGGTAA	360
	CCTCACCTAT TTnATCTCGA AAATATTCAT ATnTTATnCT	400
	(2) INFORMATION FOR SEQ ID NO: 1530:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 97 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1530:	•
	TAACAGTCAA CCCACCCATT AATATATATT CAACGGCTGA CTGATACGAC GAACGTCAAA	60
30	GAATATGAGA GGAATAGGGA CAAGATCATC ACACATA	97
	(2) INFORMATION FOR SEQ ID NO: 1531:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 150 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1531:	
	TCATAACGGT GCAACTTAGA GCTGACGTAT AGTTCATTCC AACTATATAC GATGTATCAA	60
45	CACCATGTTC CAGTTTTAGG TTAACGATAC TGTATACCGT ATTATGTCAG NGGCACCTTA	120
	TCTTCACGTA CTTTACGGCG AGATGATGAC	150
50	(2) INFORMATION FOR SEQ ID NO: 1532:	
<i>50</i>	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 138 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1532:	
5	ATTCATTCTG CTAACCAGTA AGGCAACCCC GCCAGCCTAG CCGGGTCCTC AACGACAGGA	60
	GCACGATCAT GCGCACCCGT GGCCAGGACC CAACGCTGCC CGrCCTATCC TGAAGCCAAA	120
	GGAAATGAGA TCGGAATT	138
10	(2) INFORMATION FOR SEQ ID NO: 1533:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 460 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1533:	
	GGGGnCCnGG CAATGGAGGC GTGCTTGGAT GGTGCTTGGA ATCATCCCTT TGGCCTCGAT	60
	CATAAGCTTA AACTTTTGGT GCTGGnGCCA CTGGAGGGAA ATCTTCAATT CTGGCAAATG	120
25	GTAATTnCCT ATACCAACAT TTAAGGCATG TGGTAATGCT GGCTACTCCC GCTTCGTTAT	180
	CAGCTACATG ACAAATACAG ATGCCATCAC CTTTGCGTCC ATTTTAATCG TTGATGCTTG	240
	GAAATGTTTT TTGTAAATAT CAATGTTATC CTTCGCTGTA TGTATCGCAT TTATATCTGG	300
30	TAGCAAAAAT GTTCCAACAG AAAGCCCTAT ACCTAGTTCG GCAGCTATTT TGGCAGATGT	360
	TGCGCTACTA CTTAATAACC ACATTTCTGG AAAATGATCA TGTGTGGTGC ACTACGATCG	420
35	ACTTGGTTAT CTTTATTGTT AGATAATACG GAATACGNAA	460
	(2) INFORMATION FOR SEQ ID NO: 1534:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 145 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1534:	
	TACGCTAATA AATAGTTCAC TTTTCCATTT TGTGTAGTCA GCTCATTGTA TTCTTCAATT	60
	TGCTCTTCAT TTAATGCCGC ATAAGCTTGA TCAATAATAT TTGGATTAAG TTGTCCAATA	120
50	TACTCTAACT GGTCATGATA AACAn	145
	(2) INFORMATION FOR SEO ID NO: 1535:	

5	(A) LENGTH: 151 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1535:	
10	ACGCGATTTA ATCGTTCGTT CCAACGATGT CCACTCCCCT ACTAATAATT AAAATCATTA	60
	CAAATTATTT CAAACTTTAC AATTMAAACT AACAGTTTTC TCAATAAAAT GCAAGCTTTT	120
	CTCATTTGTT ATTTAGAATG ATTATGATTT A	151
15	(2) INFORMATION FOR SEQ ID NO: 1536:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 86 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1536:	
	ATAATAGAAT CATTACAAAT TATTTCAGAC TTTACAATTA AGACTAACAG TTTTCTCAAT	60
	AAAATGCAAG CTTTTCTCAT TGTTAA	86
30	(2) INFORMATION FOR SEQ ID NO: 1537:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1537:	
40	ACCAAACTGT AAAGCCATAT ACTGAACATA TTGATAGCAT ACTCAATGAG ATCAAATTAC	60
	ATCGTGAATT TATTATAGAA GTACCTTATA TGAATTCAAG GAAATTTGAG CTACTGATTG	120
45	CTAACATTGA ACAACTTTCT GTCGAATGTC ATTTTAAGCG AACAAGTCGA AAGTTATTTA	180
	TAGAAAAGCT TAAAAGTGTT CAATATGATT TACAAAATAT ATTAGATGGC GTAACACnAG	240
	AGGGTACTGA TGGTTAAAAC AGTTTATGTA ACAGGTTACA AATCATTCGA ATTAAACATT	300
50	TTTAAAGATG ACGCACCTGA AGTACATTAT TTAAAACAAT TTATAAAACA TAAAATTGAA	. 360
	CAACTGTnGG ATGAAGGATT AGAATGGGnG TTAATACAAG	400
	(2) INFORMATION FOR SEQ ID NO: 1538:	

5	(A) LENGTH: 136 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1538:	
	-	
10	ATATCGTTAC TGCTGTATGT TTCAATATCT ATATTCATAA ATTTCAAATn CTGACACCTC	60
	AATTTCTTTA AAATAAGGGG CAGAACCCAC TATGACTATA GGATCTCTCA CAGGTCAATT	120
	CGCAAATCAC TCGTGC	136
15	(2) INFORMATION FOR SEQ ID NO: 1539:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 85 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1539:	
	TAAATATCTC GGCACAATGA TGCGGGATAT TTTTTTACAA TAGGCATAAA GGCTGGAAAA	60
	AACATATCTA GTGCTATGAT ACTTA	85
30	(2) INFORMATION FOR SEQ ID NO: 1540:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1540:	
40	ACAATTTGTT TATTTCAACA AATTATCTTT ATTCCACGAT GTGCACAAGT GGTTGAAATC	60
	AGCTGAAGAC ACG	73
	(2) INFORMATION FOR SEQ ID NO: 1541:	
45 50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1541:	

	TGCAGGAATT CGATATCAAG CTTATCGATA CCGTCGACCT CGAGGn	106
	(2) INFORMATION FOR SEQ ID NO: 1542:	
5 10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 87 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1542:	
	ACATCAACTC ACCCATAATA TATATTCACG GCTGACTGAT ACGACGAACG TCAAAGAATA	60
15	TGAGAGGAAT AGGGACAAGA TCATCAC	87
_	(2) INFORMATION FOR SEQ ID NO: 1543:	•
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1543:	
٠	GCTTATTCTG AAAAATATTT AAATTGAAGA AAAGAATATT CTAACTACGG AAGTGGTATT	60
30	AACTAATAAC TAGTATCCTT TATAAATAAA CATAAAAATA TTCAAACGAA GGTCTACTAA	120
	ATAACTATCC ATAAAGTGAG TATAAGTTTG TTTGTAAAAC TGAAGTAAAA AGCATAAGGA	180
	ATTACACTTT AAATACATAT AGTACTTACG AATAGAAAAT AATCCCTTCA ACAGTAATTT	240
35	TTAAACAAAA ATAAGTGTTG TTTTATGTTG ACTCTACTAG AATAACTTGA TATTATATAA	300
	AAGTCGTCAA ACGGCACTAA TATTTAnnAA ACAAATGTTT TAAGTTGTTG GATTTnAAAA	360
	TATTGAATTA AAGTGTAAAT TTGGACTATT GGAAATTGCG	400
40	(2) INFORMATION FOR SEQ ID NO: 1544:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 103 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1544:	
	ATAACGCTAA TCAGCCACAT TCAGTATTGT TAAATGGACA CACAAGCAGT TGATGAAAAT	60

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(2) INFORMATION FOR SEQ ID NO: 1545:

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 108 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1545:	
	GGCTGTTATT GTTGTGGAGT TAAAAATGAA GGAAAATTAT AAACATGGTA AGCGTGTTTC	60
15	TCGTATTACT TTACTTAAAC NAACGGTATA ACCATACCTA ACTTAGTA	108
	(2) INFORMATION FOR SEQ ID NO: 1546:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 554 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1546:	
	AANTATGTTT CATATATTAT GAATCTAGCC TTAATCATAT TGCATTCAAA ATAATTTTAA	60
30	AAAATGAAAA GAAAGGATTT AGCATGCAAA AATTCAAAGA CTTTTTTTAC GATGATTTAT	120
	CGGTTACACG AGGAAATTAT TTTTTAACTT TAATGGCAGC ATTTTTTATT ACTATCATTT	180
	TATTTATCGG CATAGTTGTC AGTGAAGTAC ATTTACTTTA TAGCATGCTA ATTGTATTAG	240
35	TAGGTTTAAT TCTATTGAGG CTATTCAAAA TCAATTTATT CTCTTTTAAA AAATTAACAT	300
	TGTCTCAAGT TATTTATATT ATAGGCGGTG CACTATTAAT TTATGGGTTA GATAATCTTT	360
40	ATTTATATTT TCATGACGTA CCGGCAATGA ACAACAATTA GAGCAAGCAA TACGGAAATA	420
40	CACCATTCTA TATTTCTATT TECACTGTAC CATCATCCCC GCTATTGTGG aAGAAATTGT	480
	TTTLCGCGGT ATGATAATAA GGGKTATCTT CAGAAAACAC TTGTTTTTAG GGTTAATTGT	540
45	GTCTAGTTTA GTTT	554
	(2) INFORMATION FOR SEQ ID NO: 1547:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

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	TAAAGCAACA CTTTTAATCC CTTTTGAACT TAGTTTATCC GCTAAATCAT AAGCTTCTTT	60
	TTTGCTACTT ACAAAAATCA ATCCTTGTAA AATTTCACCT GAATATCCAT AGTAATCTGT	120
5	CTTTTGAATA ATATAATTAA CTCTTTCATC AGAAGTTAAA TATCTCAGTT TAGTTACATC	180
	ATCTTCTTTA ATACCTTGAT GTACATAATC AGTCACACCA AAATAATGAA ATGGGACATA	240
10	AAATATCACT TTCTAATGCT GCTTGTAACC TTATTTCATA TGCAATATTA TAATCAAACA	300
	GTTCAAATAT ACTTAATTCA TCTGGATCTT TCTGGTGGTA GGCAGGTCAT TCCCAGCAnG	360
	AACTTAGGGT TTGGAGGTAG GTTAAAATAC TCGGTTGGAT	400
15	(2) INFORMATION FOR SEQ ID NO: 1548:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	٠
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1548:	
25	CGCTCTAGAA CTAGTGGATC CCCCGGGCTG CAGGAATTCG GCACAGCATA TCTAGTATTT	60
	TAGGACGGAG GGA	73
	(2) INFORMATION FOR SEQ ID NO: 1549:	,,
30		
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1549:	
40	GTATCCAAGC AGCTTTTAAA CAATATGGCA TAAACATTAT TAACGGCTAT GGTTTAACTG	60
٠	ATGGCACCTC TTG	73
45	(2) INFORMATION FOR SEQ ID NO: 1550:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1550:	

	GTAACATGTA TAGTGAAGTG ACTACTAAGA AGNCGTATTG TGATATTGAT AGCAGCTGAT	120
_	(2) INFORMATION FOR SEQ ID NO: 1551:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 192 base pairs (B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1551:	
15	GGTATGTATT AATTAAAATG TGGTCATGAT TGAAACAGCA ATGTAAAAAT AGCACAACAT	60
	AATTMATAAA GGAGAGAAAC GGCATGCATG AACAAGATTT TAGAATTTTA GAGGGTCAAG	120
	ATATTACTTT GCCAGAATTA GGTAGAGAAT TAGANAATAT TACAGGACAT ACGATTGCTG	180
20	ATTCTACTGG CG	192
	(2) INFORMATION FOR SEQ ID NO: 1552:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 76 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	à.
30	(5) 200 200 200 200 200 200 200 200 200 20	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1552:	
	CTAAGTTAGA TGCTAGTATA CAAGATTTAC AACAAAAGGT ACTGGAATCG AATTGTGAAC	60
35	TAGACAAACT AAACTC	76
	(2) INFORMATION FOR SEQ ID NO: 1553:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 135 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1553:	
	TGTGTTGGGG CCCCGTATAT TGAAAATTTG TTATAGGTGT ATTTCTTTGG TTAACTATTG	60
50	TTATATAACT TGTAGTTTTA GGATGTTGAT TTTGCTTACC TTGTCTGCTA TGTAATGTCA	120
	CATCAACATG ATTnA	135
55	(2) INFORMATION FOR SEQ ID NO: 1554:	

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•	(A) LENGTH: 104 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	(D) TOPOLOGY: Timear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1554:	
10	TTTGANATCA AATTCACTTC GCAAACGTGT CCAAGCGTGA GCAAAGGGCT AGATGATTAA	60
	TAGTTGCCCC ACTAACGGGA TCGCCCCAGT TATCCAACTT ATCT	104
	(2) INFORMATION FOR SEQ ID NO: 1555:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 100 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1555:	
25	AATAAGAAAC AnGACACTAG CTCACCACGA CGCGCACGGC CTGCGTGTAA AAATGTTGGT	. 60
	GGCGCGGGTT GGAGATCGTG TTCAACCAGA GCAGAAAATA	100
	(2) INFORMATION FOR SEQ ID NO: 1556:	
<i>30</i>	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 86 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEOUENCE DESCRIPTION: SEO ID NO: 1556:	
	CAATGAAATT ATTTATTATT TTAAGTGCAT TAAACCCCGA TGATGGCTGT CCGGTACCAG	60
40	GTGCATTTTG GTGCCCATGG TTTACC	86
	(2) INFORMATION FOR SEQ ID NO: 1557:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 78 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1557:	
	GTCATGTTCC CATCAAAACT AATTTGTACT TACTAAAGGC TCAGCAGCGC AACAATTAGG	60

	(2) INFORMATION FOR SEQ ID NO: 1558:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 82 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1558:	
	AACTGGTTAC AGAAATACCA CGTTCTTGTT TCAACTTTCA TCCAGTCACT TGATCGCAAA	60
15	TTTACCAGTC TTCTTCCCTT TA	82
	(2) INFORMATION FOR SEQ ID NO: 1559:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 78 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1559:	
	CCACAGCGGC ACTATAGCCA GCCCCTAATA TATACAGTAT TTGCATCTGA CTCATTGGTT	60
30	CATAAGTATA TGCAGTGA	78
	(2) INFORMATION FOR SEQ ID NO: 1560:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 76 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1560:	
	ACCATTIGCT AACTITITAG CAGCGCAATG TICTTATTAA CIGCITACGC CATCTATAAA	60
	AATAAACGTT CAACAA	76
45	(2) INFORMATION FOR SEQ ID NO: 1561:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 200 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

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	TTGGAACCCA AATTTTTTTA ATTTTCCCAA AAATTGGGGG GGGACCCCCA ATTCCCTTAA	60
_	GGGTTTTCCT TGGGGGCCGG GGGTTAATTC CACCCGGGGT TAAAATTTTC CCAAAAATTA	120
5	ATTTTNGAAA AGTTTTAATT TAAGGAAACC CATTNGTCCG GAATTTTTAC CCCATCCTTA	180
	TGGGGGGTCC CAAAGATTCC	200
10	(2) INFORMATION FOR SEQ ID NO: 1562:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1562:	
20	AACACAGAGA ATAACCAAGA GAAGACGTTT TCATCTGAAG AAAGTAACAG TAMGCCATTT	60
	ATGGAAGAAA ATCAAAACGA TGAGATAGTT ATAAAAGAAG ATTCATATAA TCCATTCGTA	120
	ACGAAAACAT CTGAAAGTTT AATAGCTGAT GATGAATCTT CTGGTTATAA TAATACACGT	180
25	GAAAAAGATG AAGACTACTT CAAAAAACAA CAAGAAATTT TACAAGAAAT GGATCAAACA	240
	TTTGATTCAA ATGATGGTAC AACTGTGCAA AATTATGAGA ATAAAGCGTC TGATGATTAT	300
30	TATGATGTAA ACGATATTAA AGGAACAAAA AGTAAAGACC CTAAACGAGG AATTCCATAT	360
	ATGGAATTGT TGGnCAGTCA TGGAACGTTA TTATTGCTCA	400
	(2) INFORMATION FOR SEQ ID NO: 1563:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 454 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1563:	
	TCTTCATCAT CTTCTAATTT ACCAGCTGGA ATTTCTAGCA ATGGTTTTC TACTGGTTTA	60
45	CGATACTGTT TCACTAATAC GACTTCTTTT TTAGGTGTCA CTGCACAAAC ArCAACTGCA	120
	CCATTATGAT AAACTAATTC TCTTGTTGAC GTTTCACCGT TTGGTAATGT CACTGTATGA	180
50	ATTTCTACAT CTACAATTTT GCCATTATAA ATAACTGTTC GATCAATTGT TTTTTCATTT	240
	AAATCCATTA TAATCACGTT CCTTTAAATT CATATTATAT ATTGATACAC TATGCTTGTT	300
	AGCTAAAGTG TATCGAAAGG AGAACAGACA TGCAAAAAAA TATATTAAAA AGTGGTATTT	360
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	AAATTATAGG ATTGTGCTGT TGAAAATGGG TATC	454
5	(2) INFORMATION FOR SEQ ID NO: 1564:	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 69 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1564:	
15	ACATCTCGCA TCGTCACGAC TTGCTTGAAC CACTAGCAGG TCAAACAAAG CTGTACAGGC	60
	AACATCTGC	69
	(2) INFORMATION FOR SEQ ID NO: 1565:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1565:	
30	TCCAGAACCA TTTTAAATCC CGGGAAATAT AATTACCTCC ACTAANGTAA TATATCCAAG	60
	CCAAGACTAA TCCTCCTTAA GCCGGTTTAA GTAACCAGGT TGAGAAGGAT TTTTTGG	117
	(2) INFORMATION FOR SEQ ID NO: 1566:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 103 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1566:	
	TATTGAGATT AACAGTCTGG GAAAAATGAA CAGCAATTGT nTAATGTGAC GATGCTGATT	60
45	ACTITITAAC AGTATCATIT AATAACTCAG AGATGCGCTT TAT	103
	(2) INFORMATION FOR SEQ ID NO: 1567:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 81 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1567:	
	AATGGATGGG ACAGCAATTA GTGCATAACG ACAATATATG CTCAATTTGT CGGCAACTGG	60
5	TTAAGAATCG TATTGTCACA A	81
	(2) INFORMATION FOR SEQ ID NO: 1568:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 80 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1568:	
	AATGGATTCA GTAGGTATTG GTGAAGCGCC AGACGCAGCT GATTTGAAAG ATGAAGGTTC	60
20	ACATACTTTT AGCATACCTT	80
	(2) INFORMATION FOR SEQ ID NO: 1569:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 95 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1569:	
	TTTTTAAATA CGATTTTAAG GAGGCCATTA TAATGGCGAG TAAAAGTAGC GAATTAATGG	60
35	TTTTGGTTAG GAATTGGTCG TTTAGGCATT CAGGA	95
	(2) INFORMATION FOR SEQ ID NO: 1570:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1570:	
	CCCAATAAAA AAAGCCTGTT GTCACAATGG TCATAGACAC GTACATACTT TAAAGGTTTC	60
50	TGTAATATAA ATATTTCATA TGCCACTTTA AAGTTGGNAC GTTCGTATGT TGTACTAA	118
	(2) INFORMATION FOR SEQ ID NO: 1571:	
<i>55</i>	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 base pairs	

(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1571:	
	GACTTGATCA ATGAAGCATT GTGTGACAAT TGGTCTGTTT GCACACCGCA CGGATTGnGC	60
10	GTCATTTATT TGTACTAATT CAAAAAACAT TGTTGTTTTC CTAG	104
	(2) INFORMATION FOR SEQ ID NO: 1572:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1572:	
	CCGAACTGTA ATGGTCCTAA TGTTTTACTC ATACCATATT GCGTAACCAT TGAGCGGCGA	60
25	TTGTGTTGCA CGTCGAGCAT TGAGACCGTT GTACTCGTAA nGTATATCTC TGTACACG	118
	(2) INFORMATION FOR SEQ ID NO: 1573:	•
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 74 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	·
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1573:	.5"
	AGGGATCAAA GGTCCATCCC CCATGCATTG GATAGTGGGG GATGACTTTT GATCCTATGT	60
	TCCAGTTGCT TATT	74
40	(2) INFORMATION FOR SEQ ID NO: 1574:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 341 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1574:	
	AACCTTTTGA GTAAATTCAC CAATACTCAT CCCCTTATCA TTTAACAAAC TTTTATTAAT	60
	GTTTTTGGTT ATATTATGAG TCTTTACTGC TTTTAGATTG TAAAAATTAT CGTCATAAAT	120

	GTAATTAATG TAATAATAGA AAAGTGTATA TATCTCATAT CGCCACCTGC TATACAACTT	240
	ATTAAATAAT TAATTCCAAG ACATATTAAT TATCTAATTA TAACCTTAGT THACGTTATT	300
5	ACATAATATA AAAATATATA ATAACTTATC CnCCGGCnCC T	341
	(2) INFORMATION FOR SEQ ID NO: 1575:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 109 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1575:	
	ACGTGTACCA ACTTTTGGGC ACCATTGATA ATANGTGTCA TAGGGTGACT CAGCATAACG	60
20	GGCAAGCCTA TTAATGATAG CCAGATTAAG ACATACAGTA CATATGTTC	109
	(2) INFORMATION FOR SEQ ID NO: 1576:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 79 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1576:	
	GCTAGATTGC GGGAATTAAC AATCATCAGC GATTTAATAT TTGCACTGGA GACGTCATGG	60
	TAATAAAAA TTGATGAGA	79
35	(2) INFORMATION FOR SEQ ID NO: 1577:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 69 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1577:	
	ATGATGGCTA TCATGAGATT GAGATGATAA TGACAACAGT TGATTTGAAA TGATCGTGTA	60
	ACTTITCAT	69
50	(2) INFORMATION FOR SEQ ID NO: 1578:	
	(i) SEQUENCE CHARACTERISTICS:	